



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:07 AM UTC

PDB ID : 6ZHK / pdb_00006zhk
Title : Crystal structure of adenosylmethionine-8-amino-7-oxononanoate amino-transferase from *Methanocaldococcus jannaschii* DSM 2661
Authors : Boyko, K.M.; Nikolaeva, T.N.; Stekhanova, T.N.; Rakitina, T.V.; Bezsudnova, E.Y.; Popov, V.O.
Deposited on : 2020-06-23
Resolution : 1.80 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
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

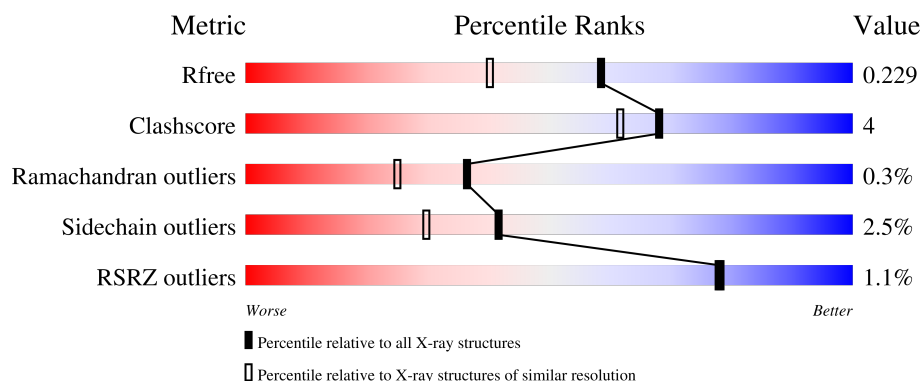
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

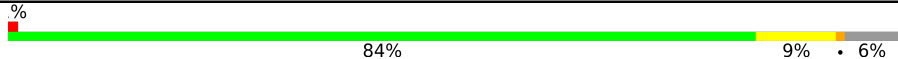
The reported resolution of this entry is 1.80 Å.

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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	466	
1	B	466	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7407 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 Adenosylmethionine-8-amino-7-oxononanoate aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	9	0
			3481	2250	561	650	20			
1	B	438	Total	C	N	O	S	0	4	0
			3477	2249	563	646	19			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q58696
A	2	HIS	-	expression tag	UNP Q58696
A	3	MET	-	variant	UNP Q58696
A	4	ASN	-	variant	UNP Q58696
A	5	LYS	-	variant	UNP Q58696
B	1	GLY	-	expression tag	UNP Q58696
B	2	HIS	-	expression tag	UNP Q58696
B	3	MET	-	variant	UNP Q58696
B	4	ASN	-	variant	UNP Q58696
B	5	LYS	-	variant	UNP Q58696

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	2	Total	Mg	0	0
			2	2		

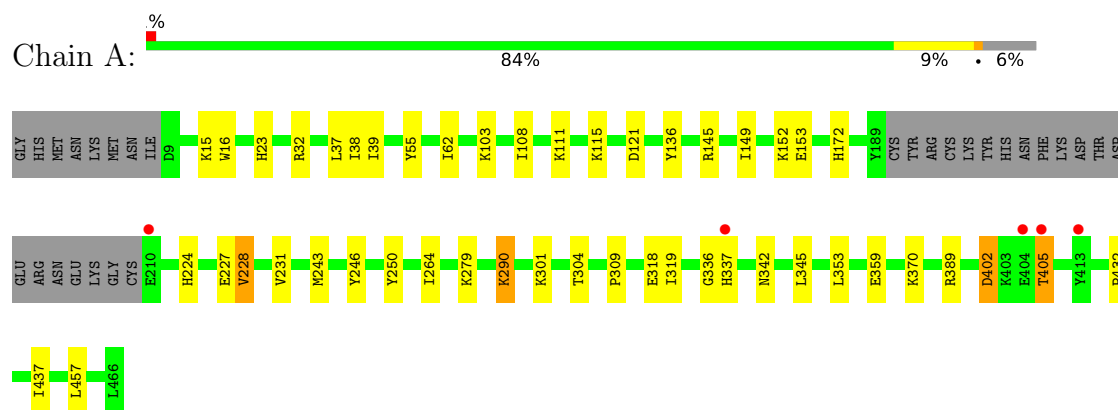
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	231	Total 231	O 231	0	0
3	B	215	Total 215	O 215	0	0

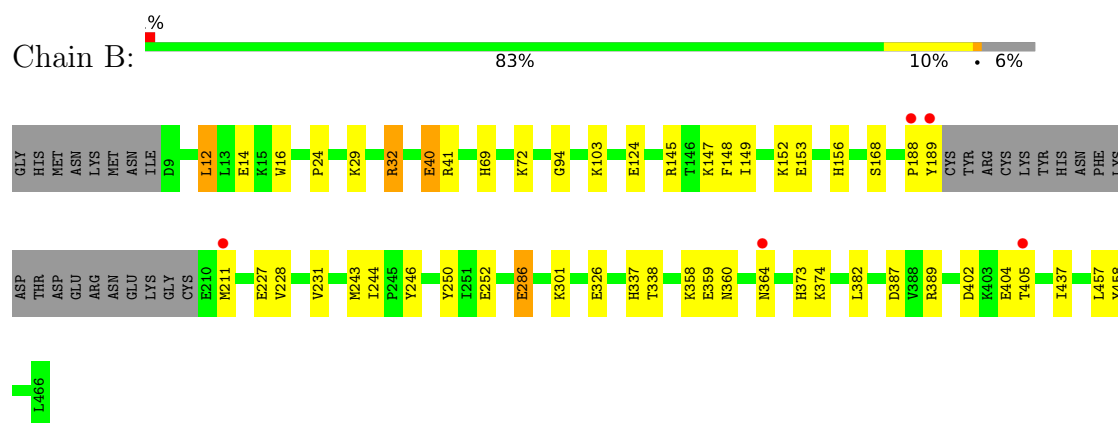
3 Residue-property plots

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: Adenosylmethionine-8-amino-7-oxononanoate aminotransferase



- Molecule 1: Adenosylmethionine-8-amino-7-oxononanoate aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	61.23Å 61.38Å 63.07Å 106.11° 93.48° 96.47°	Depositor
Resolution (Å)	60.56 – 1.80 60.56 – 1.80	Depositor EDS
% Data completeness (in resolution range)	88.5 (60.56-1.80) 88.5 (60.56-1.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.177 , 0.222 (Not available) , 0.229	Depositor DCC
R_{free} test set	3545 reflections (4.38%)	wwPDB-VP
Wilson B-factor (Å ²)	15.1	Xtriage
Anisotropy	0.944	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 36.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.019 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7407	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.36% 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: MG

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	0.78	1/3602 (0.0%)	1.19	8/4857 (0.2%)
1	B	0.81	4/3572 (0.1%)	1.19	10/4813 (0.2%)
All	All	0.80	5/7174 (0.1%)	1.19	18/9670 (0.2%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	337	HIS	CE1-NE2	8.57	1.41	1.32
1	A	23	HIS	CE1-NE2	6.41	1.39	1.32
1	B	156	HIS	CG-ND1	-5.59	1.32	1.38
1	B	69	HIS	CE1-NE2	5.47	1.38	1.32
1	B	373	HIS	CE1-NE2	5.22	1.37	1.32

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	243	MET	CA-C-N	-6.54	117.88	122.59
1	A	243	MET	C-N-CA	-6.54	117.88	122.59
1	B	338	THR	CA-CB-OG1	-6.37	100.04	109.60
1	B	243	MET	CA-C-N	-6.32	118.04	122.59
1	B	243	MET	C-N-CA	-6.32	118.04	122.59
1	A	318	GLU	CB-CG-CD	5.82	122.50	112.60
1	A	32	ARG	CG-CD-NE	-5.66	99.55	112.00
1	B	337	HIS	CA-CB-CG	-5.56	108.24	113.80
1	B	32	ARG	CB-CG-CD	-5.48	98.69	111.30
1	B	286	GLU	CB-CG-CD	5.47	121.90	112.60
1	B	211	MET	CA-C-N	5.35	128.19	120.38
1	B	211	MET	C-N-CA	5.35	128.19	120.38
1	A	304	THR	CA-CB-OG1	-5.13	101.91	109.60
1	B	252	GLU	CB-CG-CD	5.05	121.19	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	359	GLU	CB-CG-CD	5.05	121.18	112.60
1	B	40	GLU	CB-CG-CD	-5.02	104.07	112.60
1	A	172	HIS	CA-C-N	5.01	125.54	119.98
1	A	172	HIS	C-N-CA	5.01	125.54	119.98

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	3481	0	3455	31	0
1	B	3477	0	3484	30	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
3	A	231	0	0	2	0
3	B	215	0	0	2	0
All	All	7407	0	6939	50	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 4.

All (50) 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:402:ASP:HB3	1:A:405:THR:HG23	1.41	0.99
1:A:115[B]:LYS:HZ1	1:B:32:ARG:HH21	1.24	0.85
1:A:115[B]:LYS:NZ	1:B:32:ARG:NH2	2.34	0.76
1:A:115[B]:LYS:NZ	1:B:32:ARG:HH21	1.84	0.74
1:A:108:ILE:HG23	3:A:675:HOH:O	1.94	0.68
1:A:402:ASP:CB	1:A:405:THR:HG23	2.22	0.63
1:B:149:ILE:HB	1:B:231:VAL:HG22	1.81	0.62
1:A:115[B]:LYS:HZ3	1:B:32:ARG:NH2	1.99	0.60
1:A:121:ASP:OD2	1:B:124:GLU:OE2	2.20	0.60
1:A:290:LYS:O	1:A:290:LYS:HD3	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:ILE:HB	1:A:231:VAL:HG22	1.86	0.58
1:B:387:ASP:OD2	1:B:389:ARG:HD3	2.06	0.56
1:B:402:ASP:HB3	1:B:405:THR:OG1	2.09	0.53
1:A:16:TRP:CE2	1:B:103:LYS:HD2	2.45	0.52
1:A:37:LEU:HD11	1:A:55:TYR:CE2	2.46	0.51
1:B:246:TYR:HD2	1:B:250:TYR:CD1	2.30	0.50
1:A:108:ILE:HD13	1:A:353:LEU:HD22	1.94	0.49
1:A:136:TYR:CE1	1:A:319[A]:ILE:HD13	2.47	0.49
1:A:115[B]:LYS:HZ1	1:B:32:ARG:NH2	1.95	0.49
1:B:145:ARG:HD2	1:B:228:VAL:O	2.13	0.49
1:A:103:LYS:HE2	1:B:16:TRP:CZ2	2.48	0.48
1:A:38[A]:ILE:CD1	1:B:94:GLY:HA3	2.43	0.48
1:A:336:GLY:HA3	1:B:24:PRO:HB2	1.95	0.48
1:B:437:ILE:HD13	1:B:457:LEU:HD11	1.96	0.48
1:B:147:LYS:HD2	1:B:227:GLU:OE2	2.14	0.47
1:B:168:SER:HB3	3:B:783:HOH:O	2.15	0.46
1:A:37:LEU:HG	1:A:39:ILE:HD11	1.98	0.46
1:B:40:GLU:OE1	1:B:41:ARG:NH1	2.49	0.46
1:A:145:ARG:HD2	1:A:228:VAL:O	2.17	0.45
1:B:359:GLU:O	1:B:364:ASN:ND2	2.49	0.45
1:B:14[A]:GLU:HG2	3:B:775:HOH:O	2.16	0.45
1:B:402:ASP:OD1	1:B:404:GLU:HG2	2.17	0.45
1:A:264:ILE:HD11	1:A:319[A]:ILE:CD1	2.47	0.44
1:B:12:LEU:HD12	1:B:12:LEU:HA	1.85	0.43
1:A:38[A]:ILE:HD12	1:B:94:GLY:HA3	1.99	0.43
1:B:148:PHE:CD1	1:B:148:PHE:C	2.97	0.43
1:A:246:TYR:HD2	1:A:250:TYR:CD1	2.37	0.43
1:A:309:PRO:O	1:A:345:LEU:HD13	2.19	0.43
1:B:152:LYS:O	1:B:153:GLU:HB2	2.18	0.42
1:A:136:TYR:CD1	1:A:319[A]:ILE:HD13	2.55	0.42
1:B:188:PRO:HG2	1:B:246:TYR:CE2	2.55	0.42
1:A:437:ILE:HD13	1:A:457:LEU:HD11	2.02	0.41
1:A:290:LYS:HD3	1:A:290:LYS:C	2.45	0.41
1:B:382:LEU:HD21	1:B:458:TYR:CE2	2.56	0.41
1:A:224:HIS:O	1:A:227:GLU:HG2	2.21	0.41
1:A:279:LYS:HE3	3:A:804:HOH:O	2.19	0.41
1:B:189:TYR:CD2	1:B:244:ILE:HG21	2.56	0.40
1:A:152:LYS:O	1:A:153:GLU:HB2	2.21	0.40
1:A:342:ASN:HB3	1:A:345:LEU:HG	2.02	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	443/466 (95%)	429 (97%)	12 (3%)	2 (0%)	24	14
1	B	438/466 (94%)	426 (97%)	11 (2%)	1 (0%)	43	31
All	All	881/932 (94%)	855 (97%)	23 (3%)	3 (0%)	36	25

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	301	LYS
1	B	301	LYS
1	A	62	ILE

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	373/398 (94%)	362 (97%)	11 (3%)	37	25
1	B	371/398 (93%)	362 (98%)	9 (2%)	43	31
All	All	744/796 (94%)	724 (97%)	20 (3%)	42	27

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	LYS
1	A	111	LYS
1	A	228	VAL

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Mol	Chain	Res	Type
1	A	290	LYS
1	A	337[A]	HIS
1	A	337[B]	HIS
1	A	370	LYS
1	A	389	ARG
1	A	402	ASP
1	A	405	THR
1	A	432	PRO
1	B	12	LEU
1	B	29	LYS
1	B	72[A]	LYS
1	B	72[B]	LYS
1	B	286	GLU
1	B	326	GLU
1	B	358	LYS
1	B	360	ASN
1	B	374	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	186	ASN
1	A	322	GLN
1	B	80	ASN
1	B	135	GLN
1	B	322	GLN
1	B	384	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

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	438/466 (93%)	-0.18	5 (1%) 78 78	9, 19, 36, 76	9 (2%)
1	B	438/466 (93%)	-0.18	5 (1%) 78 78	12, 19, 39, 68	4 (0%)
All	All	876/932 (93%)	-0.18	10 (1%) 78 78	9, 19, 38, 76	13 (1%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	189	TYR	3.8
1	A	210	GLU	3.0
1	B	364	ASN	2.9
1	B	188	PRO	2.6
1	A	404	GLU	2.6
1	A	337[A]	HIS	2.6
1	A	413	TYR	2.4
1	B	211	MET	2.4
1	A	405	THR	2.4
1	B	405	THR	2.1

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
2	MG	B	502	1/1	0.97	0.06	35,35,35,35	0
2	MG	A	501	1/1	0.98	0.09	18,18,18,18	0
2	MG	B	501	1/1	0.99	0.06	17,17,17,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.