



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 01:39 pm GMT

PDB ID : 4B1H  
Title : Structure of human PARG catalytic domain in complex with ADP-ribose  
Authors : Brassington, C.; Ellston, J.; Hassall, G.; Holdgate, G.; Mcalister, M.; Smith, G.; Tucker, J.A.; Watson, M.  
Deposited on : 2012-07-10  
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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

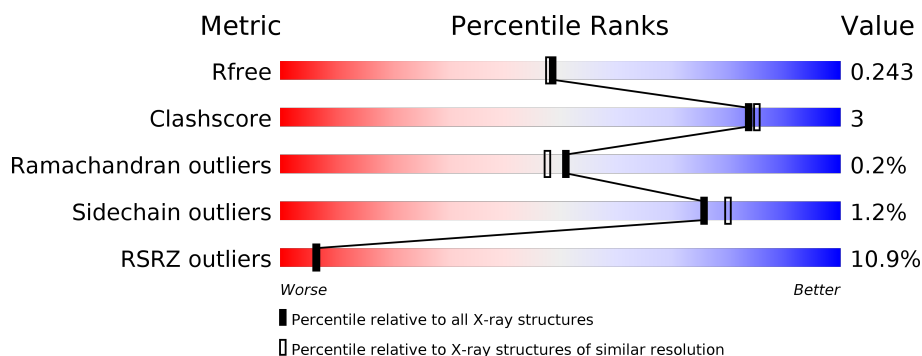
# 1 Overall quality at a glance

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))
$R_{free}$	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	531	

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
2	BME	A	1603	-	-	-	X
3	DTV	A	1711	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	A	1965	-	-	-	X
5	AR6	A	1967	-	-	-	X

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 4614 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.

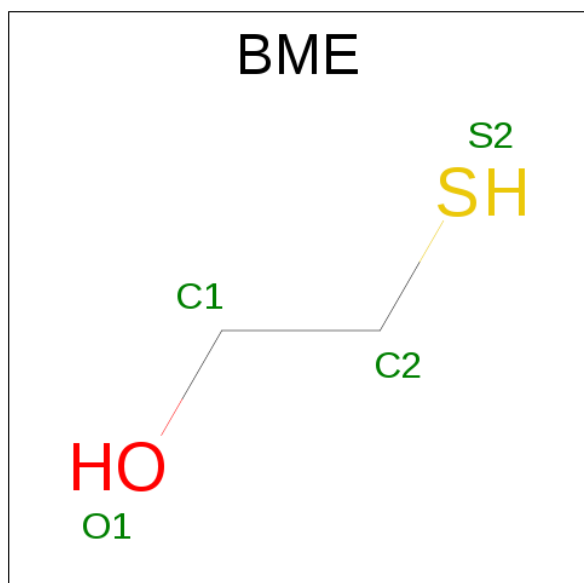
- Molecule 1 is a protein called POLY(ADP-RIBOSE) GLYCOHYDROLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	507	4155	2649	719	760	27	0	11	0

There are 8 discrepancies between the modelled and reference sequences:

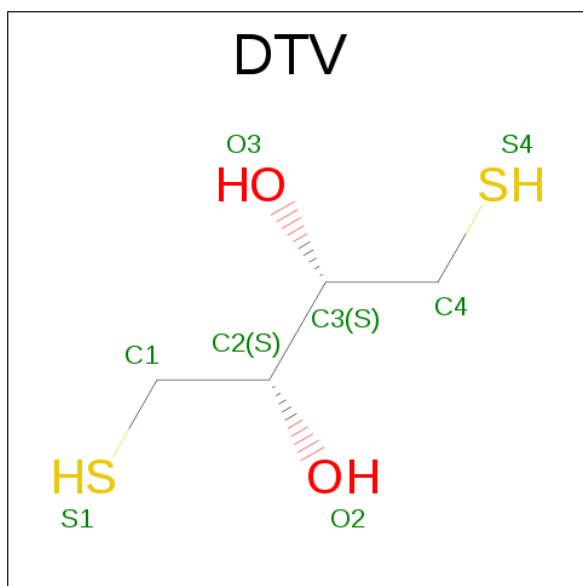
Chain	Residue	Modelled	Actual	Comment	Reference
A	446	GLY	-	EXPRESSION TAG	UNP Q86W56
A	447	SER	-	EXPRESSION TAG	UNP Q86W56
A	616	ALA	LYS	ENGINEERED MUTATION	UNP Q86W56
A	617	ALA	GLN	ENGINEERED MUTATION	UNP Q86W56
A	618	ALA	LYS	ENGINEERED MUTATION	UNP Q86W56
A	688	ALA	GLU	ENGINEERED MUTATION	UNP Q86W56
A	689	ALA	LYS	ENGINEERED MUTATION	UNP Q86W56
A	690	ALA	LYS	ENGINEERED MUTATION	UNP Q86W56

- Molecule 2 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C<sub>2</sub>H<sub>6</sub>OS).



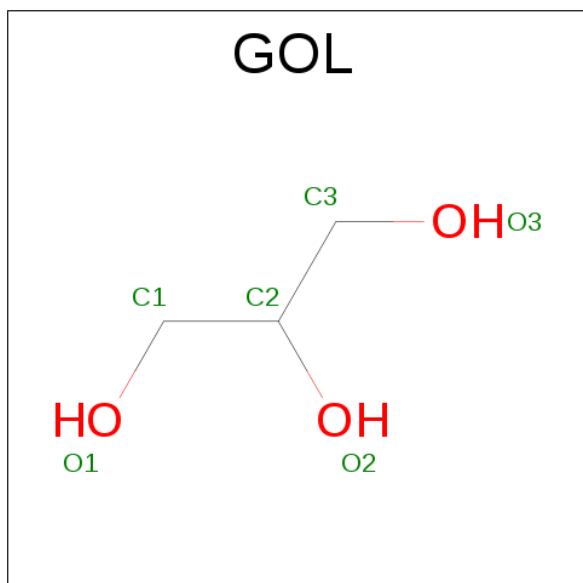
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 3 is (2S,3S)-1,4-DIMERCAPTOBUTANE-2,3-DIOL (three-letter code: DTV) (formula:  $C_4H_{10}O_2S_2$ ).



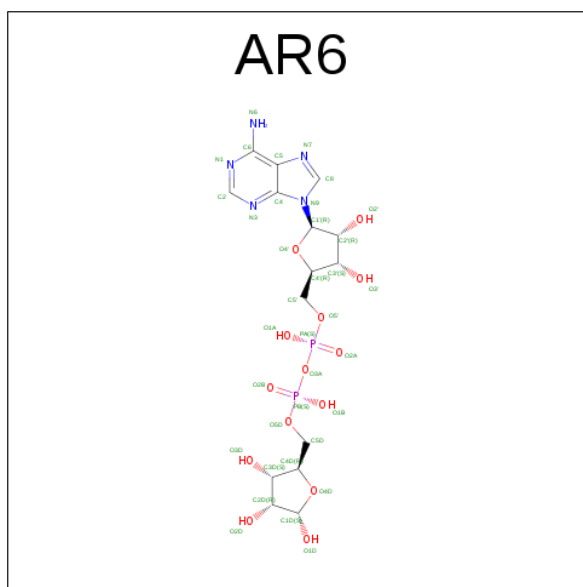
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			8	4	2	2		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



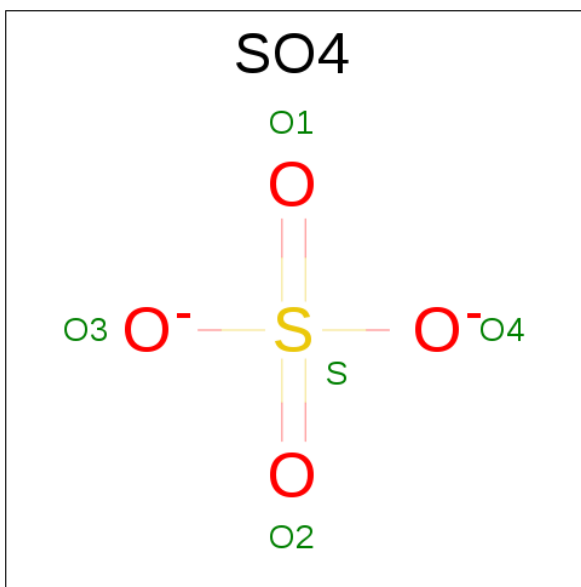
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is [(2R,3S,4R,5R)-5-(6-AMINOPURIN-9-YL)-3,4-DIHYDROXY-OXOLAN-2-YL]METHYL [HYDROXY-[(2R,3S,4R,5S)-3,4,5-TRIHYDROXYOXOLAN-2-YL]METHOXY]PHOSPHORYL] HYDROGEN PHOSPHATE (three-letter code: AR6) (formula:  $C_{15}H_{23}N_5O_{14}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
5	A	1	Total	C	N			0	0
			11	6	5				

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



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

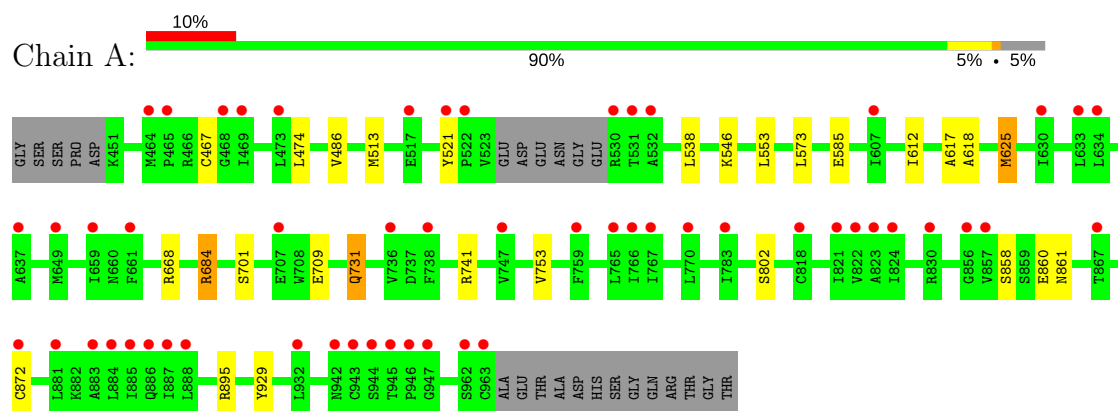
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	378	Total	O	0	0
			378	378		

### 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 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: POLY(ADP-RIBOSE) GLYCOHYDROLASE





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.93Å 90.66Å 94.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.35 – 2.00 27.29 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.6 (27.35-2.00) 98.6 (27.29-2.00)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.29 (at 1.99Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.204 , 0.241 0.207 , 0.243	Depositor DCC
$R_{free}$ test set	1961 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.4	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 38.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.53$ , $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4614	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.27% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical 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: GOL, CSO, AR6, BME, SO4, DTV

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	0.70	0/4242	0.71	2/5749 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	895	ARG	NE-CZ-NH2	-5.35	117.62	120.30
1	A	668	ARG	NE-CZ-NH2	-5.27	117.67	120.30

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	4155	0	4055	23	0
2	A	4	0	5	0	0
3	A	8	0	9	0	0
4	A	12	0	16	1	0
5	A	47	0	25	1	0
6	A	10	0	0	0	0
7	A	378	0	0	3	0
All	All	4614	0	4110	23	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 (23) 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:684[B]:ARG:O	1:A:684[B]:ARG:HD3	1.72	0.89
1:A:474:LEU:O	1:A:486[A]:VAL:HG11	1.84	0.78
1:A:872[B]:CYS:O	1:A:872[B]:CYS:SG	2.55	0.64
1:A:684[A]:ARG:HE	1:A:684[A]:ARG:HA	1.68	0.59
1:A:684[B]:ARG:C	1:A:684[B]:ARG:HD3	2.18	0.59
1:A:546:LYS:HA	7:A:2090:HOH:O	2.04	0.58
1:A:741:ARG:NH2	7:A:2270:HOH:O	2.31	0.57
1:A:513:MET:CE	1:A:612:ILE:HD12	2.34	0.56
1:A:684[A]:ARG:HE	1:A:684[A]:ARG:CA	2.20	0.54
1:A:929:TYR:OH	7:A:2333:HOH:O	2.11	0.51
1:A:513:MET:HE2	1:A:612:ILE:HD12	1.94	0.50
1:A:553:LEU:HD23	1:A:573:LEU:HD21	1.96	0.48
1:A:709:GLU:CD	1:A:709:GLU:H	2.17	0.47
1:A:858:SER:OG	1:A:860:GLU:OE1	2.31	0.47
1:A:731:GLN:H	1:A:731:GLN:HE21	1.61	0.47
1:A:513:MET:HE1	1:A:612:ILE:HD12	1.97	0.46
1:A:585:GLU:O	4:A:1965:GOL:O3	2.33	0.46
1:A:467[A]:CSO:O	1:A:861:ASN:HA	2.17	0.45
1:A:684[B]:ARG:C	1:A:684[B]:ARG:CD	2.85	0.44
1:A:625:MET:HB3	1:A:625:MET:HE3	1.91	0.43
1:A:486[B]:VAL:HG22	5:A:1967:AR6:N1	2.34	0.43
1:A:521:TYR:CZ	1:A:538:LEU:HD22	2.56	0.41
1:A:617:ALA:O	1:A:618:ALA:HB3	2.21	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	512/531 (96%)	501 (98%)	10 (2%)	1 (0%)	51	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	753	VAL

### 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	441/461 (96%)	435 (99%)	6 (1%)	71	76

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

Mol	Chain	Res	Type
1	A	625	MET
1	A	684[A]	ARG
1	A	684[B]	ARG
1	A	701	SER
1	A	731	GLN
1	A	802	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	731	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules 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
1	CSO	A	467[A]	1	4,6,7	2.11	1 (25%)	1,6,8	1.92	0
1	CSO	A	467[B]	1	5,5,7	1.53	1 (20%)	2,5,8	1.23	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
1	CSO	A	467[A]	1	-	0/1/5/7	0/0/0/0
1	CSO	A	467[B]	1	-	0/1/4/7	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	467[B]	CSO	CA-C	2.94	1.54	1.50
1	A	467[A]	CSO	CA-C	4.11	1.55	1.50

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	467[A]	CSO	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

8 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	$\# Z  > 2$
2	BME	A	1603	1	3,3,3	0.32	0	2,2,2	0.57	0
3	DTV	A	1711	1	7,7,7	0.38	0	4,8,8	1.26	0
4	GOL	A	1964	-	5,5,5	0.45	0	5,5,5	0.34	0
4	GOL	A	1965	-	5,5,5	0.45	0	5,5,5	0.37	0
5	AR6	A	1966	-	34,39,39	0.55	0	36,60,60	0.64	0
5	AR6	A	1967	-	10,12,39	0.88	1 (10%)	8,17,60	0.93	0
6	SO4	A	1968	-	4,4,4	0.26	0	6,6,6	0.83	0
6	SO4	A	1969	-	4,4,4	0.18	0	6,6,6	0.19	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
2	BME	A	1603	1	-	0/1/1/1	0/0/0/0
3	DTV	A	1711	1	-	0/8/8/8	0/0/0/0
4	GOL	A	1964	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1965	-	-	0/4/4/4	0/0/0/0
5	AR6	A	1966	-	-	0/18/54/54	0/4/4/4
5	AR6	A	1967	-	-	0/0/0/54	0/2/2/4
6	SO4	A	1968	-	-	0/0/0/0	0/0/0/0
6	SO4	A	1969	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1967	AR6	C2-N3	2.04	1.35	1.32

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1965	GOL	1	0
5	A	1967	AR6	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, 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	506/531 (95%)	0.62	55 (10%) 6 6	18, 28, 45, 65	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	963	CYS	6.9
1	A	944	SER	6.8
1	A	945	THR	6.0
1	A	884	LEU	5.4
1	A	649	MET	4.9
1	A	946	PRO	4.9
1	A	943	CYS	4.8
1	A	947	GLY	4.6
1	A	531	THR	4.1
1	A	767	ILE	4.0
1	A	856	GLY	3.8
1	A	634	LEU	3.7
1	A	521	TYR	3.7
1	A	522	PRO	3.6
1	A	469	ILE	3.6
1	A	887	ILE	3.5
1	A	473	LEU	3.4
1	A	885	ILE	3.4
1	A	824	ILE	3.2
1	A	962	SER	3.2
1	A	736	VAL	3.2
1	A	530	ARG	2.9
1	A	630	ILE	2.9
1	A	888	LEU	2.9
1	A	881	LEU	2.9
1	A	532	ALA	2.8
1	A	823	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	830	ARG	2.8
1	A	468	GLY	2.8
1	A	821	ILE	2.8
1	A	942	ASN	2.7
1	A	759	PHE	2.7
1	A	857	VAL	2.7
1	A	867	THR	2.7
1	A	766	ILE	2.6
1	A	765	LEU	2.6
1	A	517	GLU	2.6
1	A	637	ALA	2.6
1	A	464	MET	2.5
1	A	872[A]	CYS	2.5
1	A	932	LEU	2.5
1	A	465	PRO	2.4
1	A	661	PHE	2.3
1	A	707	GLU	2.3
1	A	747	VAL	2.3
1	A	886	GLN	2.3
1	A	659	ILE	2.2
1	A	783	ILE	2.2
1	A	883	ALA	2.2
1	A	607	ILE	2.2
1	A	738	PHE	2.2
1	A	770	LEU	2.1
1	A	822	VAL	2.1
1	A	818	CYS	2.1
1	A	633	LEU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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. 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	CSO	A	467[A]	7/8	0.68	0.29	-	37,43,44,45	7
1	CSO	A	467[B]	6/8	0.68	0.29	-	40,44,45,45	6

### 6.3 Carbohydrates [i](#)

There are no carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	AR6	A	1967	11/36	0.69	0.34	10.01	37,46,48,48	0
2	BME	A	1603	4/4	0.86	0.29	9.08	46,47,47,53	0
4	GOL	A	1965	6/6	0.72	0.24	5.61	48,50,51,52	0
3	DTV	A	1711	8/8	0.47	0.54	4.99	54,62,70,72	0
6	SO4	A	1968	5/5	0.94	0.15	-0.24	41,41,45,45	0
5	AR6	A	1966	36/36	0.92	0.13	-0.45	28,32,35,35	0
4	GOL	A	1964	6/6	0.69	0.34	-	72,72,72,72	0
6	SO4	A	1969	5/5	0.83	0.33	-	84,84,85,85	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.