



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 08:55 AM GMT

PDB ID : 4C8O  
Title : Binary complex of the large fragment of DNA polymerase I from *Thermus Aquaticus* with the artificial base pair dNaM-d5SICS at the postinsertion site (sequence context 2)  
Authors : Betz, K.; Malyshev, D.A.; Lavergne, T.; Welte, W.; Diederichs, K.; Romesberg, F.E.; Marx, A.  
Deposited on : 2013-10-01  
Resolution : 1.75 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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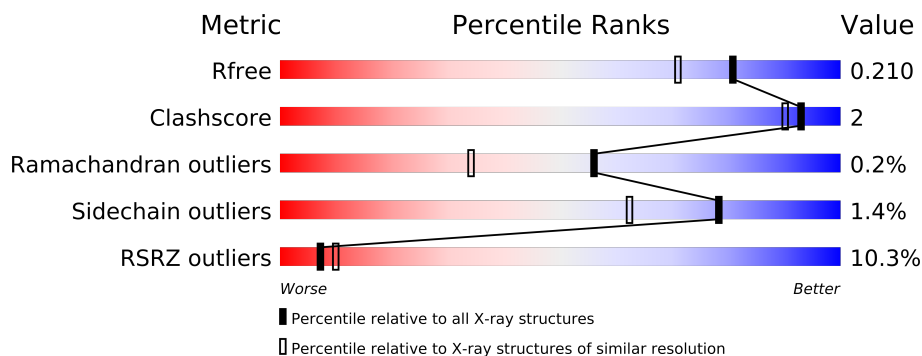
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 1.75 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))
$R_{free}$	66092	1134 (1.76-1.76)
Clashscore	79885	1304 (1.76-1.76)
Ramachandran outliers	78287	1288 (1.76-1.76)
Sidechain outliers	78261	1288 (1.76-1.76)
RSRZ outliers	66119	1135 (1.76-1.76)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	540	<div><div></div><div></div></div>
2	B	11	<div><div></div><div></div></div>
3	C	14	<div><div></div><div></div></div>

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	SO4	A	1833	-	X
4	SO4	A	1837	-	X
4	SO4	A	1838	-	X
4	SO4	A	1841	-	X
7	TRS	C	1216	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 9712 atoms, of which 4644 are hydrogens and 0 are deuterium.

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 DNA POLYMERASE I, THERMOSTABLE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	540	Total	C	H	N	O	S	0	5	0
			8680	2742	4365	772	788	13			

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

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
2	B	11	Total	C	H	N	O	P	S	0	0	0
			352	110	128	41	62	10	1			

- Molecule 3 is a DNA chain called 5'-D(\*TP\*TP\*CP\*BMNP\*GP\*CP\*GP\*CP\*CP\*GP\*TP\*GP\*GP\*CP)-3'.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	12	Total	C	H	N	O	P			
			387	121	139	42	73	12	0	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

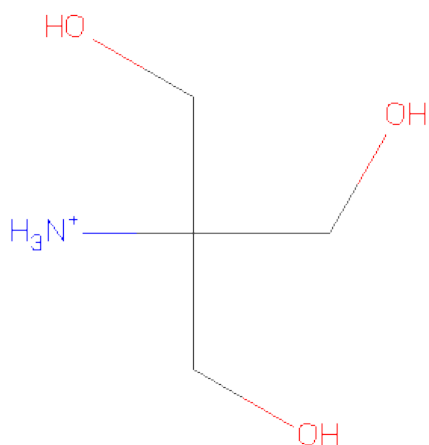
- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Cl	0	0
			1	1		

- Molecule 7 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula:  $C_4H_{12}NO_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	C	1	Total	C	H	N	O	0	0
			20	4	12	1	3		

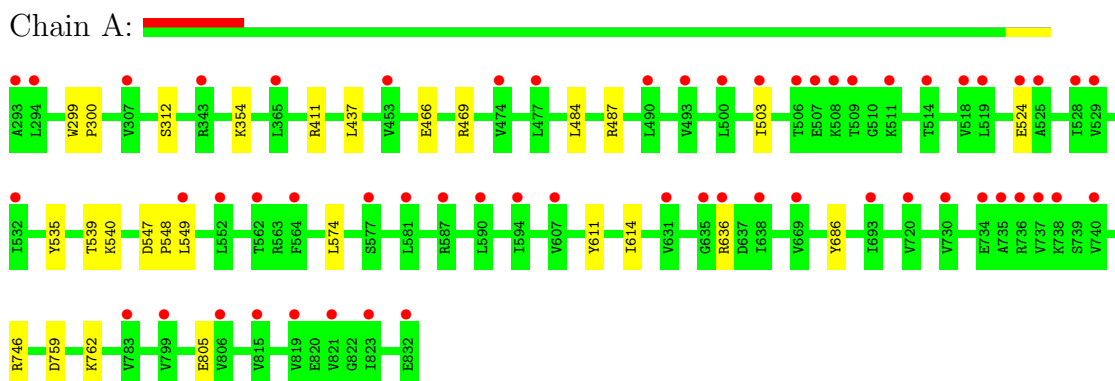
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	220	Total	O	0	0
			220	220		
8	B	10	Total	O	0	0
			10	10		
8	C	6	Total	O	0	0
			6	6		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: DNA POLYMERASE I, THERMOSTABLE



- Molecule 2: 5'-D(\*GP\*CP\*CP\*AP\*CP\*GP\*GP\*CP\*GP\*CP\*LHOP)-3'



- Molecule 3: 5'-D(\*TP\*TP\*CP\*BMNP\*GP\*CP\*GP\*CP\*CP\*GP\*TP\*GP\*GP\*CP)-3'



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.80Å 99.19Å 203.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.88 – 1.75 47.88 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.88-1.75) 99.6 (47.88-1.75)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.08 (at 1.75Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.185 , 0.212 0.186 , 0.210	Depositor DCC
$R_{free}$ test set	3301 reflections (4.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	35.5	Xtriage
Anisotropy	0.535	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 44.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 66201 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	9712	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CL, LHO, BMN, SO4, TRS

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	0.28	0/4420	0.48	0/5988
2	B	0.52	0/225	0.78	0/345
3	C	0.84	2/250 (0.8%)	1.15	4/381 (1.0%)
All	All	0.35	2/4895 (0.0%)	0.56	4/6714 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	210	DC	C4'-O4'	-7.07	1.38	1.45
3	C	210	DC	C2'-C1'	6.57	1.58	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	210	DC	O4'-C1'-C2'	9.70	113.66	105.90
3	C	210	DC	C3'-C2'-C1'	-9.04	91.65	102.50
3	C	210	DC	O4'-C4'-C3'	-5.75	102.20	104.50
3	C	210	DC	C4'-C3'-C2'	5.62	108.15	103.10

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4315	4365	0	14	0
2	B	224	128	0	1	0
3	C	248	139	0	1	0
4	A	35	0	0	1	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
7	C	8	12	0	0	0
8	A	220	0	0	5	0
8	B	10	0	0	0	0
8	C	6	0	0	0	0
All	All	5068	4644	0	16	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

All (16) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:759:ASP:OD2	8:A:2193:HOH:O	2.16	0.63
1:A:762:LYS:NZ	8:A:2067:HOH:O	2.35	0.58
1:A:686:TYR:OH	4:A:1839:SO4:O1	2.24	0.55
1:A:746:ARG:NE	8:A:2173:HOH:O	2.38	0.54
1:A:540:LYS:NZ	8:A:2113:HOH:O	2.41	0.52
3:C:204:DC:C6	3:C:205:BMN:H23	2.46	0.51
1:A:299:TRP:CG	1:A:300:PRO:HA	2.47	0.49
1:A:611:TYR:HB3	1:A:614:ILE:HB	1.95	0.47
1:A:549:LEU:N	8:A:2120:HOH:O	2.33	0.47
1:A:524:GLU:N	1:A:524:GLU:OE1	2.47	0.47
1:A:547:ASP:HB2	1:A:548:PRO:HD3	1.99	0.44
1:A:466:GLU:OE1	1:A:469:ARG:NH1	2.51	0.41
1:A:437:LEU:HD22	1:A:574:LEU:HD22	2.02	0.41
2:B:104:DC:H2'	2:B:105:DA:C8	2.55	0.41
1:A:535:TYR:CZ	1:A:539[A]:THR:HG22	2.56	0.41

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	543/540 (101%)	532 (98%)	10 (2%)	1 (0%)	56 34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	503	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	446/441 (101%)	440 (99%)	6 (1%)	80 65

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	354	LYS
1	A	411	ARG
1	A	484	LEU
1	A	487	ARG
1	A	636	ARG
1	A	805	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	613	GLN
1	A	627	ASN
1	A	754	GLN
1	A	782	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	$\# Z  > 2$
2	LHO	B	112	2	23,25,26	1.77	2 (8%)	31,36,39	0.90	2 (6%)
3	BMN	C	205	3	23,25,26	0.58	1 (4%)	32,35,38	0.88	2 (6%)

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	LHO	B	112	2	-	0/5/21/22	0/1/3/3
3	BMN	C	205	3	-	0/10/23/24	0/1/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	112	LHO	C5-N1	7.31	1.41	1.36
3	C	205	BMN	P-OP1	2.68	1.49	1.46
2	B	112	LHO	P-OP1	2.56	1.49	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	112	LHO	C9-C4-C5	-3.98	122.12	124.22
3	C	205	BMN	C2-C1-C6	2.91	121.94	117.04
3	C	205	BMN	C4'-O4'-C1'	-2.56	105.28	109.27
2	B	112	LHO	C5-N1-C1'	-2.26	117.75	120.82

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	SO4	A	1833	-	4,4,4	0.21	0	6,6,6	0.08	0
4	SO4	A	1834	-	4,4,4	0.25	0	6,6,6	0.09	0
4	SO4	A	1837	-	4,4,4	0.20	0	6,6,6	0.07	0
4	SO4	A	1838	-	4,4,4	0.22	0	6,6,6	0.06	0
4	SO4	A	1839	-	4,4,4	0.21	0	6,6,6	0.10	0
4	SO4	A	1840	-	4,4,4	0.19	0	6,6,6	0.08	0
4	SO4	A	1841	-	4,4,4	0.20	0	6,6,6	0.07	0
7	TRS	C	1216	-	7,7,7	1.04	1 (14%)	9,9,9	0.51	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
4	SO4	A	1833	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1834	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1837	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1838	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1839	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1840	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1841	-	-	0/0/0/0	0/0/0/0
7	TRS	C	1216	-	-	0/9/9/9	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	C	1216	TRS	C-N	-2.70	1.46	1.50

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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 ⓘ

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	540/540 (100%)	0.67	57 (10%) 7 9	33, 47, 83, 131	0
2	B	10/11 (90%)	0.12	0 100 100	51, 57, 67, 71	0
3	C	12/14 (85%)	0.61	1 (8%) 11 16	44, 61, 129, 132	0
All	All	562/565 (99%)	0.66	58 (10%) 7 10	33, 48, 84, 132	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	740	VAL	8.0
1	A	737	VAL	6.9
1	A	529	VAL	6.2
1	A	636	ARG	6.1
1	A	528	ILE	5.5
1	A	635	GLY	5.5
1	A	509	THR	5.4
1	A	519	LEU	5.2
1	A	736	ARG	5.1
1	A	493	VAL	4.9
1	A	474	VAL	4.8
1	A	525	ALA	4.8
1	A	293	ALA	4.6
1	A	343	ARG	4.5
3	C	205	BMN	4.5
1	A	735	ALA	4.3
1	A	738	LYS	4.2
1	A	734	GLU	4.2
1	A	532	ILE	4.2
1	A	631	VAL	4.2
1	A	821	VAL	4.2
1	A	806	VAL	4.1
1	A	503	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	730	VAL	3.6
1	A	477	LEU	3.5
1	A	799	VAL	3.4
1	A	507	GLU	3.3
1	A	518	VAL	3.3
1	A	587	ARG	3.3
1	A	506	THR	3.2
1	A	638	ILE	3.1
1	A	832	GLU	3.1
1	A	508	LYS	3.1
1	A	669	VAL	3.0
1	A	819	VAL	2.8
1	A	490	LEU	2.7
1	A	365	LEU	2.6
1	A	783	VAL	2.5
1	A	500	LEU	2.5
1	A	307	VAL	2.5
1	A	294	LEU	2.5
1	A	524	GLU	2.5
1	A	815	VAL	2.4
1	A	720	VAL	2.3
1	A	511	LYS	2.3
1	A	823	ILE	2.3
1	A	564	PHE	2.3
1	A	562	THR	2.2
1	A	581	LEU	2.2
1	A	549	LEU	2.2
1	A	577	SER	2.2
1	A	693	ILE	2.2
1	A	514	THR	2.2
1	A	453	VAL	2.1
1	A	607	VAL	2.1
1	A	594	ILE	2.1
1	A	552	LEU	2.0
1	A	590	LEU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	BMN	C	205	23/24	0.16	0.51	97,135,174,190	0
2	LHO	B	112	23/24	0.14	0.03	46,62,87,96	0

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	SO4	A	1833	5/5	0.43	22.68	112,112,112,116	5
7	TRS	C	1216	8/8	0.29	8.55	69,91,112,118	0
4	SO4	A	1841	5/5	0.13	5.76	79,81,97,107	5
4	SO4	A	1837	5/5	0.24	3.30	35,52,56,57	5
4	SO4	A	1838	5/5	0.16	3.19	90,90,100,100	5
4	SO4	A	1839	5/5	0.14	0.97	61,64,69,71	5
4	SO4	A	1840	5/5	0.12	0.76	73,82,95,97	5
4	SO4	A	1834	5/5	0.14	-0.06	58,59,65,68	5
6	CL	A	1836	1/1	0.12	-0.85	74,74,74,74	0
5	MG	A	1835	1/1	0.08	-1.33	66,66,66,66	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.