



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 07:05 pm BST

PDB ID : 3G2D  
Title : Complex of Mth0212 and a 4 bp dsDNA with 3'-overhang  
Authors : Lakomek, K.; Dickmanns, A.; Ficner, R.  
Deposited on : 2009-01-31  
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

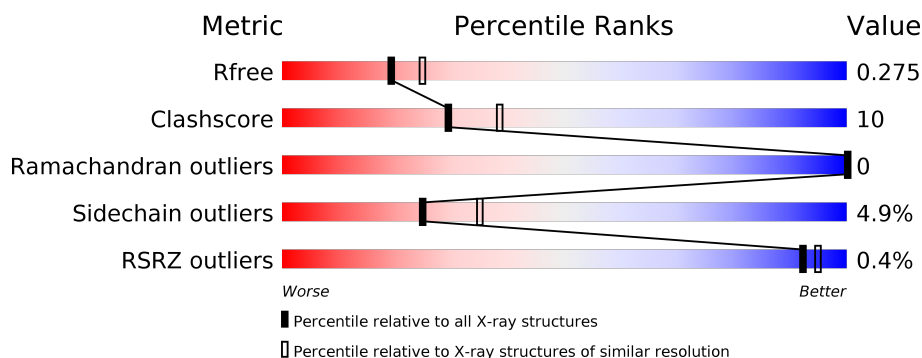
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 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	265	<div> <div>78%</div> <div>17%</div> <div>• •</div> </div>
1	B	265	<div> <div>80%</div> <div>15%</div> <div>• •</div> </div>
2	G	9	<div> <div>11%</div> <div>22%</div> <div>11%</div> <div>56%</div> </div>
2	H	9	<div> <div>11%</div> <div>22%</div> <div>11%</div> <div>56%</div> </div>
3	I	10	<div> <div>30%</div> <div>60%</div> <div>10%</div> </div>
3	K	10	<div> <div>30%</div> <div>30%</div> <div>20%</div> <div>20%</div> </div>

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	269	-	-	X	-
5	PG4	A	270	-	-	X	-

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 5190 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 Exodeoxyribonuclease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	256	Total	C	N	O	S	0	1	0
			2140	1374	375	383	8			
1	B	255	Total	C	N	O	S	0	0	0
			2127	1365	373	381	8			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	THR	ENGINEERED MUTATION	UNP O26314
A	151	ASN	ASP	ENGINEERED MUTATION	UNP O26314
A	258	LEU	-	EXPRESSION TAG	UNP O26314
A	259	GLU	-	EXPRESSION TAG	UNP O26314
A	260	HIS	-	EXPRESSION TAG	UNP O26314
A	261	HIS	-	EXPRESSION TAG	UNP O26314
A	262	HIS	-	EXPRESSION TAG	UNP O26314
A	263	HIS	-	EXPRESSION TAG	UNP O26314
A	264	HIS	-	EXPRESSION TAG	UNP O26314
A	265	HIS	-	EXPRESSION TAG	UNP O26314
B	2	ALA	THR	ENGINEERED MUTATION	UNP O26314
B	151	ASN	ASP	ENGINEERED MUTATION	UNP O26314
B	258	LEU	-	EXPRESSION TAG	UNP O26314
B	259	GLU	-	EXPRESSION TAG	UNP O26314
B	260	HIS	-	EXPRESSION TAG	UNP O26314
B	261	HIS	-	EXPRESSION TAG	UNP O26314
B	262	HIS	-	EXPRESSION TAG	UNP O26314
B	263	HIS	-	EXPRESSION TAG	UNP O26314
B	264	HIS	-	EXPRESSION TAG	UNP O26314
B	265	HIS	-	EXPRESSION TAG	UNP O26314

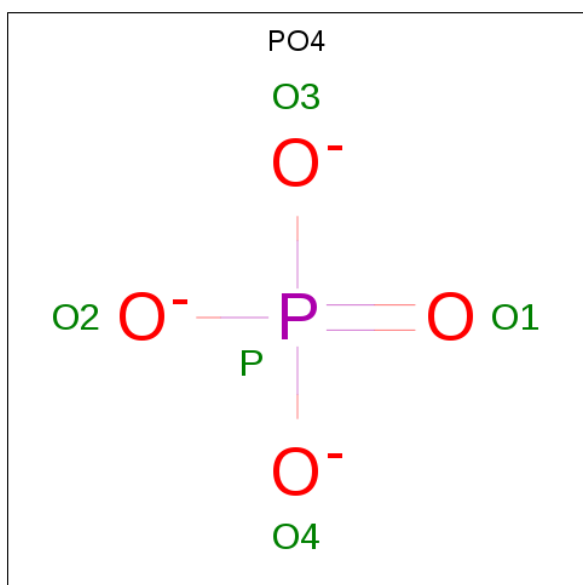
- Molecule 2 is a DNA chain called 5'-D(\*CP\*GP\*CP\*G\*CP\*AP\*GP\*GP\*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	4	Total	C	N	O	P	0	0	0
			81	39	18	21	3			
2	H	4	Total	C	N	O	P	0	0	0
			81	39	18	21	3			

- Molecule 3 is a DNA chain called 5'-D(\*CP\*CP\*TP\*GP\*UP\*GP\*CP\*GP\*AP\*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	K	8	Total	C	N	O	P	0	0	0
			159	76	28	48	7			
3	I	9	Total	C	N	O	P	0	0	0
			180	86	33	53	8			

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



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

- Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



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		
5	A	1	Total	C	O	0	0
			13	8	5		
5	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

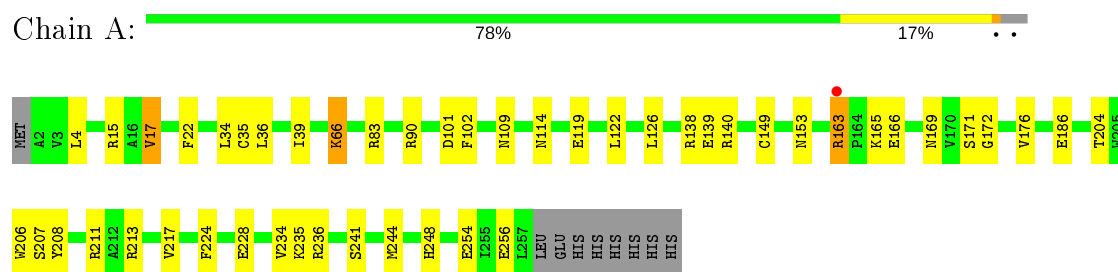
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	145	Total	O	0	0
			145	145		
7	B	141	Total	O	0	0
			141	141		
7	G	5	Total	O	0	0
			5	5		
7	K	9	Total	O	0	0
			9	9		
7	H	8	Total	O	0	0
			8	8		
7	I	5	Total	O	0	0
			5	5		

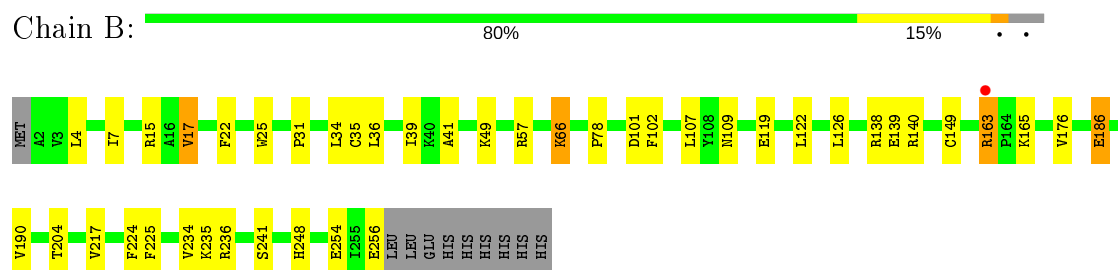
### 3 Residue-property plots [i](#)

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.

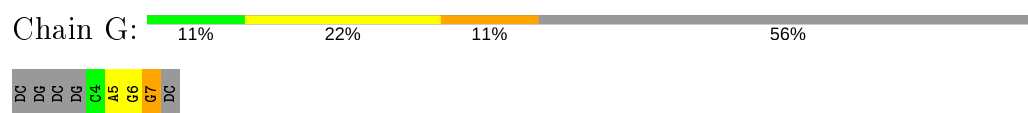
- Molecule 1: Exodeoxyribonuclease



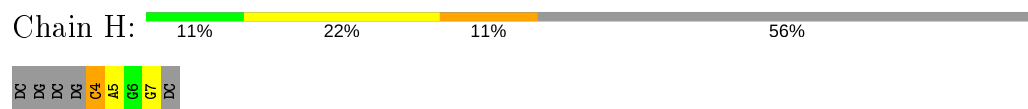
- Molecule 1: Exodeoxyribonuclease



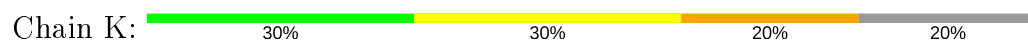
- Molecule 2: 5'-D(\*CP\*GP\*CP\*G\*CP\*AP\*GP\*GP\*C)-3'



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



- Molecule 3: 5'-D(\*CP\*CP\*TP\*GP\*UP\*GP\*CP\*GP\*AP\*T)-3'







● Molecule 3: 5'-D(\*CP\*CP\*TP\*GP\*UP\*GP\*CP\*GP\*AP\*T)-3'



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	44.60Å 81.30Å 97.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.55 – 2.30 48.55 – 2.30	Depositor EDS
% Data completeness (in resolution range)	93.5 (48.55-2.30) 93.4 (48.55-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.90 (at 2.29Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.214 , 0.279 0.210 , 0.275	Depositor DCC
$R_{free}$ test set	1470 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.6	Xtriage
Anisotropy	1.090	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 24.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.479 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5190	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.59% 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, PO4, 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	0.53	0/2201	0.66	1/2968 (0.0%)
1	B	0.54	0/2185	0.67	1/2946 (0.0%)
2	G	0.89	0/91	1.69	1/139 (0.7%)
2	H	1.00	0/91	2.11	5/139 (3.6%)
3	I	0.83	0/201	1.66	4/308 (1.3%)
3	K	0.97	0/177	1.76	4/271 (1.5%)
All	All	0.59	0/4946	0.88	16/6771 (0.2%)

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	7	DG	O4'-C1'-N9	10.51	115.36	108.00
3	I	6	DG	O4'-C4'-C3'	-9.39	100.37	106.00
2	H	7	DG	O4'-C1'-N9	8.51	113.96	108.00
3	K	2	DC	C1'-O4'-C4'	-7.90	102.20	110.10
3	I	6	DG	O4'-C1'-N9	7.31	113.12	108.00

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	2140	0	2082	48	0
1	B	2127	0	2065	33	0
2	G	81	0	46	2	0
2	H	81	0	46	2	0
3	I	180	0	101	4	0
3	K	159	0	90	4	0
4	A	15	0	0	0	0
5	A	39	0	54	20	0
5	B	13	0	18	2	0
6	A	30	0	40	2	0
6	B	6	0	8	0	0
6	K	6	0	8	0	0
7	A	145	0	0	5	0
7	B	141	0	0	5	0
7	G	5	0	0	0	0
7	H	8	0	0	0	0
7	I	5	0	0	0	0
7	K	9	0	0	0	0
All	All	5190	0	4558	90	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 10.

The worst 5 of 90 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:163:ARG:HG3	1:A:163:ARG:HH21	1.19	1.04
1:B:163:ARG:HH21	1:B:163:ARG:HG3	1.18	1.04
1:A:163:ARG:HH22	1:A:217:VAL:HG13	1.26	0.97
1:B:163:ARG:HH22	1:B:217:VAL:HG13	1.28	0.95
1:B:66:LYS:H	1:B:66:LYS:HD2	1.32	0.94

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	255/265 (96%)	248 (97%)	7 (3%)	0	100	100
1	B	253/265 (96%)	243 (96%)	10 (4%)	0	100	100
All	All	508/530 (96%)	491 (97%)	17 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	227/235 (97%)	216 (95%)	11 (5%)	25	36
1	B	225/235 (96%)	214 (95%)	11 (5%)	25	35
All	All	452/470 (96%)	430 (95%)	22 (5%)	25	35

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	234	VAL
1	B	34	LEU
1	B	234	VAL
1	A	235	LYS
1	B	17	VAL

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	114	ASN

### 5.3.3 RNA ⓘ

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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

14 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	$\# Z  > 2$
5	PG4	B	266	-	12,12,12	0.59	0	11,11,11	0.61	0
6	GOL	A	273	-	5,5,5	0.41	0	5,5,5	0.30	0
5	PG4	A	272	-	12,12,12	0.72	0	11,11,11	0.74	0
4	PO4	A	267	-	4,4,4	0.95	0	6,6,6	0.32	0
5	PG4	A	269	-	12,12,12	0.87	0	11,11,11	1.03	1 (9%)
6	GOL	A	271	-	5,5,5	0.58	0	5,5,5	0.63	0
6	GOL	A	276	-	5,5,5	0.40	0	5,5,5	0.20	0
6	GOL	A	275	-	5,5,5	0.34	0	5,5,5	0.26	0
6	GOL	K	11	-	5,5,5	0.30	0	5,5,5	0.42	0
5	PG4	A	270	-	12,12,12	0.90	0	11,11,11	0.86	0
4	PO4	A	268	-	4,4,4	0.80	0	6,6,6	0.67	0
6	GOL	B	267	-	5,5,5	0.40	0	5,5,5	0.37	0
6	GOL	A	274	-	5,5,5	0.37	0	5,5,5	0.18	0
4	PO4	A	266	-	4,4,4	0.91	0	6,6,6	0.49	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
5	PG4	B	266	-	-	6/10/10/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GOL	A	273	-	-	0/4/4/4	-
5	PG4	A	272	-	-	3/10/10/10	-
5	PG4	A	269	-	-	6/10/10/10	-
5	PG4	A	270	-	-	7/10/10/10	-
6	GOL	A	276	-	-	4/4/4/4	-
6	GOL	A	275	-	-	4/4/4/4	-
6	GOL	K	11	-	-	1/4/4/4	-
6	GOL	A	271	-	-	2/4/4/4	-
6	GOL	B	267	-	-	0/4/4/4	-
6	GOL	A	274	-	-	2/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	269	PG4	O4-C6-C5	2.06	119.70	110.39

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	271	GOL	C1-C2-C3-O3
6	A	276	GOL	O1-C1-C2-C3
6	A	276	GOL	C1-C2-C3-O3
6	A	275	GOL	O1-C1-C2-C3
6	A	275	GOL	C1-C2-C3-O3

There are no ring outliers.

6 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	266	PG4	2	0
6	A	273	GOL	1	0
5	A	272	PG4	1	0
5	A	269	PG4	7	0
6	A	275	GOL	1	0
5	A	270	PG4	12	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 [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, 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	256/265 (96%)	-0.22	1 (0%) 92 95	15, 24, 34, 41	0
1	B	255/265 (96%)	-0.28	1 (0%) 92 95	15, 23, 34, 39	0
2	G	4/9 (44%)	-0.26	0 100 100	29, 39, 56, 61	0
2	H	4/9 (44%)	-0.34	0 100 100	29, 38, 54, 65	0
3	I	8/10 (80%)	0.00	0 100 100	33, 35, 102, 112	0
3	K	7/10 (70%)	-0.08	0 100 100	32, 34, 80, 86	0
All	All	534/568 (94%)	-0.24	2 (0%) 92 95	15, 24, 35, 112	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	163	ARG	3.9
1	A	163	ARG	3.5

### 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 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
6	GOL	K	11	6/6	0.54	0.25	77,78,78,78	0
5	PG4	A	272	13/13	0.67	0.32	79,81,83,83	0
6	GOL	A	275	6/6	0.74	0.31	65,66,66,67	0
6	GOL	A	276	6/6	0.81	0.15	49,51,51,52	0
6	GOL	A	273	6/6	0.83	0.15	53,54,54,55	0
5	PG4	B	266	13/13	0.85	0.15	54,55,56,57	0
6	GOL	B	267	6/6	0.87	0.18	53,54,54,54	0
6	GOL	A	271	6/6	0.88	0.20	32,33,34,35	0
5	PG4	A	270	13/13	0.88	0.22	45,51,54,55	0
5	PG4	A	269	13/13	0.89	0.21	32,37,39,39	0
6	GOL	A	274	6/6	0.90	0.26	49,51,52,52	0
4	PO4	A	267	5/5	0.92	0.14	50,51,52,53	0
4	PO4	A	266	5/5	0.92	0.16	87,88,88,88	0
4	PO4	A	268	5/5	0.95	0.14	54,54,55,56	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.