



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:31 PM UTC

PDB ID : 7LNV / pdb_00007lnv
Title : Apo Structure of Isopentenyl Phosphate Kinase from Candidatus
methanomethylophilus alvus
Authors : Thomas, L.M.; Singh, S.; Scull, E.M.; Bourne, C.R.
Deposited on : 2021-02-08
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 ⓘ 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

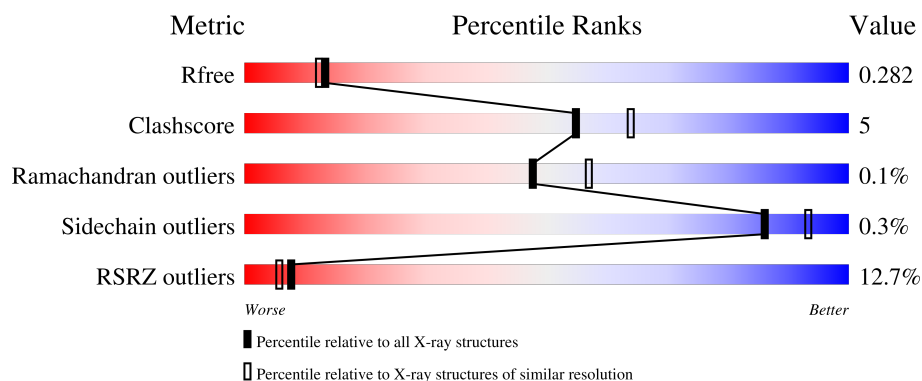
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (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 $\leq 5\%$. 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	279	12% 75% 8% 17%
1	B	279	9% 81% 11% 8%
1	C	279	12% 77% 12% 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5867 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 Isopentenyl phosphate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	0	1	0
			1780	1113	315	334	18			
1	B	256	Total	C	N	O	S	0	0	0
			1951	1217	345	370	19			
1	C	247	Total	C	N	O	S	0	0	0
			1885	1178	331	358	18			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP A0A3G3II74
A	-18	GLY	-	expression tag	UNP A0A3G3II74
A	-17	SER	-	expression tag	UNP A0A3G3II74
A	-16	SER	-	expression tag	UNP A0A3G3II74
A	-15	HIS	-	expression tag	UNP A0A3G3II74
A	-14	HIS	-	expression tag	UNP A0A3G3II74
A	-13	HIS	-	expression tag	UNP A0A3G3II74
A	-12	HIS	-	expression tag	UNP A0A3G3II74
A	-11	HIS	-	expression tag	UNP A0A3G3II74
A	-10	HIS	-	expression tag	UNP A0A3G3II74
A	-9	SER	-	expression tag	UNP A0A3G3II74
A	-8	SER	-	expression tag	UNP A0A3G3II74
A	-7	GLY	-	expression tag	UNP A0A3G3II74
A	-6	LEU	-	expression tag	UNP A0A3G3II74
A	-5	VAL	-	expression tag	UNP A0A3G3II74
A	-4	PRO	-	expression tag	UNP A0A3G3II74
A	-3	ARG	-	expression tag	UNP A0A3G3II74
A	-2	GLY	-	expression tag	UNP A0A3G3II74
A	-1	SER	-	expression tag	UNP A0A3G3II74
A	0	HIS	-	expression tag	UNP A0A3G3II74
B	-19	MET	-	initiating methionine	UNP A0A3G3II74
B	-18	GLY	-	expression tag	UNP A0A3G3II74
B	-17	SER	-	expression tag	UNP A0A3G3II74

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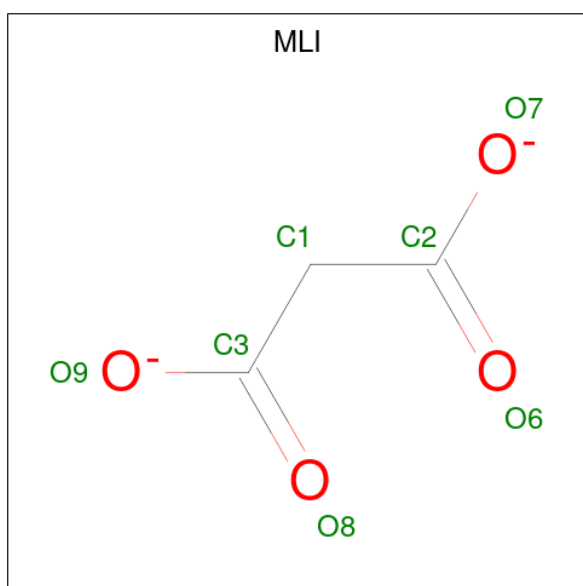
Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	SER	-	expression tag	UNP A0A3G3II74
B	-15	HIS	-	expression tag	UNP A0A3G3II74
B	-14	HIS	-	expression tag	UNP A0A3G3II74
B	-13	HIS	-	expression tag	UNP A0A3G3II74
B	-12	HIS	-	expression tag	UNP A0A3G3II74
B	-11	HIS	-	expression tag	UNP A0A3G3II74
B	-10	HIS	-	expression tag	UNP A0A3G3II74
B	-9	SER	-	expression tag	UNP A0A3G3II74
B	-8	SER	-	expression tag	UNP A0A3G3II74
B	-7	GLY	-	expression tag	UNP A0A3G3II74
B	-6	LEU	-	expression tag	UNP A0A3G3II74
B	-5	VAL	-	expression tag	UNP A0A3G3II74
B	-4	PRO	-	expression tag	UNP A0A3G3II74
B	-3	ARG	-	expression tag	UNP A0A3G3II74
B	-2	GLY	-	expression tag	UNP A0A3G3II74
B	-1	SER	-	expression tag	UNP A0A3G3II74
B	0	HIS	-	expression tag	UNP A0A3G3II74
C	-19	MET	-	initiating methionine	UNP A0A3G3II74
C	-18	GLY	-	expression tag	UNP A0A3G3II74
C	-17	SER	-	expression tag	UNP A0A3G3II74
C	-16	SER	-	expression tag	UNP A0A3G3II74
C	-15	HIS	-	expression tag	UNP A0A3G3II74
C	-14	HIS	-	expression tag	UNP A0A3G3II74
C	-13	HIS	-	expression tag	UNP A0A3G3II74
C	-12	HIS	-	expression tag	UNP A0A3G3II74
C	-11	HIS	-	expression tag	UNP A0A3G3II74
C	-10	HIS	-	expression tag	UNP A0A3G3II74
C	-9	SER	-	expression tag	UNP A0A3G3II74
C	-8	SER	-	expression tag	UNP A0A3G3II74
C	-7	GLY	-	expression tag	UNP A0A3G3II74
C	-6	LEU	-	expression tag	UNP A0A3G3II74
C	-5	VAL	-	expression tag	UNP A0A3G3II74
C	-4	PRO	-	expression tag	UNP A0A3G3II74
C	-3	ARG	-	expression tag	UNP A0A3G3II74
C	-2	GLY	-	expression tag	UNP A0A3G3II74
C	-1	SER	-	expression tag	UNP A0A3G3II74
C	0	HIS	-	expression tag	UNP A0A3G3II74

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 3 is MALONATE ION (CCD ID: MLI) (formula: $C_3H_2O_4$).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	73	Total 73	O 73	0	0
4	B	112	Total 112	O 112	0	0
4	C	40	Total 40	O 40	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	194.39Å 45.63Å 113.87Å 90.00° 121.20° 90.00°	Depositor
Resolution (Å)	37.29 – 2.20 37.29 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.7 (37.29-2.20) 88.5 (37.29-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.228 , 0.281 0.227 , 0.282	Depositor DCC
R_{free} test set	2006 reflections (4.55%)	wwPDB-VP
Wilson B-factor (Å ²)	24.8	Xtriage
Anisotropy	0.530	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5867	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.14% 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

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	0.14	0/1804	0.32	0/2425
1	B	0.14	0/1976	0.31	0/2659
1	C	0.12	0/1908	0.28	0/2568
All	All	0.13	0/5688	0.30	0/7652

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	1780	0	1805	15	0
1	B	1951	0	1986	18	0
1	C	1885	0	1924	22	0
2	A	6	0	8	1	0
2	B	6	0	8	0	0
3	B	7	0	2	0	0
3	C	7	0	2	0	0
4	A	73	0	0	1	0
4	B	112	0	0	1	0
4	C	40	0	0	1	0
All	All	5867	0	5735	54	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 5.

All (54) 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:224:ASP:H	1:A:227:ARG:HB3	1.49	0.78
1:B:81:LEU:HA	1:B:84:MET:HE2	1.69	0.75
1:A:164:LYS:HZ3	1:A:164:LYS:HB2	1.54	0.71
1:C:165:VAL:HG23	1:C:227:ARG:HD2	1.79	0.63
1:B:63:VAL:H	1:B:67:GLN:HE22	1.46	0.63
1:C:81:LEU:HA	1:C:84:MET:HE2	1.82	0.62
1:C:11:ILE:HG13	1:C:12:THR:HG23	1.86	0.58
1:C:120:ILE:H	1:C:120:ILE:HD12	1.69	0.58
1:B:205:VAL:O	1:B:209:THR:OG1	2.21	0.57
1:B:64:ASP:H	1:B:67:GLN:NE2	2.02	0.57
1:B:108:GLU:OE1	1:B:141:LYS:NZ	2.35	0.57
1:C:16:GLU:HB2	1:C:19:LYS:HB2	1.86	0.55
1:C:191:VAL:HG22	1:C:216:MET:HE3	1.88	0.55
1:A:149:GLY:H	2:A:301:GOL:H32	1.71	0.55
1:C:245:LYS:NZ	4:C:404:HOH:O	2.40	0.54
1:A:191:VAL:HB	1:A:254:ALA:HA	1.89	0.54
1:B:97:VAL:HG21	1:C:75:MET:HE2	1.89	0.54
1:B:17:TYR:CD1	1:B:18:HIS:HB2	2.43	0.53
1:C:202:ASP:HB3	1:C:205:VAL:HG22	1.90	0.53
1:C:212:VAL:O	1:C:216:MET:HG3	2.10	0.52
1:A:11:ILE:HG13	1:A:12:THR:HG23	1.92	0.51
1:B:9:SER:HA	1:B:14:LYS:HE3	1.94	0.50
1:C:4:ILE:HD11	1:C:244:LEU:HD21	1.93	0.49
1:B:2:ILE:HG23	1:B:164:LYS:HB3	1.94	0.49
1:C:196:LEU:HD12	1:C:220:LEU:HD12	1.95	0.48
1:B:221:ARG:HG2	1:B:258:MET:HG3	1.95	0.48
1:C:196:LEU:HD22	1:C:213:HIS:CE1	2.48	0.48
1:A:161:ASP:OD2	1:A:227:ARG:NH2	2.45	0.48
1:A:35:SER:HA	1:A:245:LYS:HD3	1.95	0.47
1:B:245:LYS:NZ	4:B:411:HOH:O	2.46	0.47
1:B:162:PRO:O	1:B:227:ARG:HD3	2.15	0.46
1:B:107:MET:HE2	1:B:137:VAL:HB	1.97	0.46
1:C:23:GLU:CD	1:C:23:GLU:H	2.24	0.46
1:A:220:LEU:O	1:A:223:THR:OG1	2.34	0.45
1:A:17:TYR:HA	1:A:47:SER:HB2	1.98	0.45
1:A:110:GLY:O	1:A:151:GLN:NE2	2.49	0.45
1:B:107:MET:HE3	1:B:145:ALA:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:31:GLU:HB3	1:C:241:TYR:HB2	1.99	0.45
1:B:35:SER:HA	1:B:245:LYS:HD3	1.99	0.45
1:B:159:MET:HE2	1:B:159:MET:HB3	1.77	0.45
1:A:120:ILE:H	1:A:120:ILE:HD12	1.81	0.44
1:C:48:PHE:CD2	1:C:81:LEU:HB2	2.54	0.43
1:A:172:ASP:OD1	1:A:239:ARG:NH1	2.48	0.42
1:B:33:ARG:HD3	1:B:92:GLN:O	2.19	0.42
1:A:14:LYS:HB3	1:A:14:LYS:HE2	1.78	0.42
1:A:159:MET:HE2	1:A:159:MET:HB3	1.88	0.41
1:B:111:LYS:HB3	1:B:111:LYS:HE3	1.64	0.41
1:C:68:ILE:HB	1:C:69:PRO:HD3	2.02	0.41
1:C:208:VAL:O	1:C:209:THR:OG1	2.32	0.41
1:C:164:LYS:HE3	1:C:164:LYS:HB2	1.85	0.41
1:A:14:LYS:NZ	4:A:409:HOH:O	2.41	0.41
1:C:19:LYS:HA	1:C:19:LYS:HD3	1.90	0.41
1:C:169:SER:OG	1:C:170:ASP:N	2.52	0.41
1:C:71:ALA:O	1:C:75:MET:HG3	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	227/279 (81%)	219 (96%)	7 (3%)	1 (0%)	30	34
1	B	252/279 (90%)	244 (97%)	8 (3%)	0	100	100
1	C	243/279 (87%)	229 (94%)	14 (6%)	0	100	100
All	All	722/837 (86%)	692 (96%)	29 (4%)	1 (0%)	48	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	49	GLY

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	195/234 (83%)	195 (100%)	0	100	100
1	B	215/234 (92%)	213 (99%)	2 (1%)	70	84
1	C	208/234 (89%)	208 (100%)	0	100	100
All	All	618/702 (88%)	616 (100%)	2 (0%)	86	93

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	204	THR
1	B	214	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	18	HIS
1	B	67	GLN
1	B	151	GLN
1	C	151	GLN
1	C	213	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](#)

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](#)

4 ligands 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	MLI	B	301	-	6,6,6	1.31	0	7,7,7	1.06	0
3	MLI	C	301	-	6,6,6	1.36	0	7,7,7	1.04	0
2	GOL	B	302	-	5,5,5	0.99	0	5,5,5	1.02	0
2	GOL	A	301	-	5,5,5	0.98	0	5,5,5	0.94	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
3	MLI	B	301	-	-	2/4/4/4	-
3	MLI	C	301	-	-	4/4/4/4	-
2	GOL	B	302	-	-	0/4/4/4	-
2	GOL	A	301	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	301	MLI	C2-C1-C3-O8
3	B	301	MLI	C2-C1-C3-O9

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Mol	Chain	Res	Type	Atoms
3	C	301	MLI	C3-C1-C2-O6
3	C	301	MLI	C3-C1-C2-O7
3	C	301	MLI	C2-C1-C3-O8
3	C	301	MLI	C2-C1-C3-O9

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	GOL	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

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	232/279 (83%)	0.57	33 (14%) 6 4	16, 32, 74, 91	1 (0%)
1	B	256/279 (91%)	0.61	26 (10%) 12 9	17, 32, 60, 69	0
1	C	247/279 (88%)	1.17	34 (13%) 6 5	26, 43, 66, 87	0
All	All	735/837 (87%)	0.79	93 (12%) 8 6	16, 38, 67, 91	1 (0%)

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	210	GLY	5.3
1	C	49	GLY	5.2
1	B	206	ALA	4.9
1	B	200	LEU	4.8
1	C	208	VAL	4.6
1	B	17	TYR	4.5
1	B	205	VAL	4.4
1	B	203	ILE	4.3
1	A	255	LYS	4.3
1	C	207	ASP	4.2
1	A	226	ASN	4.1
1	A	174	LEU	4.0
1	C	209	THR	4.0
1	C	256	GLY	3.9
1	A	257	GLY	3.9
1	B	144	PHE	3.9
1	B	209	THR	3.8
1	C	206	ALA	3.7
1	C	18	HIS	3.7
1	B	-5	VAL	3.6
1	C	51	VAL	3.6
1	C	1	MET	3.6
1	C	196	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	228	ARG	3.5
1	A	218	ALA	3.5
1	A	214	SER	3.4
1	A	220	LEU	3.4
1	C	15	SER	3.4
1	A	256	GLY	3.4
1	B	50	HIS	3.4
1	A	191	VAL	3.3
1	A	176	THR	3.2
1	B	18	HIS	3.2
1	B	-3	ARG	3.2
1	C	17	TYR	3.2
1	C	176	THR	3.2
1	B	51	VAL	3.1
1	A	190	GLU	3.1
1	A	179	PRO	3.1
1	B	210	GLY	3.1
1	B	145	ALA	2.9
1	A	185	ALA	2.9
1	C	220	LEU	2.9
1	C	211	GLY	2.8
1	B	63	VAL	2.8
1	A	0	HIS	2.8
1	A	216	MET	2.7
1	A	177	ALA	2.7
1	C	50	HIS	2.7
1	B	110	GLY	2.7
1	C	241	TYR	2.6
1	A	217	GLU	2.6
1	C	16	GLU	2.6
1	A	215	LYS	2.6
1	A	221	ARG	2.5
1	A	225	ARG	2.5
1	C	186	ARG	2.5
1	C	222	MET	2.5
1	A	189	GLY	2.5
1	C	193	ARG	2.5
1	C	221	ARG	2.5
1	A	184	LYS	2.5
1	A	175	TYR	2.4
1	A	222	MET	2.4
1	A	224	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	188	ILE	2.4
1	B	52	ILE	2.4
1	A	254	ALA	2.3
1	C	199	ALA	2.3
1	B	113	ILE	2.3
1	C	63	VAL	2.3
1	B	207	ASP	2.3
1	B	68	ILE	2.3
1	C	14	LYS	2.3
1	B	15	SER	2.3
1	B	57	ALA	2.3
1	C	54	LYS	2.3
1	B	137	VAL	2.3
1	C	173	GLY	2.2
1	B	111	LYS	2.2
1	A	173	GLY	2.2
1	A	186	ARG	2.1
1	C	89	LEU	2.1
1	B	65	ASP	2.1
1	A	249	VAL	2.1
1	A	253	VAL	2.1
1	C	175	TYR	2.1
1	C	124	ALA	2.1
1	C	171	ILE	2.1
1	B	-2	GLY	2.1
1	A	178	ASP	2.0
1	C	52	ILE	2.0
1	C	194	LYS	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
2	GOL	B	302	6/6	0.82	0.15	39,40,41,42	0
2	GOL	A	301	6/6	0.85	0.12	29,32,36,37	0
3	MLI	C	301	7/7	0.91	0.10	31,33,38,41	0
3	MLI	B	301	7/7	0.92	0.11	29,30,32,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.