



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 02:41 PM UTC

PDB ID : 4UDK / pdb_00004udk
Title : Crystal structure of b-1,4-mannopyranosyl-chitobiose phosphorylase at 1.76 Angstrom from unknown human gut bacteria (Uhgb_MP) in complex with N-acetyl-D-glucosamine, beta-D-mannopyranose and inorganic phosphate
Authors : Ladeveze, S.; Cioci, G.; Potocki-Veronese, G.; Tranier, S.; Mourey, L.
Deposited on : 2014-12-10
Resolution : 1.76 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

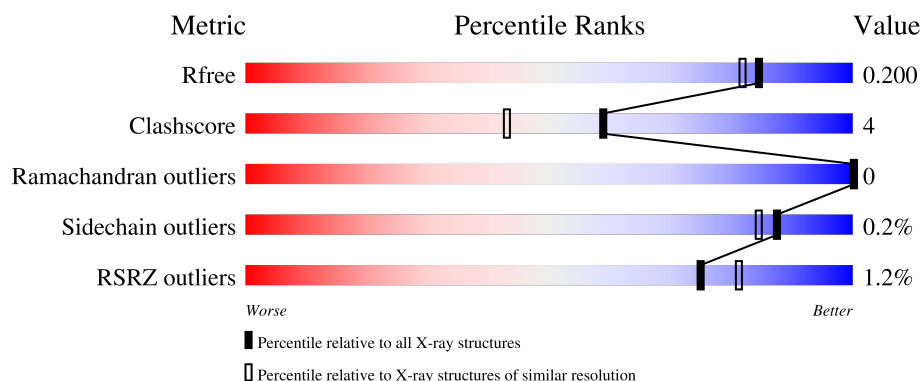
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.76 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	347	84% 8% 8%
1	B	347	81% 11% 8%
1	C	347	83% 9% 8%
1	D	347	83% 9% 8%
1	F	347	82% 9% 8%

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Mol	Chain	Length	Quality of chain
2	E	347	% 84% 8% 7%

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
4	BMA	A	329	-	-	X	-
4	BMA	D	329	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 17398 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 UHGB_MP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	0	11	0
			2648	1710	445	476	17			
1	B	320	Total	C	N	O	S	0	15	0
			2686	1734	449	486	17			
1	C	319	Total	C	N	O	S	0	10	0
			2628	1699	437	475	17			
1	D	320	Total	C	N	O	S	0	14	0
			2679	1725	451	486	17			
1	F	320	Total	C	N	O	S	0	12	0
			2657	1713	447	480	17			

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP D9ZDQ9
A	-18	GLY	-	expression tag	UNP D9ZDQ9
A	-17	SER	-	expression tag	UNP D9ZDQ9
A	-16	SER	-	expression tag	UNP D9ZDQ9
A	-15	HIS	-	expression tag	UNP D9ZDQ9
A	-14	HIS	-	expression tag	UNP D9ZDQ9
A	-13	HIS	-	expression tag	UNP D9ZDQ9
A	-12	HIS	-	expression tag	UNP D9ZDQ9
A	-11	HIS	-	expression tag	UNP D9ZDQ9
A	-10	HIS	-	expression tag	UNP D9ZDQ9
A	-9	SER	-	expression tag	UNP D9ZDQ9
A	-8	SER	-	expression tag	UNP D9ZDQ9
A	-7	GLY	-	expression tag	UNP D9ZDQ9
A	-6	LEU	-	expression tag	UNP D9ZDQ9
A	-5	VAL	-	expression tag	UNP D9ZDQ9
A	-4	PRO	-	expression tag	UNP D9ZDQ9
A	-3	ARG	-	expression tag	UNP D9ZDQ9
A	-2	GLY	-	expression tag	UNP D9ZDQ9
A	-1	SER	-	expression tag	UNP D9ZDQ9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	expression tag	UNP D9ZDQ9
B	-19	MET	-	expression tag	UNP D9ZDQ9
B	-18	GLY	-	expression tag	UNP D9ZDQ9
B	-17	SER	-	expression tag	UNP D9ZDQ9
B	-16	SER	-	expression tag	UNP D9ZDQ9
B	-15	HIS	-	expression tag	UNP D9ZDQ9
B	-14	HIS	-	expression tag	UNP D9ZDQ9
B	-13	HIS	-	expression tag	UNP D9ZDQ9
B	-12	HIS	-	expression tag	UNP D9ZDQ9
B	-11	HIS	-	expression tag	UNP D9ZDQ9
B	-10	HIS	-	expression tag	UNP D9ZDQ9
B	-9	SER	-	expression tag	UNP D9ZDQ9
B	-8	SER	-	expression tag	UNP D9ZDQ9
B	-7	GLY	-	expression tag	UNP D9ZDQ9
B	-6	LEU	-	expression tag	UNP D9ZDQ9
B	-5	VAL	-	expression tag	UNP D9ZDQ9
B	-4	PRO	-	expression tag	UNP D9ZDQ9
B	-3	ARG	-	expression tag	UNP D9ZDQ9
B	-2	GLY	-	expression tag	UNP D9ZDQ9
B	-1	SER	-	expression tag	UNP D9ZDQ9
B	0	HIS	-	expression tag	UNP D9ZDQ9
C	-19	MET	-	expression tag	UNP D9ZDQ9
C	-18	GLY	-	expression tag	UNP D9ZDQ9
C	-17	SER	-	expression tag	UNP D9ZDQ9
C	-16	SER	-	expression tag	UNP D9ZDQ9
C	-15	HIS	-	expression tag	UNP D9ZDQ9
C	-14	HIS	-	expression tag	UNP D9ZDQ9
C	-13	HIS	-	expression tag	UNP D9ZDQ9
C	-12	HIS	-	expression tag	UNP D9ZDQ9
C	-11	HIS	-	expression tag	UNP D9ZDQ9
C	-10	HIS	-	expression tag	UNP D9ZDQ9
C	-9	SER	-	expression tag	UNP D9ZDQ9
C	-8	SER	-	expression tag	UNP D9ZDQ9
C	-7	GLY	-	expression tag	UNP D9ZDQ9
C	-6	LEU	-	expression tag	UNP D9ZDQ9
C	-5	VAL	-	expression tag	UNP D9ZDQ9
C	-4	PRO	-	expression tag	UNP D9ZDQ9
C	-3	ARG	-	expression tag	UNP D9ZDQ9
C	-2	GLY	-	expression tag	UNP D9ZDQ9
C	-1	SER	-	expression tag	UNP D9ZDQ9
C	0	HIS	-	expression tag	UNP D9ZDQ9
D	-19	MET	-	expression tag	UNP D9ZDQ9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-18	GLY	-	expression tag	UNP D9ZDQ9
D	-17	SER	-	expression tag	UNP D9ZDQ9
D	-16	SER	-	expression tag	UNP D9ZDQ9
D	-15	HIS	-	expression tag	UNP D9ZDQ9
D	-14	HIS	-	expression tag	UNP D9ZDQ9
D	-13	HIS	-	expression tag	UNP D9ZDQ9
D	-12	HIS	-	expression tag	UNP D9ZDQ9
D	-11	HIS	-	expression tag	UNP D9ZDQ9
D	-10	HIS	-	expression tag	UNP D9ZDQ9
D	-9	SER	-	expression tag	UNP D9ZDQ9
D	-8	SER	-	expression tag	UNP D9ZDQ9
D	-7	GLY	-	expression tag	UNP D9ZDQ9
D	-6	LEU	-	expression tag	UNP D9ZDQ9
D	-5	VAL	-	expression tag	UNP D9ZDQ9
D	-4	PRO	-	expression tag	UNP D9ZDQ9
D	-3	ARG	-	expression tag	UNP D9ZDQ9
D	-2	GLY	-	expression tag	UNP D9ZDQ9
D	-1	SER	-	expression tag	UNP D9ZDQ9
D	0	HIS	-	expression tag	UNP D9ZDQ9
F	-19	MET	-	expression tag	UNP D9ZDQ9
F	-18	GLY	-	expression tag	UNP D9ZDQ9
F	-17	SER	-	expression tag	UNP D9ZDQ9
F	-16	SER	-	expression tag	UNP D9ZDQ9
F	-15	HIS	-	expression tag	UNP D9ZDQ9
F	-14	HIS	-	expression tag	UNP D9ZDQ9
F	-13	HIS	-	expression tag	UNP D9ZDQ9
F	-12	HIS	-	expression tag	UNP D9ZDQ9
F	-11	HIS	-	expression tag	UNP D9ZDQ9
F	-10	HIS	-	expression tag	UNP D9ZDQ9
F	-9	SER	-	expression tag	UNP D9ZDQ9
F	-8	SER	-	expression tag	UNP D9ZDQ9
F	-7	GLY	-	expression tag	UNP D9ZDQ9
F	-6	LEU	-	expression tag	UNP D9ZDQ9
F	-5	VAL	-	expression tag	UNP D9ZDQ9
F	-4	PRO	-	expression tag	UNP D9ZDQ9
F	-3	ARG	-	expression tag	UNP D9ZDQ9
F	-2	GLY	-	expression tag	UNP D9ZDQ9
F	-1	SER	-	expression tag	UNP D9ZDQ9
F	0	HIS	-	expression tag	UNP D9ZDQ9

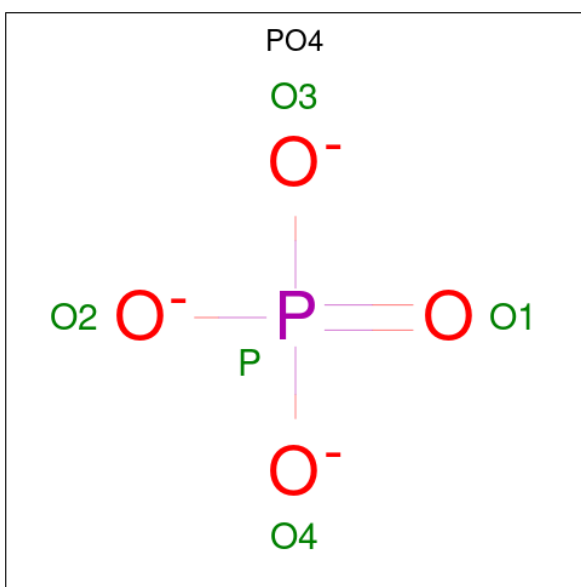
- Molecule 2 is a protein called UHGB_MP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	321	Total	C	N	O	S	0	8	0
			2636	1701	441	477	17			

There are 21 discrepancies between the modelled and reference sequences:

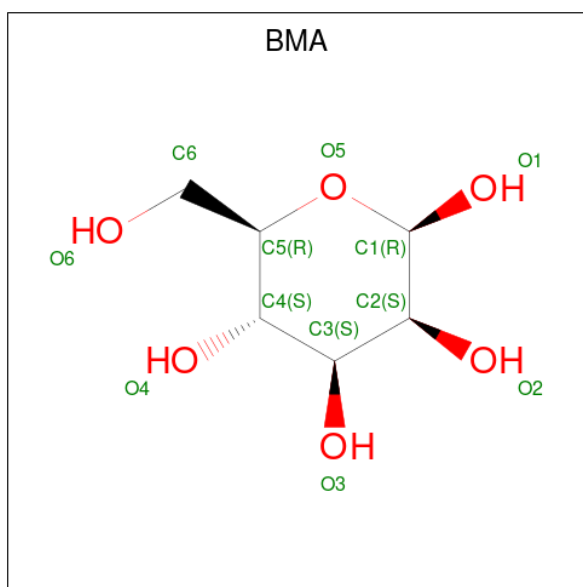
Chain	Residue	Modelled	Actual	Comment	Reference
E	-19	MET	-	expression tag	UNP D9ZDQ9
E	-18	GLY	-	expression tag	UNP D9ZDQ9
E	-17	SER	-	expression tag	UNP D9ZDQ9
E	-16	SER	-	expression tag	UNP D9ZDQ9
E	-15	HIS	-	expression tag	UNP D9ZDQ9
E	-14	HIS	-	expression tag	UNP D9ZDQ9
E	-13	HIS	-	expression tag	UNP D9ZDQ9
E	-12	HIS	-	expression tag	UNP D9ZDQ9
E	-11	HIS	-	expression tag	UNP D9ZDQ9
E	-10	HIS	-	expression tag	UNP D9ZDQ9
E	-9	SER	-	expression tag	UNP D9ZDQ9
E	-8	SER	-	expression tag	UNP D9ZDQ9
E	-7	GLY	-	expression tag	UNP D9ZDQ9
E	-6	LEU	-	expression tag	UNP D9ZDQ9
E	-5	VAL	-	expression tag	UNP D9ZDQ9
E	-4	PRO	-	expression tag	UNP D9ZDQ9
E	-3	ARG	-	expression tag	UNP D9ZDQ9
E	-2	GLY	-	expression tag	UNP D9ZDQ9
E	-1	SER	-	expression tag	UNP D9ZDQ9
E	0	HIS	-	expression tag	UNP D9ZDQ9
E	7	ILE	VAL	conflict	UNP D9ZDQ9

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



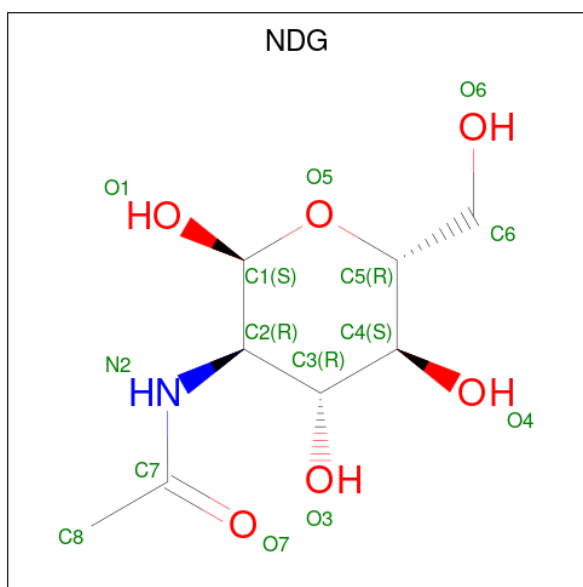
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	E	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is beta-D-mannopyranose (CCD ID: BMA) (formula: C₆H₁₂O₆).



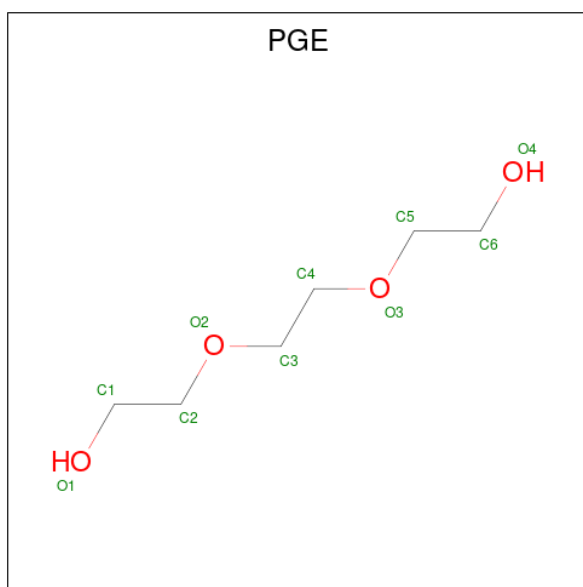
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	6	6		
4	B	1	Total	C	O	0	0
			12	6	6		
4	C	1	Total	C	O	0	0
			12	6	6		
4	D	1	Total	C	O	0	0
			12	6	6		
4	E	1	Total	C	O	0	0
			12	6	6		
4	F	1	Total	C	O	0	0
			12	6	6		

- Molecule 5 is 2-acetamido-2-deoxy-alpha-D-glucopyranose (CCD ID: NDG) (formula: $C_8H_{15}NO_6$).



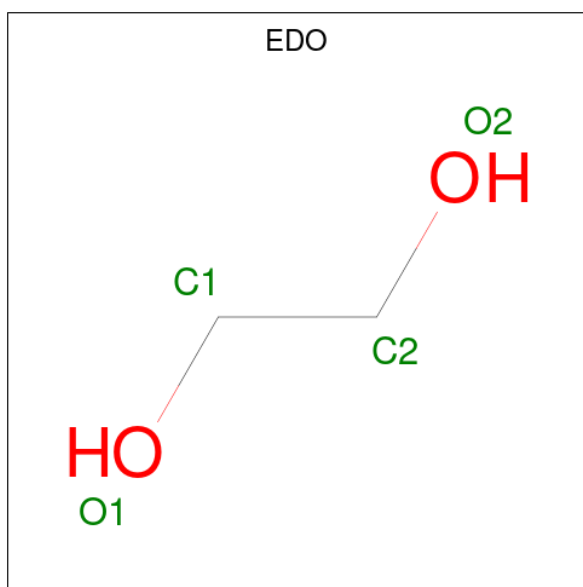
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			15	8	1	6		
5	B	1	Total	C	N	O	0	0
			15	8	1	6		
5	C	1	Total	C	N	O	0	0
			15	8	1	6		
5	D	1	Total	C	N	O	0	0
			15	8	1	6		
5	E	1	Total	C	N	O	0	0
			15	8	1	6		
5	F	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 6 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			10	6	4		
6	D	1	Total	C	O	0	0
			10	6	4		
6	E	1	Total	C	O	0	0
			10	6	4		

- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

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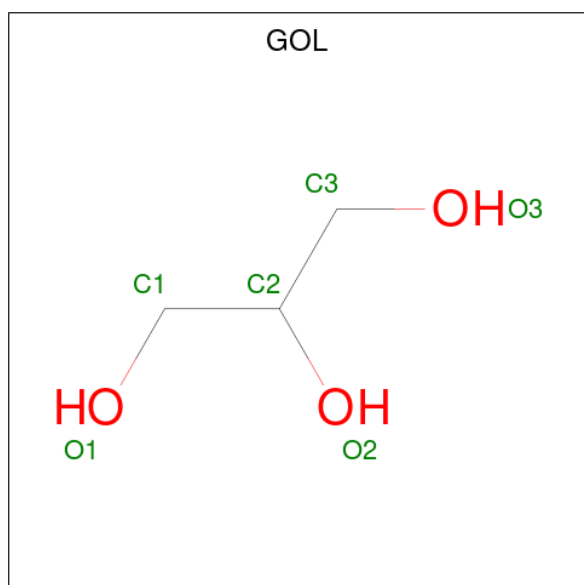
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	D	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	F	1	Total C O 4 2 2	0	0
7	F	1	Total C O 4 2 2	0	0

- Molecule 8 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total K 1 1	0	0
8	B	1	Total K 1 1	0	0
8	C	1	Total K 1 1	0	0
8	D	1	Total K 1 1	0	0
8	E	1	Total K 1 1	0	0
8	F	1	Total K 1 1	0	0

- Molecule 9 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

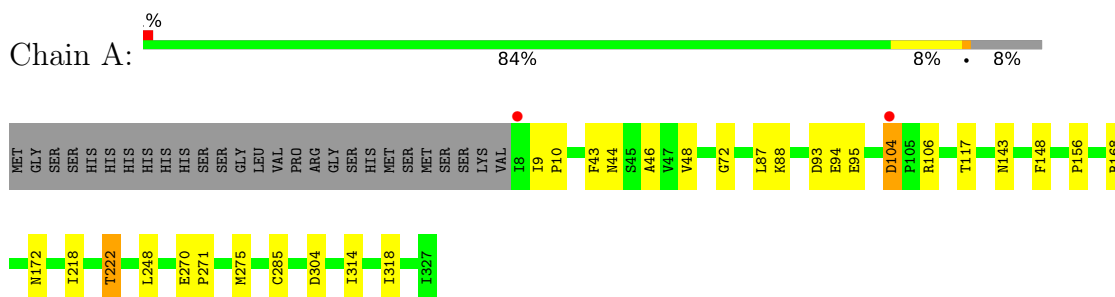
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	238	Total	O	0	0
			238	238		
10	B	226	Total	O	0	0
			226	226		
10	C	218	Total	O	0	0
			218	218		
10	D	181	Total	O	0	0
			181	181		
10	E	188	Total	O	0	0
			188	188		
10	F	153	Total	O	0	0
			153	153		

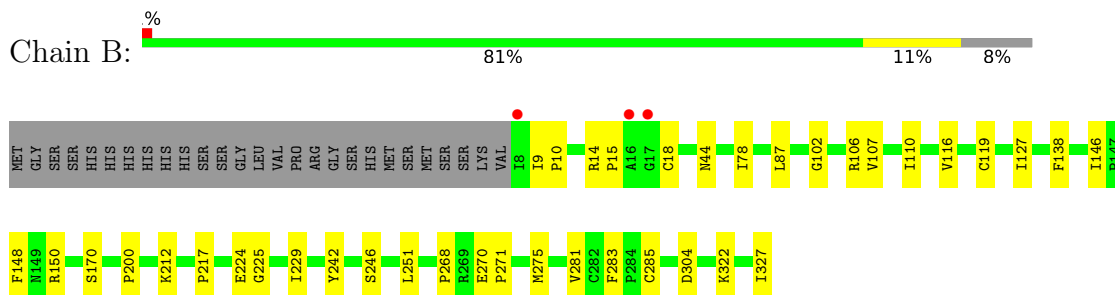
3 Residue-property plots [i](#)

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.

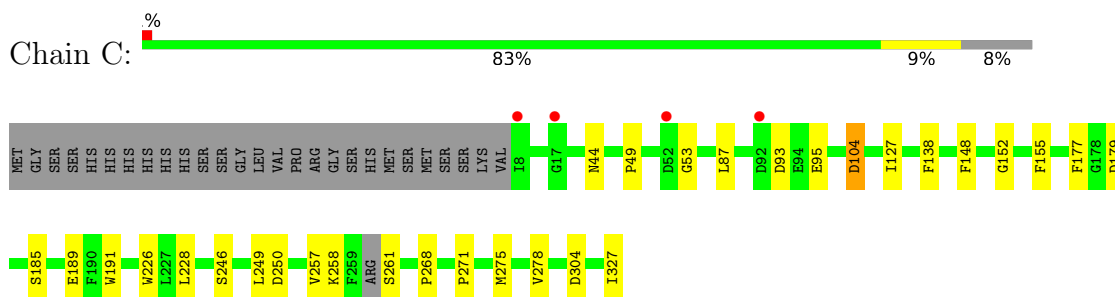
• Molecule 1: UHGB_MP



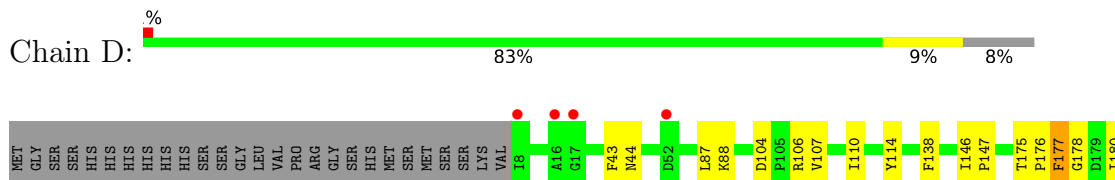
• Molecule 1: UHGB_MP

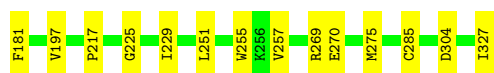


• Molecule 1: UHGB_MP

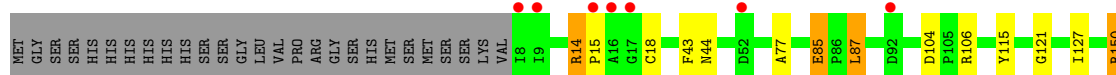
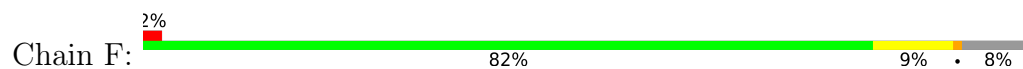


• Molecule 1: UHGB_MP

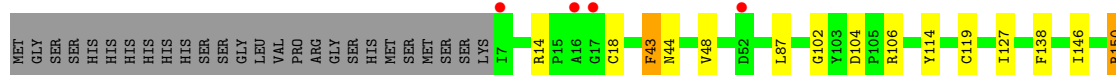
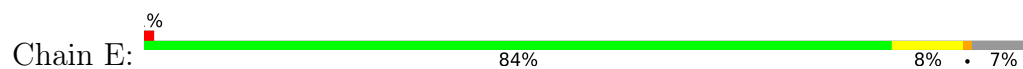




• Molecule 1: UHGB_MP



• Molecule 2: UHGB_MP



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.74Å 140.89Å 168.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	108.17 – 1.76 108.17 – 1.76	Depositor EDS
% Data completeness (in resolution range)	99.6 (108.17-1.76) 99.9 (108.17-1.76)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 1.76Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.158 , 0.192 0.171 , 0.200	Depositor DCC
R_{free} test set	9956 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	19.5	Xtriage
Anisotropy	0.097	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 34.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	17398	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, PO4, NDG, K, PGE, BMA, EDO

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	1.24	13/2741 (0.5%)	1.07	5/3736 (0.1%)
1	B	1.20	7/2776 (0.3%)	1.01	3/3785 (0.1%)
1	C	1.25	11/2717 (0.4%)	1.01	0/3703
1	D	1.14	8/2769 (0.3%)	1.00	0/3772
1	F	1.15	6/2747 (0.2%)	1.03	5/3744 (0.1%)
2	E	1.18	7/2726 (0.3%)	1.06	4/3716 (0.1%)
All	All	1.19	52/16476 (0.3%)	1.03	17/22456 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

The worst 5 of 52 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	222	THR	N-CA	8.21	1.51	1.46
1	C	53	GLY	C-O	-7.87	1.17	1.24
1	C	104[A]	ASP	C-O	-6.96	1.15	1.24
1	C	104[B]	ASP	C-O	-6.96	1.15	1.24
1	A	156	PRO	CA-C	6.48	1.58	1.52

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	46[A]	ALA	N-CA-C	6.32	120.90	107.70
1	A	46[B]	ALA	N-CA-C	6.32	120.90	107.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	314	ILE	CA-C-N	-6.20	112.62	119.19
1	A	314	ILE	C-N-CA	-6.20	112.62	119.19
2	E	150	ARG	CG-CD-NE	-6.13	98.51	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	104[B]	ASP	Mainchain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2648	0	2503	20	0
1	B	2686	0	2541	26	0
1	C	2628	0	2476	19	0
1	D	2679	0	2518	27	0
1	F	2657	0	2498	30	0
2	E	2636	0	2482	21	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
4	A	12	0	12	6	0
4	B	12	0	10	2	0
4	C	12	0	12	5	0
4	D	12	0	12	6	0
4	E	12	0	12	2	0
4	F	12	0	12	5	0
5	A	15	0	12	1	0
5	B	15	0	11	1	0
5	C	15	0	12	0	0
5	D	15	0	12	0	0
5	E	15	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	15	0	12	1	0
6	A	10	0	14	0	0
6	D	10	0	14	0	0
6	E	10	0	14	2	0
7	A	4	0	6	0	0
7	D	4	0	6	0	0
7	E	4	0	6	0	0
7	F	8	0	12	2	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
8	C	1	0	0	0	0
8	D	1	0	0	0	0
8	E	1	0	0	0	0
8	F	1	0	0	0	0
9	B	6	0	8	0	0
9	C	6	0	8	0	0
10	A	238	0	0	2	0
10	B	226	0	0	1	0
10	C	218	0	0	1	0
10	D	181	0	0	0	0
10	E	188	0	0	0	0
10	F	153	0	0	2	0
All	All	17398	0	15247	140	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 140 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)
2:E:44[A]:ASN:ND2	2:E:104[A]:ASP:HA	1.75	1.01
2:E:44[A]:ASN:ND2	2:E:104[A]:ASP:OD1	1.98	0.95
2:E:44[A]:ASN:HD22	2:E:104[A]:ASP:HA	1.31	0.92
1:D:44[A]:ASN:ND2	1:D:104[A]:ASP:HA	1.87	0.88
1:F:44[A]:ASN:HD22	1:F:104[A]:ASP:HA	1.38	0.88

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	329/347 (95%)	314 (95%)	15 (5%)	0	100	100
1	B	333/347 (96%)	317 (95%)	16 (5%)	0	100	100
1	C	324/347 (93%)	309 (95%)	15 (5%)	0	100	100
1	D	332/347 (96%)	315 (95%)	17 (5%)	0	100	100
1	F	330/347 (95%)	316 (96%)	14 (4%)	0	100	100
2	E	327/347 (94%)	308 (94%)	19 (6%)	0	100	100
All	All	1975/2082 (95%)	1879 (95%)	96 (5%)	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	282/298 (95%)	281 (100%)	1 (0%)	84	80
1	B	288/298 (97%)	288 (100%)	0	100	100
1	C	280/298 (94%)	280 (100%)	0	100	100
1	D	285/298 (96%)	285 (100%)	0	100	100
1	F	282/298 (95%)	280 (99%)	2 (1%)	76	67
2	E	280/298 (94%)	279 (100%)	1 (0%)	84	80
All	All	1697/1788 (95%)	1693 (100%)	4 (0%)	87	84

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	GLU
2	E	309	LEU
1	F	85	GLU
1	F	87	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	151	ASN
2	E	172	ASN
1	F	172	ASN
1	F	40	ASN
1	F	151	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 34 ligands modelled in this entry, 6 are monoatomic - leaving 28 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
7	EDO	A	332	-	3,3,3	0.18	0	2,2,2	0.90	0
4	BMA	C	329	-	12,12,12	1.47	1 (8%)	17,17,17	3.68	9 (52%)
6	PGE	E	331	-	9,9,9	0.70	0	8,8,8	1.29	1 (12%)
3	PO4	E	328	-	4,4,4	1.03	0	6,6,6	1.00	0
7	EDO	F	331	-	3,3,3	0.40	0	2,2,2	0.34	0
5	NDG	B	330	-	15,15,15	0.86	1 (6%)	21,21,21	1.78	8 (38%)
3	PO4	A	328	-	4,4,4	1.35	1 (25%)	6,6,6	0.63	0
3	PO4	D	328	-	4,4,4	0.48	0	6,6,6	1.10	0
3	PO4	F	328	-	4,4,4	0.63	0	6,6,6	0.61	0
4	BMA	F	329	-	12,12,12	1.09	1 (8%)	17,17,17	3.25	9 (52%)
4	BMA	A	329	-	12,12,12	1.42	1 (8%)	17,17,17	3.98	8 (47%)
3	PO4	C	328	-	4,4,4	1.75	1 (25%)	6,6,6	0.97	0
7	EDO	D	332	-	3,3,3	0.56	0	2,2,2	0.25	0
4	BMA	D	329	-	12,12,12	1.29	1 (8%)	17,17,17	3.74	8 (47%)
5	NDG	F	330	-	15,15,15	0.76	0	21,21,21	1.43	5 (23%)
7	EDO	E	569	-	3,3,3	0.17	0	2,2,2	0.75	0
5	NDG	C	330	-	15,15,15	1.19	1 (6%)	21,21,21	1.53	4 (19%)
5	NDG	A	330	-	15,15,15	1.01	1 (6%)	21,21,21	1.95	5 (23%)
6	PGE	A	331	-	9,9,9	0.50	0	8,8,8	0.78	0
4	BMA	E	329	-	12,12,12	1.04	1 (8%)	17,17,17	3.69	9 (52%)
5	NDG	E	330	-	15,15,15	0.79	0	21,21,21	1.36	3 (14%)
7	EDO	F	569	-	3,3,3	0.32	0	2,2,2	0.51	0
3	PO4	B	328	-	4,4,4	1.17	0	6,6,6	1.13	1 (16%)
9	GOL	C	331	-	5,5,5	0.85	0	5,5,5	1.66	2 (40%)
6	PGE	D	331	-	9,9,9	0.38	0	8,8,8	0.79	0
5	NDG	D	330	-	15,15,15	0.73	0	21,21,21	1.81	4 (19%)
9	GOL	B	331	-	5,5,5	0.28	0	5,5,5	0.42	0
4	BMA	B	329	-	12,12,12	1.13	1 (8%)	17,17,17	2.88	9 (52%)

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
7	EDO	A	332	-	-	1/1/1/1	-
4	BMA	C	329	-	-	2/2/22/22	0/1/1/1
6	PGE	E	331	-	-	3/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EDO	F	331	-	-	1/1/1/1	-
4	BMA	B	329	-	-	2/2/22/22	0/1/1/1
5	NDG	B	330	-	-	0/6/26/26	0/1/1/1
4	BMA	F	329	-	-	2/2/22/22	0/1/1/1
4	BMA	A	329	-	-	2/2/22/22	0/1/1/1
7	EDO	D	332	-	-	1/1/1/1	-
4	BMA	D	329	-	-	2/2/22/22	0/1/1/1
5	NDG	F	330	-	-	0/6/26/26	0/1/1/1
7	EDO	E	569	-	-	1/1/1/1	-
5	NDG	C	330	-	-	0/6/26/26	0/1/1/1
5	NDG	A	330	-	-	0/6/26/26	0/1/1/1
6	PGE	A	331	-	-	5/7/7/7	-
4	BMA	E	329	-	-	2/2/22/22	0/1/1/1
5	NDG	E	330	-	-	0/6/26/26	0/1/1/1
7	EDO	F	569	-	-	1/1/1/1	-
9	GOL	C	331	-	-	3/4/4/4	-
6	PGE	D	331	-	-	2/7/7/7	-
9	GOL	B	331	-	-	2/4/4/4	-
5	NDG	D	330	-	-	0/6/26/26	0/1/1/1

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	329	BMA	C1-C2	3.60	1.60	1.52
4	C	329	BMA	C1-C2	3.55	1.60	1.52
5	C	330	NDG	O7-C7	-3.34	1.15	1.23
5	A	330	NDG	O7-C7	-3.26	1.16	1.23
4	D	329	BMA	C1-C2	3.07	1.59	1.52

The worst 5 of 85 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	329	BMA	O2-C2-C1	7.38	126.28	109.25
4	A	329	BMA	O1-C1-C2	7.37	130.38	108.98
4	C	329	BMA	O2-C2-C1	7.24	125.97	109.25
4	D	329	BMA	C1-O5-C5	7.15	127.49	113.65
4	C	329	BMA	O1-C1-C2	7.09	129.55	108.98

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	B	331	GOL	O1-C1-C2-O2
9	B	331	GOL	O1-C1-C2-C3
9	C	331	GOL	C1-C2-C3-O3
4	F	329	BMA	O5-C5-C6-O6
4	A	329	BMA	O5-C5-C6-O6

There are no ring outliers.

11 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	329	BMA	5	0
6	E	331	PGE	2	0
7	F	331	EDO	2	0
5	B	330	NDG	1	0
4	F	329	BMA	5	0
4	A	329	BMA	6	0
4	D	329	BMA	6	0
5	F	330	NDG	1	0
5	A	330	NDG	1	0
4	E	329	BMA	2	0
4	B	329	BMA	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	103:TYR	C	104[B]:ASP	N	0.51

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	320/347 (92%)	-0.39	2 (0%) 85 89	7, 16, 30, 47	11 (3%)
1	B	320/347 (92%)	-0.37	3 (0%) 81 86	6, 17, 30, 51	15 (4%)
1	C	319/347 (91%)	-0.39	4 (1%) 75 81	6, 17, 32, 52	10 (3%)
1	D	320/347 (92%)	-0.21	4 (1%) 75 81	8, 20, 34, 47	14 (4%)
1	F	320/347 (92%)	-0.08	7 (2%) 62 69	8, 22, 38, 53	12 (3%)
2	E	321/347 (92%)	-0.20	4 (1%) 76 82	8, 19, 33, 47	8 (2%)
All	All	1920/2082 (92%)	-0.27	24 (1%) 75 81	6, 19, 34, 53	70 (3%)

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	8	ILE	4.5
1	C	8	ILE	4.0
1	F	8	ILE	3.7
1	A	8	ILE	3.5
1	B	16	ALA	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 oligosaccharides 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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BMA	D	329	12/12	0.75	0.20	23,28,33,34	12
4	BMA	A	329	12/12	0.76	0.21	19,26,31,34	12
4	BMA	B	329	12/12	0.78	0.17	31,50,62,62	0
4	BMA	E	329	12/12	0.78	0.20	21,27,29,31	12
4	BMA	C	329	12/12	0.79	0.23	22,30,34,37	12
4	BMA	F	329	12/12	0.79	0.22	25,31,35,39	12
9	GOL	C	331	6/6	0.79	0.18	39,41,46,47	0
7	EDO	D	332	4/4	0.80	0.17	50,54,55,57	0
6	PGE	A	331	10/10	0.81	0.15	38,44,47,47	0
7	EDO	F	331	4/4	0.82	0.17	40,45,47,53	0
9	GOL	B	331	6/6	0.84	0.15	42,45,47,53	0
7	EDO	A	332	4/4	0.86	0.17	38,39,42,45	0
6	PGE	D	331	10/10	0.87	0.13	43,46,61,62	0
7	EDO	F	569	4/4	0.88	0.15	41,42,42,46	0
7	EDO	E	569	4/4	0.88	0.14	41,41,41,45	0
6	PGE	E	331	10/10	0.88	0.13	35,42,47,49	0
5	NDG	B	330	15/15	0.89	0.11	27,30,32,32	0
5	NDG	F	330	15/15	0.90	0.10	21,26,27,27	0
5	NDG	A	330	15/15	0.91	0.09	21,24,27,27	0
5	NDG	E	330	15/15	0.92	0.08	20,23,25,26	0
8	K	B	333	1/1	0.92	0.31	58,58,58,58	0
5	NDG	C	330	15/15	0.92	0.08	21,23,25,25	0
5	NDG	D	330	15/15	0.92	0.08	23,26,27,28	0
8	K	C	333	1/1	0.93	0.31	54,54,54,54	0
8	K	A	333	1/1	0.94	0.30	56,56,56,56	0
8	K	F	333	1/1	0.94	0.34	62,62,62,62	0
8	K	E	333	1/1	0.95	0.27	49,49,49,49	0
8	K	D	333	1/1	0.97	0.21	59,59,59,59	0
3	PO4	B	328	5/5	0.99	0.03	14,14,15,18	0
3	PO4	C	328	5/5	0.99	0.02	13,14,15,16	0
3	PO4	E	328	5/5	0.99	0.03	14,16,17,17	0
3	PO4	F	328	5/5	0.99	0.03	16,16,17,20	0
3	PO4	A	328	5/5	1.00	0.02	13,13,14,15	0
3	PO4	D	328	5/5	1.00	0.03	16,17,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.