



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 06:52 PM BST

PDB ID : 3VDC  
Title : E. coli (lacZ) beta-galactosidase (N460T) in complex with IPTG  
Authors : Wheatley, R.W.; Kappelhoff, J.C.; Hahn, J.N.; Dugdale, M.L.; Dutkoski, M.J.;  
Tamman, S.D.; Fraser, M.E.; Huber, R.E.  
Deposited on : 2012-01-04  
Resolution : 2.55 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

<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 : 2.13.1  
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) : 2.13.1

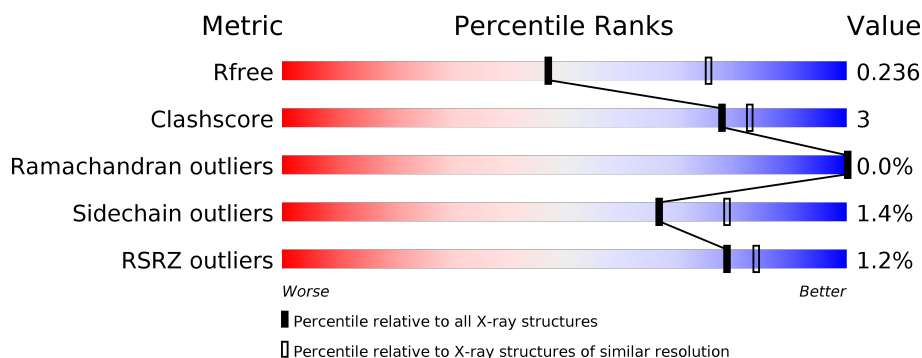
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	1052	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 89%, green 89%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>89%</span> <span>8%</span> </div> </div>
1	B	1052	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 89%, green 89%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>89%</span> <span>7%</span> </div> </div>
1	C	1052	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 87%, green 87%, grey 10%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>87%</span> <span>10%</span> </div> </div>
1	D	1052	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 88%, green 88%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>88%</span> <span>8%</span> </div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 34583 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 Beta-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1015	Total	C	N	O	S	0	0	0
			8156	5159	1444	1515	38			
1	B	1015	Total	C	N	O	S	0	0	0
			8156	5159	1444	1515	38			
1	C	1015	Total	C	N	O	S	0	0	0
			8156	5159	1444	1515	38			
1	D	1015	Total	C	N	O	S	0	0	0
			8156	5159	1444	1515	38			

There are 152 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-28	MET	-	expression tag	UNP P00722
A	-27	GLY	-	expression tag	UNP P00722
A	-26	GLY	-	expression tag	UNP P00722
A	-25	SER	-	expression tag	UNP P00722
A	-24	HIS	-	expression tag	UNP P00722
A	-23	HIS	-	expression tag	UNP P00722
A	-22	HIS	-	expression tag	UNP P00722
A	-21	HIS	-	expression tag	UNP P00722
A	-20	HIS	-	expression tag	UNP P00722
A	-19	HIS	-	expression tag	UNP P00722
A	-18	GLY	-	expression tag	UNP P00722
A	-17	MET	-	expression tag	UNP P00722
A	-16	ALA	-	expression tag	UNP P00722
A	-15	SER	-	expression tag	UNP P00722
A	-14	MET	-	expression tag	UNP P00722
A	-13	THR	-	expression tag	UNP P00722
A	-12	GLY	-	expression tag	UNP P00722
A	-11	GLY	-	expression tag	UNP P00722
A	-10	GLN	-	expression tag	UNP P00722
A	-9	GLN	-	expression tag	UNP P00722
A	-8	MET	-	expression tag	UNP P00722

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLY	-	expression tag	UNP P00722
A	-6	ARG	-	expression tag	UNP P00722
A	-5	ASP	-	expression tag	UNP P00722
A	-4	LEU	-	expression tag	UNP P00722
A	-3	TYR	-	expression tag	UNP P00722
A	-2	ASP	-	expression tag	UNP P00722
A	-1	ASP	-	expression tag	UNP P00722
A	0	ASP	-	expression tag	UNP P00722
A	1	ASP	-	expression tag	UNP P00722
A	2	LYS	-	expression tag	UNP P00722
A	3	ASP	-	expression tag	UNP P00722
A	4	PRO	-	expression tag	UNP P00722
A	5	MET	-	expression tag	UNP P00722
A	6	ILE	-	expression tag	UNP P00722
A	7	ASP	-	expression tag	UNP P00722
A	8	PRO	-	expression tag	UNP P00722
A	460	THR	ASN	engineered mutation	UNP P00722
B	-28	MET	-	expression tag	UNP P00722
B	-27	GLY	-	expression tag	UNP P00722
B	-26	GLY	-	expression tag	UNP P00722
B	-25	SER	-	expression tag	UNP P00722
B	-24	HIS	-	expression tag	UNP P00722
B	-23	HIS	-	expression tag	UNP P00722
B	-22	HIS	-	expression tag	UNP P00722
B	-21	HIS	-	expression tag	UNP P00722
B	-20	HIS	-	expression tag	UNP P00722
B	-19	HIS	-	expression tag	UNP P00722
B	-18	GLY	-	expression tag	UNP P00722
B	-17	MET	-	expression tag	UNP P00722
B	-16	ALA	-	expression tag	UNP P00722
B	-15	SER	-	expression tag	UNP P00722
B	-14	MET	-	expression tag	UNP P00722
B	-13	THR	-	expression tag	UNP P00722
B	-12	GLY	-	expression tag	UNP P00722
B	-11	GLY	-	expression tag	UNP P00722
B	-10	GLN	-	expression tag	UNP P00722
B	-9	GLN	-	expression tag	UNP P00722
B	-8	MET	-	expression tag	UNP P00722
B	-7	GLY	-	expression tag	UNP P00722
B	-6	ARG	-	expression tag	UNP P00722
B	-5	ASP	-	expression tag	UNP P00722
B	-4	LEU	-	expression tag	UNP P00722

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	TYR	-	expression tag	UNP P00722
B	-2	ASP	-	expression tag	UNP P00722
B	-1	ASP	-	expression tag	UNP P00722
B	0	ASP	-	expression tag	UNP P00722
B	1	ASP	-	expression tag	UNP P00722
B	2	LYS	-	expression tag	UNP P00722
B	3	ASP	-	expression tag	UNP P00722
B	4	PRO	-	expression tag	UNP P00722
B	5	MET	-	expression tag	UNP P00722
B	6	ILE	-	expression tag	UNP P00722
B	7	ASP	-	expression tag	UNP P00722
B	8	PRO	-	expression tag	UNP P00722
B	460	THR	ASN	engineered mutation	UNP P00722
C	-28	MET	-	expression tag	UNP P00722
C	-27	GLY	-	expression tag	UNP P00722
C	-26	GLY	-	expression tag	UNP P00722
C	-25	SER	-	expression tag	UNP P00722
C	-24	HIS	-	expression tag	UNP P00722
C	-23	HIS	-	expression tag	UNP P00722
C	-22	HIS	-	expression tag	UNP P00722
C	-21	HIS	-	expression tag	UNP P00722
C	-20	HIS	-	expression tag	UNP P00722
C	-19	HIS	-	expression tag	UNP P00722
C	-18	GLY	-	expression tag	UNP P00722
C	-17	MET	-	expression tag	UNP P00722
C	-16	ALA	-	expression tag	UNP P00722
C	-15	SER	-	expression tag	UNP P00722
C	-14	MET	-	expression tag	UNP P00722
C	-13	THR	-	expression tag	UNP P00722
C	-12	GLY	-	expression tag	UNP P00722
C	-11	GLY	-	expression tag	UNP P00722
C	-10	GLN	-	expression tag	UNP P00722
C	-9	GLN	-	expression tag	UNP P00722
C	-8	MET	-	expression tag	UNP P00722
C	-7	GLY	-	expression tag	UNP P00722
C	-6	ARG	-	expression tag	UNP P00722
C	-5	ASP	-	expression tag	UNP P00722
C	-4	LEU	-	expression tag	UNP P00722
C	-3	TYR	-	expression tag	UNP P00722
C	-2	ASP	-	expression tag	UNP P00722
C	-1	ASP	-	expression tag	UNP P00722
C	0	ASP	-	expression tag	UNP P00722

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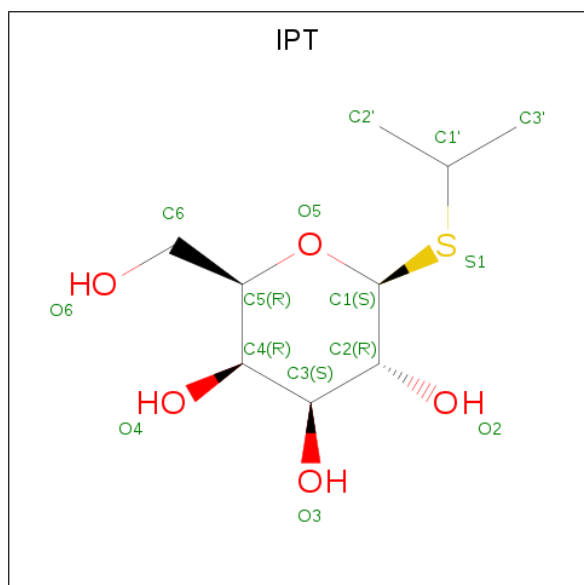
Chain	Residue	Modelled	Actual	Comment	Reference
C	1	ASP	-	expression tag	UNP P00722
C	2	LYS	-	expression tag	UNP P00722
C	3	ASP	-	expression tag	UNP P00722
C	4	PRO	-	expression tag	UNP P00722
C	5	MET	-	expression tag	UNP P00722
C	6	ILE	-	expression tag	UNP P00722
C	7	ASP	-	expression tag	UNP P00722
C	8	PRO	-	expression tag	UNP P00722
C	460	THR	ASN	engineered mutation	UNP P00722
D	-28	MET	-	expression tag	UNP P00722
D	-27	GLY	-	expression tag	UNP P00722
D	-26	GLY	-	expression tag	UNP P00722
D	-25	SER	-	expression tag	UNP P00722
D	-24	HIS	-	expression tag	UNP P00722
D	-23	HIS	-	expression tag	UNP P00722
D	-22	HIS	-	expression tag	UNP P00722
D	-21	HIS	-	expression tag	UNP P00722
D	-20	HIS	-	expression tag	UNP P00722
D	-19	HIS	-	expression tag	UNP P00722
D	-18	GLY	-	expression tag	UNP P00722
D	-17	MET	-	expression tag	UNP P00722
D	-16	ALA	-	expression tag	UNP P00722
D	-15	SER	-	expression tag	UNP P00722
D	-14	MET	-	expression tag	UNP P00722
D	-13	THR	-	expression tag	UNP P00722
D	-12	GLY	-	expression tag	UNP P00722
D	-11	GLY	-	expression tag	UNP P00722
D	-10	GLN	-	expression tag	UNP P00722
D	-9	GLN	-	expression tag	UNP P00722
D	-8	MET	-	expression tag	UNP P00722
D	-7	GLY	-	expression tag	UNP P00722
D	-6	ARG	-	expression tag	UNP P00722
D	-5	ASP	-	expression tag	UNP P00722
D	-4	LEU	-	expression tag	UNP P00722
D	-3	TYR	-	expression tag	UNP P00722
D	-2	ASP	-	expression tag	UNP P00722
D	-1	ASP	-	expression tag	UNP P00722
D	0	ASP	-	expression tag	UNP P00722
D	1	ASP	-	expression tag	UNP P00722
D	2	LYS	-	expression tag	UNP P00722
D	3	ASP	-	expression tag	UNP P00722
D	4	PRO	-	expression tag	UNP P00722

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Chain	Residue	Modelled	Actual	Comment	Reference
D	5	MET	-	expression tag	UNP P00722
D	6	ILE	-	expression tag	UNP P00722
D	7	ASP	-	expression tag	UNP P00722
D	8	PRO	-	expression tag	UNP P00722
D	460	THR	ASN	engineered mutation	UNP P00722

- Molecule 2 is 1-methylethyl 1-thio-beta-D-galactopyranoside (three-letter code: IPT) (formula:  $C_9H_{18}O_5S$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			15	9	5	1		
2	B	1	Total	C	O	S	0	0
			15	9	5	1		
2	C	1	Total	C	O	S	0	0
			15	9	5	1		
2	D	1	Total	C	O	S	0	0
			15	9	5	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

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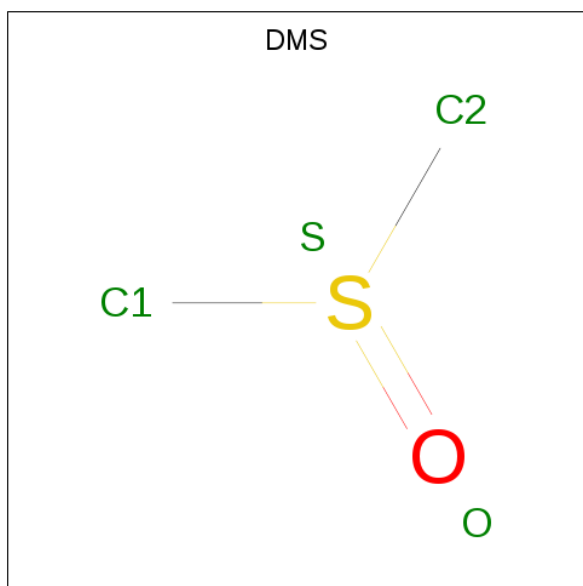
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	2	Total	Mg	0	0
			2	2		
3	C	2	Total	Mg	0	0
			2	2		

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	3	Total	Na	0	0
			3	3		
4	A	3	Total	Na	0	0
			3	3		
4	D	2	Total	Na	0	0
			2	2		
4	C	2	Total	Na	0	0
			2	2		

- Molecule 5 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C<sub>2</sub>H<sub>6</sub>OS).



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

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

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

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

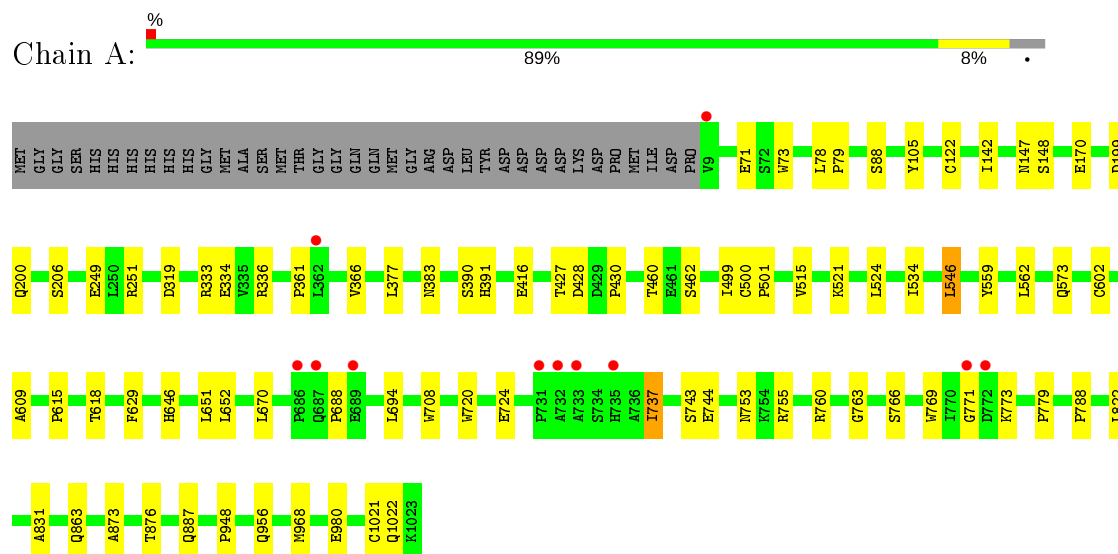
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	441	Total	O	0	0
			441	441		
6	B	421	Total	O	0	0
			421	421		
6	C	397	Total	O	0	0
			397	397		
6	D	438	Total	O	0	0
			438	438		

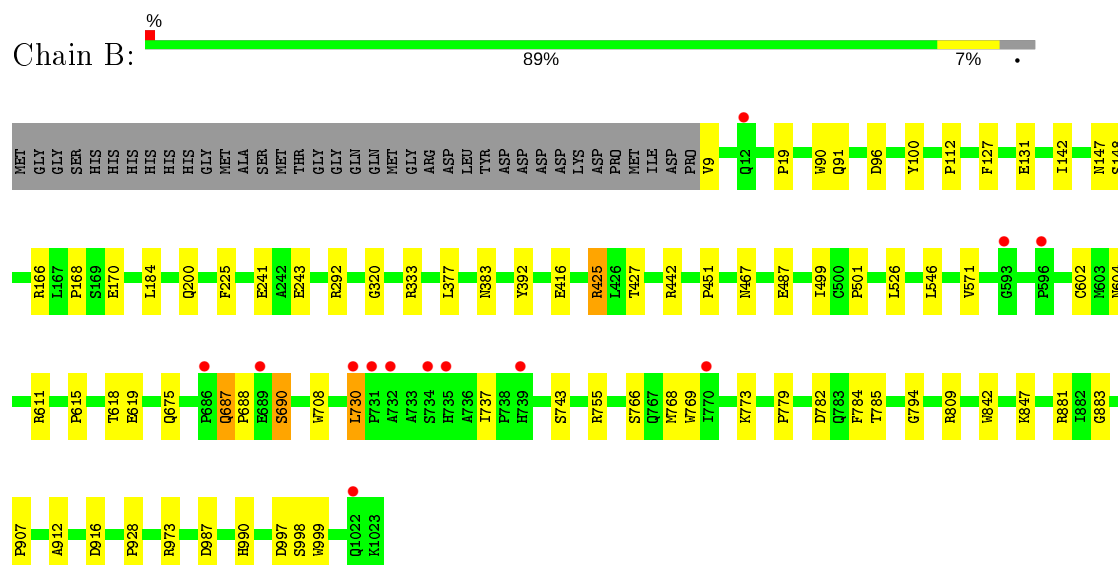
### 3 Residue-property plots [i](#)

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.

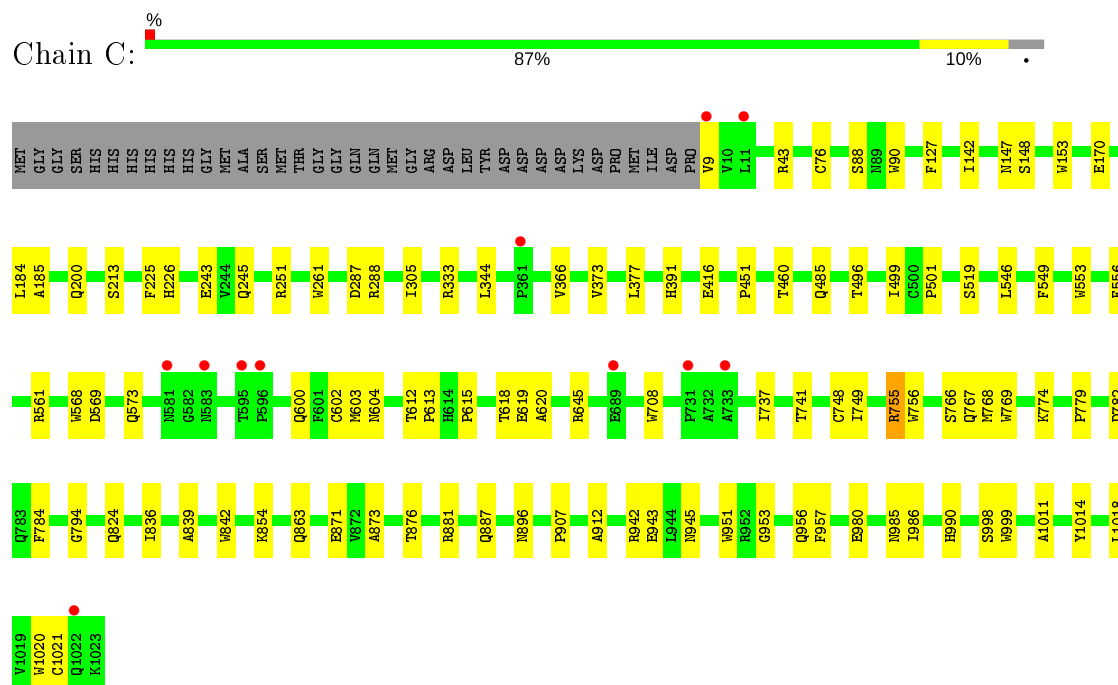
#### • Molecule 1: Beta-galactosidase



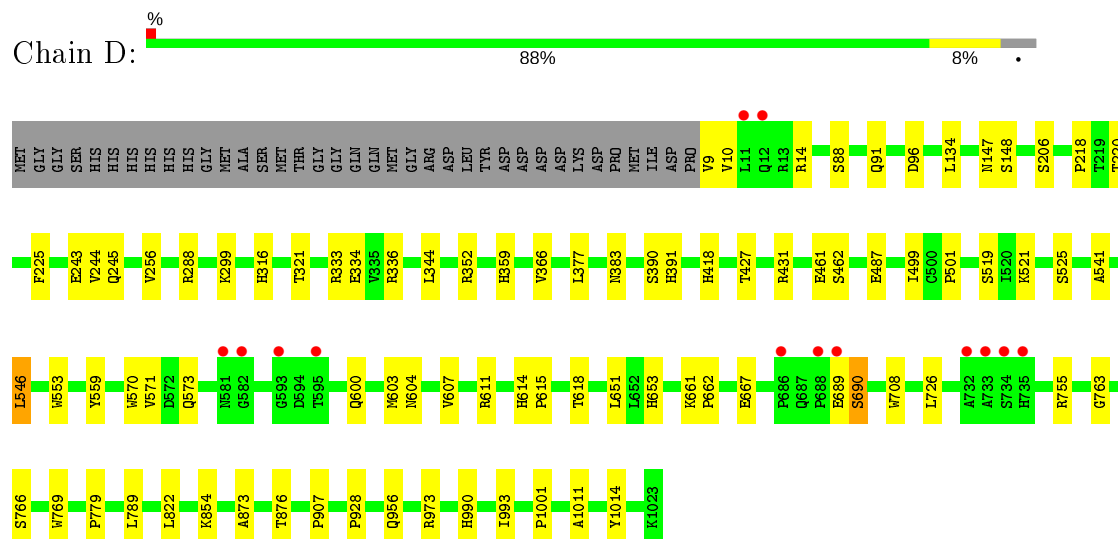
#### • Molecule 1: Beta-galactosidase



#### • Molecule 1: Beta-galactosidase



- Molecule 1: Beta-galactosidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	151.18Å 161.06Å 201.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	126.21 – 2.55 125.80 – 2.55	Depositor EDS
% Data completeness (in resolution range)	100.0 (126.21-2.55) 95.7 (125.80-2.55)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.10 (at 2.55Å)	Xtriage
Refinement program	REFMAC 5.5.0109, CNS	Depositor
R, $R_{free}$	0.179 , 0.236 0.177 , 0.236	Depositor DCC
$R_{free}$ test set	2164 reflections (1.41%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.8	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 43.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	34583	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.58 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.6774e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: NA, MG, DMS, IPT

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	0.43	0/8398	0.58	0/11457
1	B	0.43	0/8398	0.57	0/11457
1	C	0.42	0/8398	0.56	0/11457
1	D	0.43	0/8398	0.57	0/11457
All	All	0.43	0/33592	0.57	0/45828

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 [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	8156	0	7754	45	0
1	B	8156	0	7754	46	0
1	C	8156	0	7754	54	0
1	D	8156	0	7754	45	0
2	A	15	0	17	0	0
2	B	15	0	18	0	0
2	C	15	0	17	1	0
2	D	15	0	17	0	0
3	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	3	0	0	0	0
4	B	3	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
5	A	40	0	60	3	0
5	B	48	0	72	3	0
5	C	44	0	66	1	0
5	D	52	0	78	2	0
6	A	441	0	0	3	0
6	B	421	0	0	3	0
6	C	397	0	0	1	0
6	D	438	0	0	5	0
All	All	34583	0	31361	183	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 (183) 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:B:766:SER:HA	1:B:779:PRO:HB3	1.57	0.86
1:D:377:LEU:HD22	1:D:708:TRP:HA	1.58	0.84
1:C:245:GLN:HG2	1:C:288:ARG:HG2	1.62	0.79
1:A:377:LEU:HD22	1:A:708:TRP:HA	1.69	0.74
1:B:383:ASN:HA	5:B:8003:DMS:H11	1.69	0.73
1:D:88:SER:HA	1:D:366:VAL:HG21	1.72	0.71
1:C:142:ILE:HG12	1:C:170:GLU:HG2	1.75	0.68
1:B:755:ARG:HB3	1:B:769:TRP:HB2	1.76	0.68
1:D:245:GLN:HG2	1:D:288:ARG:HG2	1.75	0.68
1:C:755:ARG:HB2	1:C:769:TRP:HB2	1.79	0.65
1:D:615:PRO:O	1:D:618:THR:HG22	1.96	0.65
1:D:766:SER:HA	1:D:779:PRO:HB3	1.80	0.63
1:D:499:ILE:HG22	1:D:501:PRO:HD3	1.81	0.62
1:A:887:GLN:NE2	1:A:980:GLU:O	2.33	0.62
1:C:615:PRO:O	1:C:618:THR:HG22	2.01	0.61
1:C:986:ILE:HG21	1:C:1018:LEU:HD11	1.83	0.60
1:B:91:GLN:HG3	1:B:96:ASP:OD1	2.02	0.59
1:A:766:SER:HA	1:A:779:PRO:HB3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:ILE:HG12	1:B:170:GLU:HG2	1.82	0.59
1:A:615:PRO:O	1:A:618:THR:HG22	2.03	0.58
1:B:782:ASP:HB2	1:B:842:TRP:CH2	2.38	0.58
1:A:427:THR:HG21	1:A:462:SER:HB3	1.85	0.58
1:A:200:GLN:HA	1:A:416:GLU:OE1	2.03	0.58
1:A:249:GLU:HG2	1:A:251:ARG:CZ	2.34	0.58
1:B:928:PRO:HB2	1:B:973:ARG:HH11	1.68	0.58
1:C:794:GLY:HA2	1:C:998:SER:O	2.03	0.58
1:C:887:GLN:NE2	1:C:980:GLU:O	2.39	0.56
1:D:873:ALA:O	1:D:876:THR:HG22	2.05	0.56
1:A:334:GLU:OE1	1:A:336:ARG:NH1	2.39	0.56
1:C:766:SER:HA	1:C:779:PRO:HB3	1.88	0.55
1:A:499:ILE:HG22	1:A:501:PRO:HD3	1.89	0.55
1:A:873:ALA:O	1:A:876:THR:HG22	2.07	0.54
1:B:241:GLU:HG3	1:B:292:ARG:HG2	1.90	0.54
1:A:737:ILE:HD12	1:A:831:ALA:O	2.09	0.53
1:C:88:SER:HA	1:C:366:VAL:HG21	1.90	0.53
1:B:377:LEU:HD22	1:B:708:TRP:HA	1.90	0.53
1:C:756:TRP:CD1	1:C:768:MET:HG2	2.45	0.52
1:C:245:GLN:HG2	1:C:288:ARG:CG	2.37	0.52
1:D:427:THR:HG21	1:D:462:SER:HB3	1.90	0.52
1:C:499:ILE:HG22	1:C:501:PRO:HD3	1.92	0.52
1:C:377:LEU:HD22	1:C:708:TRP:HA	1.91	0.52
1:C:767:GLN:NE2	1:C:774:LYS:HE3	2.23	0.52
1:B:100:TYR:CE1	1:B:602:CYS:HB3	2.45	0.52
1:D:689:GLU:O	1:D:690:SER:HB3	2.09	0.52
1:D:928:PRO:HB2	1:D:973:ARG:HH11	1.74	0.52
1:B:200:GLN:HA	1:B:416:GLU:OE1	2.10	0.52
1:A:73:TRP:CE2	1:A:122:CYS:HB3	2.45	0.51
1:C:225:PHE:HA	1:C:243:GLU:O	2.10	0.51
1:C:451:PRO:HB3	5:C:8001:DMS:O	2.11	0.51
1:D:334:GLU:OE1	1:D:336:ARG:NH1	2.42	0.51
1:D:1011:ALA:HB3	1:D:1014:TYR:CZ	2.46	0.51
1:C:600:GLN:HB2	1:C:603:MET:HE2	1.93	0.51
1:B:9:VAL:HG22	1:C:9:VAL:HG22	1.92	0.51
1:D:614:HIS:HB3	6:D:4145:HOH:O	2.12	0.50
1:C:768:MET:HE1	1:C:1020:TRP:CZ2	2.47	0.50
1:D:418:HIS:CE1	1:D:461:GLU:OE2	2.65	0.50
1:B:675:GLN:HG3	6:B:4168:HOH:O	2.12	0.49
1:B:451:PRO:HA	5:B:8001:DMS:H22	1.95	0.49
1:A:430:PRO:HD3	5:A:8009:DMS:H13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:743:SER:O	1:A:760:ARG:NH1	2.40	0.48
1:B:166:ARG:HG3	1:B:392:TYR:HB2	1.95	0.48
1:C:782:ASP:HB2	1:C:842:TRP:CH2	2.47	0.48
1:A:646:HIS:HB3	6:A:4022:HOH:O	2.12	0.48
1:A:788:PRO:HD2	1:A:968:MET:HB2	1.96	0.48
1:B:425:ARG:HH12	1:C:287:ASP:CG	2.15	0.48
1:A:763:GLY:HA3	1:A:822:LEU:HD13	1.96	0.48
1:B:9:VAL:HG13	1:C:9:VAL:HG13	1.96	0.48
1:B:571:VAL:HG21	1:B:611:ARG:NH1	2.28	0.47
1:B:425:ARG:NH1	1:C:287:ASP:OD2	2.46	0.47
1:B:883:GLY:HA3	1:B:987:ASP:HA	1.96	0.47
1:C:153:TRP:HB2	1:C:185:ALA:HB3	1.96	0.47
1:C:200:GLN:HA	1:C:416:GLU:OE1	2.15	0.47
1:A:383:ASN:HA	5:A:8003:DMS:H11	1.97	0.47
1:A:863:GLN:HG2	1:A:1021:CYS:HB3	1.97	0.47
1:D:571:VAL:HG21	1:D:611:ARG:NH1	2.30	0.47
1:A:629:PHE:HB3	1:A:720:TRP:HH2	1.79	0.47
1:C:896:ASN:HB3	1:C:945:ASN:HB2	1.96	0.47
1:B:809:ARG:HD3	6:B:4161:HOH:O	2.14	0.47
1:A:361:PRO:HB3	1:A:609:ALA:HB1	1.98	0.46
1:D:316:HIS:HB2	1:D:321:THR:O	2.16	0.46
1:D:546:LEU:HA	6:D:4227:HOH:O	2.15	0.46
1:A:753:ASN:O	1:A:771:GLY:N	2.46	0.46
1:C:305:ILE:HD11	1:C:645:ARG:HB3	1.96	0.46
1:D:600:GLN:HB2	1:D:603:MET:HE2	1.97	0.46
1:A:524:LEU:HD11	1:A:562:LEU:HG	1.96	0.46
1:B:225:PHE:HA	1:B:243:GLU:O	2.16	0.46
1:D:352:ARG:HG2	1:D:553:TRP:CH2	2.51	0.46
1:A:743:SER:OG	1:A:744:GLU:N	2.48	0.46
1:B:615:PRO:O	1:B:618:THR:HG22	2.16	0.46
1:D:755:ARG:HB3	1:D:769:TRP:HB2	1.98	0.45
1:B:784:PHE:HA	1:B:881:ARG:O	2.15	0.45
1:A:948:PRO:HB2	1:A:1022:GLN:HG3	1.99	0.45
1:D:653:HIS:CD2	1:D:667:GLU:HG2	2.52	0.45
1:C:485:GLN:HA	1:C:496:THR:OG1	2.16	0.45
1:C:784:PHE:HA	1:C:881:ARG:O	2.16	0.45
1:C:943:GLU:HA	1:C:951:TRP:O	2.17	0.45
1:D:570:TRP:O	1:D:607:VAL:HG22	2.16	0.45
1:D:218:PRO:HB2	1:D:220:THR:O	2.17	0.45
1:A:336:ARG:HD2	6:A:4259:HOH:O	2.17	0.45
1:B:127:PHE:CE1	1:B:184:LEU:HG	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:730:LEU:H	1:B:730:LEU:HG	1.56	0.45
1:A:88:SER:HA	1:A:366:VAL:HG21	1.98	0.45
1:C:957:PHE:HA	1:C:985:ASN:O	2.17	0.45
1:B:782:ASP:OD1	1:B:842:TRP:HH2	2.00	0.44
1:C:43:ARG:HD2	1:C:261:TRP:CD2	2.51	0.44
1:C:391:HIS:CG	1:C:460:THR:HG21	2.53	0.44
1:A:521:LYS:HG2	1:A:559:TYR:CZ	2.53	0.44
1:B:782:ASP:HB2	1:B:842:TRP:CZ2	2.53	0.44
1:D:147:ASN:HB3	1:D:206:SER:HA	1.99	0.44
1:D:225:PHE:HA	1:D:243:GLU:O	2.18	0.44
1:D:9:VAL:HG13	1:D:10:VAL:N	2.33	0.44
1:D:431:ARG:NH2	6:D:4353:HOH:O	2.51	0.44
1:A:147:ASN:HA	1:A:148:SER:HA	1.67	0.43
1:A:390:SER:HA	1:A:391:HIS:HA	1.84	0.43
1:C:147:ASN:HA	1:C:148:SER:HA	1.71	0.43
1:D:147:ASN:HA	1:D:148:SER:HA	1.77	0.43
1:B:785:THR:O	1:B:881:ARG:HD2	2.18	0.43
1:C:824:GLN:HB3	1:C:839:ALA:HB3	1.99	0.43
1:C:854:LYS:NZ	6:C:4157:HOH:O	2.50	0.43
1:B:687:GLN:HG3	1:B:688:PRO:HD2	2.00	0.43
1:A:391:HIS:CG	1:A:460:THR:HG21	2.53	0.43
1:C:871:GLU:OE1	1:D:726:LEU:HD22	2.17	0.43
1:D:763:GLY:HA3	1:D:822:LEU:HD13	2.01	0.43
1:D:383:ASN:HA	5:D:8003:DMS:H11	2.00	0.43
1:D:541:ALA:HB3	1:D:604:ASN:O	2.19	0.43
1:B:320:GLY:HA2	5:B:8006:DMS:O	2.19	0.43
1:B:794:GLY:HA2	1:B:998:SER:O	2.18	0.43
1:C:873:ALA:O	1:C:876:THR:HG22	2.17	0.43
1:D:1001:PRO:O	5:D:8006:DMS:H11	2.18	0.43
1:A:105:TYR:CE1	1:A:199:ASP:HB2	2.54	0.43
1:B:127:PHE:HE1	1:B:184:LEU:HG	1.84	0.43
1:B:168:PRO:O	1:B:442:ARG:NH2	2.52	0.43
1:D:487:GLU:HB3	6:D:4041:HOH:O	2.18	0.43
1:D:854:LYS:NZ	6:D:4033:HOH:O	2.52	0.43
1:A:500:CYS:HA	1:A:534:ILE:O	2.19	0.42
1:B:768:MET:HB2	1:B:768:MET:HE3	1.96	0.42
1:C:863:GLN:HG2	1:C:1021:CYS:HB3	2.01	0.42
1:C:549:PHE:CE2	1:C:620:ALA:HA	2.53	0.42
1:C:612:THR:HA	1:C:613:PRO:HD3	1.92	0.42
1:A:948:PRO:O	1:A:1022:GLN:HA	2.18	0.42
1:C:942:ARG:HA	1:C:953:GLY:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:499:ILE:HG22	1:B:501:PRO:HD3	2.01	0.42
1:B:526:LEU:HD23	1:B:526:LEU:HA	1.90	0.42
1:C:561:ARG:HD3	1:D:525:SER:O	2.18	0.42
1:C:568:TRP:CD2	1:C:569:ASP:HB3	2.54	0.42
1:D:377:LEU:CD2	1:D:708:TRP:HA	2.39	0.42
1:A:724:GLU:O	1:B:847:LYS:NZ	2.53	0.42
1:C:907:PRO:HG2	1:C:990:HIS:O	2.19	0.42
1:D:789:LEU:HD11	1:D:993:ILE:HG22	2.02	0.42
1:A:573:GLN:HB2	1:A:602:CYS:O	2.20	0.42
1:C:127:PHE:CE1	1:C:184:LEU:HG	2.54	0.42
1:D:521:LYS:HG2	1:D:559:TYR:CZ	2.55	0.42
1:D:661:LYS:HA	1:D:662:PRO:HD3	1.90	0.42
1:A:147:ASN:HB3	1:A:206:SER:HA	2.02	0.42
1:C:749:ILE:HD11	1:C:836:ILE:HD11	2.00	0.42
1:D:91:GLN:HG3	1:D:96:ASP:OD1	2.20	0.42
1:C:573:GLN:HB2	1:C:602:CYS:O	2.20	0.42
1:B:166:ARG:HG3	1:B:392:TYR:CB	2.50	0.41
1:B:147:ASN:HA	1:B:148:SER:HA	1.71	0.41
1:C:999:TRP:CD2	2:C:2001:IPT:H3'3	2.56	0.41
1:A:546:LEU:HA	6:A:4130:HOH:O	2.19	0.41
1:C:1011:ALA:HB3	1:C:1014:TYR:CZ	2.55	0.41
1:D:244:VAL:HG21	1:D:256:VAL:HG11	2.01	0.41
1:C:619:GLU:HA	1:C:912:ALA:HB2	2.03	0.41
1:A:142:ILE:HG12	1:A:170:GLU:HG2	2.02	0.41
1:A:688:PRO:HG3	1:A:694:LEU:HD21	2.03	0.41
1:B:997:ASP:HB2	1:B:999:TRP:CE2	2.56	0.41
1:A:428:ASP:O	5:A:8009:DMS:H13	2.21	0.41
1:B:907:PRO:HG2	1:B:990:HIS:O	2.21	0.41
1:C:553:TRP:CE3	1:C:556:PHE:HD2	2.39	0.41
1:D:359:HIS:CD2	1:D:573:GLN:HA	2.56	0.41
1:B:427:THR:O	1:B:467:ASN:HB2	2.21	0.41
1:B:619:GLU:HA	1:B:912:ALA:HB2	2.02	0.41
1:C:127:PHE:HE1	1:C:184:LEU:HG	1.86	0.41
1:C:373:VAL:O	1:C:377:LEU:HG	2.21	0.41
1:A:78:LEU:HA	1:A:79:PRO:HD3	1.97	0.40
1:A:670:LEU:HA	1:A:670:LEU:HD23	1.97	0.40
1:B:19:PRO:HD3	1:B:112:PRO:HB3	2.03	0.40
1:D:907:PRO:HG2	1:D:990:HIS:O	2.20	0.40
1:A:755:ARG:HB3	1:A:769:TRP:HB2	2.04	0.40
1:A:753:ASN:HB2	1:A:771:GLY:HA2	2.04	0.40
1:B:487:GLU:HB3	6:B:4078:HOH:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:390:SER:HA	1:D:391:HIS:HA	1.78	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	1013/1052 (96%)	974 (96%)	39 (4%)	0	100	100
1	B	1013/1052 (96%)	971 (96%)	41 (4%)	1 (0%)	51	65
1	C	1013/1052 (96%)	974 (96%)	39 (4%)	0	100	100
1	D	1013/1052 (96%)	966 (95%)	46 (4%)	1 (0%)	51	65
All	All	4052/4208 (96%)	3885 (96%)	165 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	690	SER
1	B	690	SER

### 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	868/898 (97%)	858 (99%)	10 (1%)	71	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	868/898 (97%)	855 (98%)	13 (2%)	65	77
1	C	868/898 (97%)	853 (98%)	15 (2%)	60	75
1	D	868/898 (97%)	859 (99%)	9 (1%)	76	84
All	All	3472/3592 (97%)	3425 (99%)	47 (1%)	67	79

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	GLU
1	A	319	ASP
1	A	333	ARG
1	A	515	VAL
1	A	546	LEU
1	A	651	LEU
1	A	652	LEU
1	A	737	ILE
1	A	773	LYS
1	A	956	GLN
1	B	90	TRP
1	B	131	GLU
1	B	333	ARG
1	B	425	ARG
1	B	546	LEU
1	B	604	ASN
1	B	687	GLN
1	B	690	SER
1	B	730	LEU
1	B	737	ILE
1	B	743	SER
1	B	773	LYS
1	B	916	ASP
1	C	76	CYS
1	C	90	TRP
1	C	213	SER
1	C	226	HIS
1	C	251	ARG
1	C	333	ARG
1	C	344	LEU
1	C	519	SER
1	C	546	LEU
1	C	604	ASN

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Mol	Chain	Res	Type
1	C	737	ILE
1	C	741	THR
1	C	748	CYS
1	C	755	ARG
1	C	956	GLN
1	D	14	ARG
1	D	134	LEU
1	D	299	LYS
1	D	333	ARG
1	D	344	LEU
1	D	519	SER
1	D	546	LEU
1	D	651	LEU
1	D	956	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	418	HIS
1	D	418	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 68 ligands modelled in this entry, 18 are monoatomic - leaving 50 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
5	DMS	D	8004	-	3,3,3	2.61	1 (33%)	3,3,3	0.66	0
5	DMS	D	8010	-	3,3,3	2.62	1 (33%)	3,3,3	0.65	0
5	DMS	B	8010	-	3,3,3	2.65	1 (33%)	3,3,3	0.63	0
5	DMS	D	8013	-	3,3,3	2.61	1 (33%)	3,3,3	0.52	0
5	DMS	A	8002	-	3,3,3	2.50	1 (33%)	3,3,3	0.42	0
5	DMS	A	8008	-	3,3,3	2.65	1 (33%)	3,3,3	0.59	0
5	DMS	A	8001	-	3,3,3	2.41	1 (33%)	3,3,3	0.69	0
5	DMS	D	8001	-	3,3,3	2.58	1 (33%)	3,3,3	0.88	0
5	DMS	A	8005	-	3,3,3	2.57	1 (33%)	3,3,3	0.58	0
5	DMS	B	8001	-	3,3,3	2.53	1 (33%)	3,3,3	0.93	0
5	DMS	B	8011	-	3,3,3	2.68	1 (33%)	3,3,3	0.70	0
5	DMS	B	8005	-	3,3,3	2.53	1 (33%)	3,3,3	0.64	0
5	DMS	D	8002	-	3,3,3	2.55	1 (33%)	3,3,3	0.65	0
5	DMS	C	8004	-	3,3,3	2.58	1 (33%)	3,3,3	0.43	0
5	DMS	C	8002	-	3,3,3	2.43	1 (33%)	3,3,3	0.51	0
5	DMS	A	8009	-	3,3,3	2.67	1 (33%)	3,3,3	0.53	0
5	DMS	C	8006	-	3,3,3	2.70	1 (33%)	3,3,3	0.75	0
5	DMS	C	8005	-	3,3,3	2.57	1 (33%)	3,3,3	0.58	0
5	DMS	B	8009	-	3,3,3	2.58	1 (33%)	3,3,3	0.68	0
2	IPT	B	2001	4	14,15,15	0.58	0	18,21,21	1.69	1 (5%)
5	DMS	B	8003	-	3,3,3	2.60	1 (33%)	3,3,3	0.64	0
5	DMS	C	8010	-	3,3,3	2.65	1 (33%)	3,3,3	0.51	0
2	IPT	C	2001	4	14,15,15	0.51	0	18,21,21	1.66	2 (11%)
5	DMS	C	8007	-	3,3,3	2.72	1 (33%)	3,3,3	0.87	0
5	DMS	C	8009	-	3,3,3	2.64	1 (33%)	3,3,3	0.49	0
5	DMS	D	8003	-	3,3,3	2.56	1 (33%)	3,3,3	0.52	0
5	DMS	A	8010	-	3,3,3	2.66	1 (33%)	3,3,3	0.68	0
5	DMS	D	8012	-	3,3,3	2.69	1 (33%)	3,3,3	0.55	0
5	DMS	B	8012	-	3,3,3	2.68	1 (33%)	3,3,3	0.73	0
5	DMS	C	8008	-	3,3,3	2.61	1 (33%)	3,3,3	0.73	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	DMS	B	8002	-	3,3,3	2.49	1 (33%)	3,3,3	0.65	0
5	DMS	C	8003	-	3,3,3	2.49	1 (33%)	3,3,3	0.47	0
5	DMS	D	8011	-	3,3,3	2.71	1 (33%)	3,3,3	0.51	0
5	DMS	D	8009	-	3,3,3	2.61	1 (33%)	3,3,3	0.64	0
5	DMS	B	8006	-	3,3,3	2.60	1 (33%)	3,3,3	0.60	0
5	DMS	B	8007	-	3,3,3	2.69	1 (33%)	3,3,3	0.58	0
5	DMS	C	8011	-	3,3,3	2.63	1 (33%)	3,3,3	0.54	0
5	DMS	B	8004	-	3,3,3	2.62	1 (33%)	3,3,3	0.45	0
5	DMS	C	8001	-	3,3,3	2.47	1 (33%)	3,3,3	0.78	0
5	DMS	B	8008	-	3,3,3	2.63	1 (33%)	3,3,3	0.46	0
5	DMS	D	8005	-	3,3,3	2.54	1 (33%)	3,3,3	0.68	0
5	DMS	A	8006	-	3,3,3	2.65	1 (33%)	3,3,3	0.66	0
5	DMS	D	8008	-	3,3,3	2.67	1 (33%)	3,3,3	0.72	0
5	DMS	D	8006	-	3,3,3	2.71	1 (33%)	3,3,3	0.80	0
5	DMS	A	8004	-	3,3,3	2.64	1 (33%)	3,3,3	0.70	0
5	DMS	A	8003	-	3,3,3	2.59	1 (33%)	3,3,3	0.60	0
2	IPT	A	2001	4	14,15,15	0.48	0	18,21,21	1.66	1 (5%)
2	IPT	D	2001	4	14,15,15	0.49	0	18,21,21	1.56	1 (5%)
5	DMS	A	8007	-	3,3,3	2.57	1 (33%)	3,3,3	0.68	0
5	DMS	D	8007	-	3,3,3	2.69	1 (33%)	3,3,3	0.72	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	IPT	D	2001	4	-	3/6/26/26	0/1/1/1
2	IPT	C	2001	4	-	4/6/26/26	0/1/1/1
2	IPT	B	2001	4	-	3/6/26/26	0/1/1/1
2	IPT	A	2001	4	-	3/6/26/26	0/1/1/1

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	8011	DMS	O-S	4.55	1.81	1.50
5	C	8007	DMS	O-S	4.54	1.80	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	8011	DMS	O-S	4.54	1.80	1.50
5	D	8006	DMS	O-S	4.53	1.80	1.50
5	C	8006	DMS	O-S	4.53	1.80	1.50
5	B	8007	DMS	O-S	4.52	1.80	1.50
5	D	8012	DMS	O-S	4.52	1.80	1.50
5	D	8007	DMS	O-S	4.50	1.80	1.50
5	B	8012	DMS	O-S	4.49	1.80	1.50
5	A	8009	DMS	O-S	4.49	1.80	1.50
5	A	8010	DMS	O-S	4.48	1.80	1.50
5	D	8008	DMS	O-S	4.46	1.80	1.50
5	C	8010	DMS	O-S	4.45	1.80	1.50
5	A	8004	DMS	O-S	4.44	1.80	1.50
5	A	8006	DMS	O-S	4.44	1.80	1.50
5	A	8008	DMS	O-S	4.43	1.80	1.50
5	C	8009	DMS	O-S	4.43	1.80	1.50
5	B	8010	DMS	O-S	4.42	1.80	1.50
5	B	8004	DMS	O-S	4.40	1.80	1.50
5	C	8011	DMS	O-S	4.40	1.80	1.50
5	B	8008	DMS	O-S	4.40	1.79	1.50
5	D	8010	DMS	O-S	4.39	1.79	1.50
5	B	8003	DMS	O-S	4.38	1.79	1.50
5	D	8004	DMS	O-S	4.37	1.79	1.50
5	D	8013	DMS	O-S	4.37	1.79	1.50
5	B	8006	DMS	O-S	4.37	1.79	1.50
5	C	8008	DMS	O-S	4.35	1.79	1.50
5	D	8001	DMS	O-S	4.35	1.79	1.50
5	A	8003	DMS	O-S	4.35	1.79	1.50
5	D	8009	DMS	O-S	4.34	1.79	1.50
5	C	8004	DMS	O-S	4.32	1.79	1.50
5	D	8003	DMS	O-S	4.32	1.79	1.50
5	A	8007	DMS	O-S	4.31	1.79	1.50
5	B	8009	DMS	O-S	4.30	1.79	1.50
5	C	8005	DMS	O-S	4.29	1.79	1.50
5	A	8005	DMS	O-S	4.29	1.79	1.50
5	D	8002	DMS	O-S	4.28	1.79	1.50
5	B	8001	DMS	O-S	4.24	1.78	1.50
5	D	8005	DMS	O-S	4.24	1.78	1.50
5	A	8002	DMS	O-S	4.23	1.78	1.50
5	B	8005	DMS	O-S	4.23	1.78	1.50
5	C	8003	DMS	O-S	4.20	1.78	1.50
5	B	8002	DMS	O-S	4.18	1.78	1.50
5	C	8001	DMS	O-S	4.14	1.78	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	8002	DMS	O-S	4.10	1.77	1.50
5	A	8001	DMS	O-S	4.03	1.77	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2001	IPT	C1-S1-C1'	5.87	118.23	100.26
2	A	2001	IPT	C1-S1-C1'	5.71	117.74	100.26
2	C	2001	IPT	C1-S1-C1'	5.70	117.70	100.26
2	D	2001	IPT	C1-S1-C1'	5.35	116.65	100.26
2	C	2001	IPT	C2-C1-S1	-2.33	107.71	111.30

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2001	IPT	C2'-C1'-S1-C1
2	B	2001	IPT	C3'-C1'-S1-C1
2	C	2001	IPT	C2'-C1'-S1-C1
2	C	2001	IPT	C3'-C1'-S1-C1
2	A	2001	IPT	C2'-C1'-S1-C1
2	A	2001	IPT	C3'-C1'-S1-C1
2	D	2001	IPT	C2'-C1'-S1-C1
2	D	2001	IPT	C3'-C1'-S1-C1
2	B	2001	IPT	O5-C5-C6-O6
2	C	2001	IPT	O5-C5-C6-O6
2	D	2001	IPT	O5-C5-C6-O6
2	A	2001	IPT	O5-C5-C6-O6
2	C	2001	IPT	C4-C5-C6-O6

There are no ring outliers.

9 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	8001	DMS	1	0
5	A	8009	DMS	2	0
5	B	8003	DMS	1	0
2	C	2001	IPT	1	0
5	D	8003	DMS	1	0
5	B	8006	DMS	1	0
5	C	8001	DMS	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	8006	DMS	1	0
5	A	8003	DMS	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	1015/1052 (96%)	-0.17	11 (1%) 80 85	25, 42, 70, 102	0
1	B	1015/1052 (96%)	-0.10	13 (1%) 77 82	23, 44, 74, 108	0
1	C	1015/1052 (96%)	-0.13	11 (1%) 80 85	24, 44, 72, 99	0
1	D	1015/1052 (96%)	-0.15	13 (1%) 77 82	25, 42, 71, 108	0
All	All	4060/4208 (96%)	-0.14	48 (1%) 79 84	23, 43, 72, 108	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	689	GLU	7.4
1	B	689	GLU	5.5
1	A	732	ALA	4.5
1	A	689	GLU	4.3
1	B	12	GLN	3.9
1	C	11	LEU	3.8
1	D	735	HIS	3.7
1	C	689	GLU	3.6
1	B	732	ALA	3.6
1	A	735	HIS	3.3
1	D	732	ALA	3.2
1	B	596	PRO	3.2
1	D	595	THR	3.2
1	D	581	ASN	3.1
1	C	583	ASN	3.1
1	D	582	GLY	3.0
1	A	733	ALA	3.0
1	B	730	LEU	3.0
1	D	11	LEU	3.0
1	D	688	PRO	2.9
1	C	9	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	596	PRO	2.8
1	A	686	PRO	2.8
1	D	734	SER	2.7
1	C	731	PRO	2.7
1	B	731	PRO	2.7
1	B	593	GLY	2.6
1	D	12	GLN	2.6
1	B	686	PRO	2.6
1	B	770	ILE	2.6
1	D	593	GLY	2.6
1	C	595	THR	2.6
1	C	1022	GLN	2.5
1	A	9	VAL	2.5
1	A	772	ASP	2.5
1	D	686	PRO	2.5
1	B	1022	GLN	2.4
1	A	731	PRO	2.3
1	A	362	LEU	2.2
1	C	733	ALA	2.2
1	A	771	GLY	2.1
1	D	733	ALA	2.1
1	B	735	HIS	2.1
1	C	361	PRO	2.1
1	C	581	ASN	2.1
1	B	734	SER	2.0
1	B	739	HIS	2.0
1	A	687	GLN	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 monosaccharides 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
4	NA	D	3101	1/1	0.85	0.09	53,53,53,53	0
5	DMS	B	8011	4/4	0.86	0.30	58,59,61,63	0
5	DMS	B	8012	4/4	0.88	0.27	78,80,81,81	0
5	DMS	D	8013	4/4	0.88	0.24	74,74,75,76	0
5	DMS	C	8011	4/4	0.90	0.21	77,78,79,79	0
4	NA	C	3101	1/1	0.90	0.08	52,52,52,52	0
5	DMS	D	8011	4/4	0.92	0.14	77,78,78,79	0
5	DMS	C	8007	4/4	0.92	0.24	64,66,67,67	0
5	DMS	C	8006	4/4	0.92	0.22	69,70,72,74	0
5	DMS	B	8007	4/4	0.93	0.18	68,69,70,73	0
2	IPT	C	2001	15/15	0.93	0.14	45,48,53,58	0
5	DMS	A	8010	4/4	0.93	0.20	59,60,61,63	0
5	DMS	D	8012	4/4	0.93	0.18	57,57,58,60	0
5	DMS	D	8009	4/4	0.93	0.20	68,69,70,71	0
5	DMS	D	8006	4/4	0.93	0.25	66,67,68,68	0
5	DMS	C	8010	4/4	0.94	0.18	64,66,66,67	0
3	MG	B	3002	1/1	0.94	0.11	51,51,51,51	0
3	MG	D	3001	1/1	0.94	0.07	54,54,54,54	0
5	DMS	B	8009	4/4	0.94	0.21	55,58,59,60	0
2	IPT	B	2001	15/15	0.95	0.12	40,47,55,56	0
4	NA	A	3103	1/1	0.95	0.09	43,43,43,43	0
5	DMS	A	8009	4/4	0.95	0.15	67,67,67,69	0
5	DMS	A	8008	4/4	0.95	0.16	59,59,59,60	0
5	DMS	A	8006	4/4	0.95	0.24	70,72,74,74	0
3	MG	A	3001	1/1	0.95	0.07	53,53,53,53	0
5	DMS	A	8007	4/4	0.95	0.21	58,59,59,60	0
5	DMS	D	8007	4/4	0.95	0.19	68,68,69,70	0
5	DMS	C	8008	4/4	0.96	0.24	58,58,60,61	0
5	DMS	B	8002	4/4	0.96	0.25	48,50,53,54	0
5	DMS	B	8004	4/4	0.96	0.23	50,53,57,57	0
5	DMS	B	8010	4/4	0.96	0.21	62,63,64,66	0
5	DMS	D	8004	4/4	0.96	0.20	60,60,61,62	0
5	DMS	B	8006	4/4	0.96	0.25	68,69,69,69	0
2	IPT	A	2001	15/15	0.96	0.12	37,44,50,52	0
5	DMS	A	8004	4/4	0.96	0.18	57,59,60,63	0
5	DMS	C	8004	4/4	0.96	0.23	63,63,64,66	0
5	DMS	C	8005	4/4	0.96	0.20	55,56,57,57	0
5	DMS	D	8005	4/4	0.97	0.28	48,48,52,55	0
5	DMS	D	8002	4/4	0.97	0.29	56,59,59,61	0
3	MG	A	3002	1/1	0.97	0.08	43,43,43,43	0
5	DMS	D	8008	4/4	0.97	0.20	55,56,58,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	DMS	B	8005	4/4	0.97	0.19	57,57,58,59	0
5	DMS	C	8009	4/4	0.97	0.20	61,62,63,66	0
3	MG	D	3002	1/1	0.97	0.12	45,45,45,45	0
3	MG	B	3001	1/1	0.97	0.08	46,46,46,46	0
3	MG	C	3001	1/1	0.97	0.09	52,52,52,52	0
2	IPT	D	2001	15/15	0.97	0.12	37,44,52,53	0
4	NA	B	3101	1/1	0.97	0.17	51,51,51,51	0
5	DMS	C	8001	4/4	0.97	0.21	38,43,44,46	0
5	DMS	A	8001	4/4	0.98	0.19	31,34,35,37	0
5	DMS	D	8001	4/4	0.98	0.23	39,41,42,43	0
3	MG	C	3002	1/1	0.98	0.14	49,49,49,49	0
5	DMS	C	8002	4/4	0.98	0.19	42,45,46,47	0
5	DMS	A	8005	4/4	0.98	0.20	53,54,57,58	0
5	DMS	B	8001	4/4	0.98	0.22	36,37,39,39	0
4	NA	D	3102	1/1	0.98	0.08	30,30,30,30	0
5	DMS	D	8003	4/4	0.98	0.27	44,46,47,48	0
5	DMS	A	8002	4/4	0.98	0.20	51,52,53,53	0
5	DMS	D	8010	4/4	0.98	0.23	57,58,58,60	0
5	DMS	A	8003	4/4	0.98	0.22	43,44,46,51	0
5	DMS	B	8003	4/4	0.98	0.23	48,50,51,51	0
4	NA	A	3101	1/1	0.98	0.16	52,52,52,52	0
4	NA	B	3104	1/1	0.98	0.12	47,47,47,47	0
5	DMS	B	8008	4/4	0.98	0.16	71,71,72,73	0
4	NA	B	3102	1/1	0.99	0.10	31,31,31,31	0
4	NA	A	3102	1/1	0.99	0.12	30,30,30,30	0
5	DMS	C	8003	4/4	0.99	0.16	42,44,45,46	0
4	NA	C	3102	1/1	0.99	0.15	33,33,33,33	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.