



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 20, 2025 – 10:09 AM EDT

PDB ID : 9OMH / pdb\_00009omh  
Title : WrtF fucosyltransferase - Apo  
Authors : Forrester, T.J.B.; Kimber, M.S.  
Deposited on : 2025-05-14  
Resolution : 1.45 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.

The types of validation reports are described at

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

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

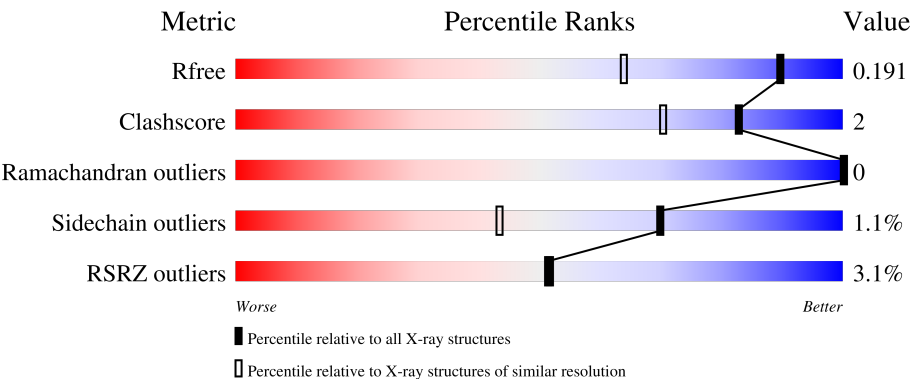
MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.46

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.45 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))
$R_{free}$	164625	1556 (1.46-1.46)
Clashscore	180529	1653 (1.46-1.46)
Ramachandran outliers	177936	1635 (1.46-1.46)
Sidechain outliers	177891	1635 (1.46-1.46)
RSRZ outliers	164620	1556 (1.46-1.46)

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  $\geq 3$ , 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	279	<div><div>%</div><div>94%</div><div>.</div><div>.</div></div>
1	B	279	<div><div>5%</div><div>87%</div><div>8%</div><div>5%</div></div>
1	C	279	<div><div>3%</div><div>87%</div><div>5%</div><div>7%</div></div>
1	D	279	<div><div>3%</div><div>93%</div><div>.</div><div>.</div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17442 atoms, of which 8186 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 Glycosyltransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	271	Total	C	H	N	O	S	0	0	0
			4167	1328	2072	358	403	6			
1	B	266	Total	C	H	N	O	S	0	0	0
			4088	1301	2039	347	395	6			
1	C	260	Total	C	H	N	O	S	0	0	0
			3998	1272	1995	337	388	6			
1	D	269	Total	C	H	N	O	S	0	0	0
			4139	1319	2060	356	398	6			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP A0A6P1C6J0
A	1	GLY	-	expression tag	UNP A0A6P1C6J0
A	268	ALA	-	expression tag	UNP A0A6P1C6J0
A	269	ALA	-	expression tag	UNP A0A6P1C6J0
A	270	ALA	-	expression tag	UNP A0A6P1C6J0
A	271	LEU	-	expression tag	UNP A0A6P1C6J0
A	272	GLU	-	expression tag	UNP A0A6P1C6J0
A	273	HIS	-	expression tag	UNP A0A6P1C6J0
A	274	HIS	-	expression tag	UNP A0A6P1C6J0
A	275	HIS	-	expression tag	UNP A0A6P1C6J0
A	276	HIS	-	expression tag	UNP A0A6P1C6J0
A	277	HIS	-	expression tag	UNP A0A6P1C6J0
A	278	HIS	-	expression tag	UNP A0A6P1C6J0
B	0	MET	-	expression tag	UNP A0A6P1C6J0
B	1	GLY	-	expression tag	UNP A0A6P1C6J0
B	268	ALA	-	expression tag	UNP A0A6P1C6J0
B	269	ALA	-	expression tag	UNP A0A6P1C6J0
B	270	ALA	-	expression tag	UNP A0A6P1C6J0
B	271	LEU	-	expression tag	UNP A0A6P1C6J0
B	272	GLU	-	expression tag	UNP A0A6P1C6J0
B	273	HIS	-	expression tag	UNP A0A6P1C6J0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	274	HIS	-	expression tag	UNP A0A6P1C6J0
B	275	HIS	-	expression tag	UNP A0A6P1C6J0
B	276	HIS	-	expression tag	UNP A0A6P1C6J0
B	277	HIS	-	expression tag	UNP A0A6P1C6J0
B	278	HIS	-	expression tag	UNP A0A6P1C6J0
C	0	MET	-	expression tag	UNP A0A6P1C6J0
C	1	GLY	-	expression tag	UNP A0A6P1C6J0
C	268	ALA	-	expression tag	UNP A0A6P1C6J0
C	269	ALA	-	expression tag	UNP A0A6P1C6J0
C	270	ALA	-	expression tag	UNP A0A6P1C6J0
C	271	LEU	-	expression tag	UNP A0A6P1C6J0
C	272	GLU	-	expression tag	UNP A0A6P1C6J0
C	273	HIS	-	expression tag	UNP A0A6P1C6J0
C	274	HIS	-	expression tag	UNP A0A6P1C6J0
C	275	HIS	-	expression tag	UNP A0A6P1C6J0
C	276	HIS	-	expression tag	UNP A0A6P1C6J0
C	277	HIS	-	expression tag	UNP A0A6P1C6J0
C	278	HIS	-	expression tag	UNP A0A6P1C6J0
D	0	MET	-	expression tag	UNP A0A6P1C6J0
D	1	GLY	-	expression tag	UNP A0A6P1C6J0
D	268	ALA	-	expression tag	UNP A0A6P1C6J0
D	269	ALA	-	expression tag	UNP A0A6P1C6J0
D	270	ALA	-	expression tag	UNP A0A6P1C6J0
D	271	LEU	-	expression tag	UNP A0A6P1C6J0
D	272	GLU	-	expression tag	UNP A0A6P1C6J0
D	273	HIS	-	expression tag	UNP A0A6P1C6J0
D	274	HIS	-	expression tag	UNP A0A6P1C6J0
D	275	HIS	-	expression tag	UNP A0A6P1C6J0
D	276	HIS	-	expression tag	UNP A0A6P1C6J0
D	277	HIS	-	expression tag	UNP A0A6P1C6J0
D	278	HIS	-	expression tag	UNP A0A6P1C6J0

- Molecule 2 is IMIDAZOLE (CCD ID: IMD) (formula:  $C_3H_5N_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	N	0	0
			10	3	5	2		
2	B	1	Total	C	H	N	0	0
			10	3	5	2		
2	C	1	Total	C	H	N	0	0
			10	3	5	2		
2	D	1	Total	C	H	N	0	0
			10	3	5	2		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Cl	0	0
			2	2		

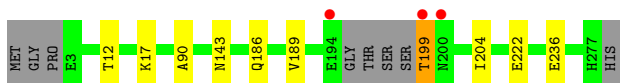
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	323	Total	O	0	0
			323	323		
4	B	215	Total	O	0	0
			215	215		
4	C	226	Total	O	0	0
			226	226		
4	D	244	Total	O	0	0
			244	244		

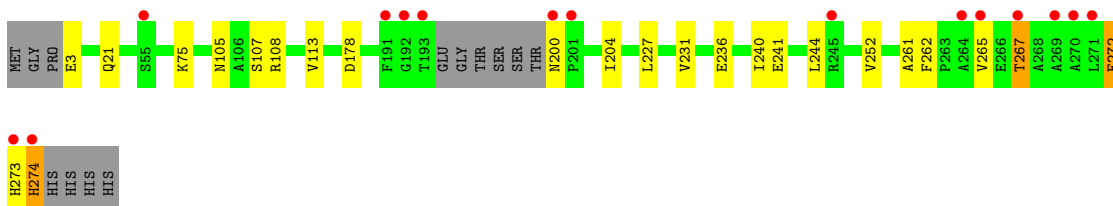
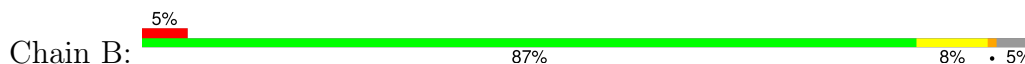
### 3 Residue-property plots [i](#)

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.

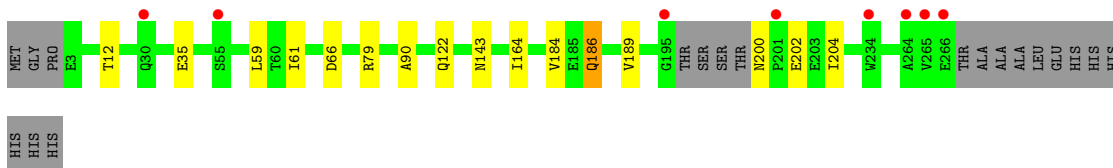
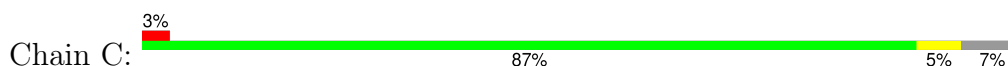
- Molecule 1: Glycosyltransferase



- Molecule 1: Glycosyltransferase



- Molecule 1: Glycosyltransferase



- Molecule 1: Glycosyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.18Å 124.29Å 64.77Å 90.00° 93.00° 90.00°	Depositor
Resolution (Å)	46.77 – 1.45 46.77 – 1.45	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.77-1.45) 92.9 (46.77-1.45)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.25 (at 1.35Å)	Xtriage
Refinement program	PHENIX 1.20.1-4487	Depositor
R, $R_{free}$	0.165 , 0.191 0.165 , 0.191	Depositor DCC
$R_{free}$ test set	10836 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.3	Xtriage
Anisotropy	0.363	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 41.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.012 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	17442	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	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 45.40 % 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 1.3291e-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: IMD, CL

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	0.20	0/2134	0.42	0/2893
1	B	0.18	0/2085	0.39	0/2826
1	C	0.18	0/2037	0.40	0/2759
1	D	0.18	0/2118	0.39	0/2871
All	All	0.19	0/8374	0.40	0/11349

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	2095	2072	2072	6	1
1	B	2049	2039	2038	17	1
1	C	2003	1995	1994	10	0
1	D	2079	2060	2059	5	0
2	A	5	5	5	0	0
2	B	5	5	5	0	0
2	C	5	5	5	0	0
2	D	5	5	5	0	0
3	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	323	0	0	3	4
4	B	215	0	0	5	1
4	C	226	0	0	3	3
4	D	244	0	0	1	2
All	All	9256	8186	8183	38	6

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 2.

All (38) 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:222:GLU:OE1	4:A:401:HOH:O	1.66	1.14
1:B:272:GLU:OE2	4:B:1001:HOH:O	2.03	0.77
1:B:75:LYS:NZ	4:B:1004:HOH:O	2.21	0.73
1:B:3:GLU:O	4:B:1002:HOH:O	2.10	0.69
1:B:107:SER:OG	4:B:1003:HOH:O	2.12	0.68
1:A:236:GLU:OE1	4:A:402:HOH:O	2.12	0.67
1:B:200:ASN:O	1:B:204:ILE:HD12	1.93	0.66
1:C:66:ASP:OD2	4:C:401:HOH:O	2.12	0.66
1:B:252:VAL:HG12	1:B:274:HIS:CG	2.37	0.59
1:D:203:GLU:N	1:D:203:GLU:OE1	2.35	0.59
1:B:231:VAL:HG12	1:B:261:ALA:HB1	1.89	0.54
1:D:222:GLU:OE1	4:D:401:HOH:O	2.17	0.53
1:D:259:GLN:NE2	1:D:266:GLU:OE2	2.42	0.52
1:B:227:LEU:O	1:B:231:VAL:HG22	2.11	0.51
1:C:200:ASN:O	1:C:204:ILE:HD12	2.10	0.51
1:C:143:ASN:O	1:C:189:VAL:HG21	2.12	0.50
1:A:199:THR:HG23	1:A:204:ILE:HD11	1.94	0.49
1:B:105:ASN:CB	1:B:113:VAL:HG21	2.44	0.48
1:B:241:GLU:OE1	1:B:241:GLU:N	2.45	0.48
1:C:59:LEU:CD1	1:C:61:ILE:HG13	2.44	0.47
1:B:262:PHE:O	1:B:265:VAL:HG22	2.15	0.47
1:C:184:VAL:HG12	1:C:186:GLN:HG3	1.97	0.45
1:C:59:LEU:HD11	1:C:61:ILE:CG1	2.48	0.44
1:B:252:VAL:HG12	1:B:274:HIS:ND1	2.33	0.44
1:A:186:GLN:NE2	4:A:412:HOH:O	2.49	0.44
1:B:272:GLU:O	1:B:273:HIS:C	2.60	0.43
1:B:21:GLN:HG3	4:B:1141:HOH:O	2.19	0.43
1:C:164:ILE:HD13	1:C:204:ILE:HG13	2.01	0.43
1:C:35:GLU:HG3	4:C:420:HOH:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:122:GLN:OE1	4:C:402:HOH:O	2.22	0.42
1:D:262:PHE:O	1:D:265:VAL:HG22	2.19	0.42
1:B:240:ILE:HG21	1:B:265:VAL:HG11	2.02	0.41
1:B:240:ILE:CG2	1:B:265:VAL:HG11	2.50	0.41
1:A:143:ASN:O	1:A:189:VAL:HG21	2.21	0.41
1:A:12:THR:HG22	1:A:90:ALA:HB2	2.03	0.41
1:C:12:THR:HG22	1:C:90:ALA:HB2	2.03	0.40
1:B:244:LEU:HD21	1:B:267:THR:HG23	2.04	0.40
1:D:226:TYR:CZ	1:D:239:ARG:HB2	2.57	0.40

All (6) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:605:HOH:O	4:D:612:HOH:O[1_556]	2.03	0.17
4:A:601:HOH:O	4:C:543:HOH:O[2_546]	2.14	0.06
1:A:17:LYS:NZ	1:B:178:ASP:O[1_656]	2.15	0.05
4:A:653:HOH:O	4:C:603:HOH:O[2_546]	2.15	0.05
4:B:1037:HOH:O	4:D:522:HOH:O[2_545]	2.17	0.03
4:A:430:HOH:O	4:C:452:HOH:O[2_546]	2.18	0.02

## 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	267/279 (96%)	262 (98%)	5 (2%)	0	100	100
1	B	262/279 (94%)	257 (98%)	5 (2%)	0	100	100
1	C	256/279 (92%)	250 (98%)	6 (2%)	0	100	100
1	D	265/279 (95%)	260 (98%)	5 (2%)	0	100	100
All	All	1050/1116 (94%)	1029 (98%)	21 (2%)	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	224/230 (97%)	223 (100%)	1 (0%)	89	78
1	B	219/230 (95%)	214 (98%)	5 (2%)	45	14
1	C	215/230 (94%)	212 (99%)	3 (1%)	62	33
1	D	222/230 (96%)	221 (100%)	1 (0%)	86	73
All	All	880/920 (96%)	870 (99%)	10 (1%)	70	43

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	199	THR
1	B	108	ARG
1	B	236	GLU
1	B	267	THR
1	B	272	GLU
1	B	274	HIS
1	C	79	ARG
1	C	186	GLN
1	C	202	GLU
1	D	178	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	ASN
1	A	143	ASN
1	C	122	GLN
1	D	143	ASN
1	D	275	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	$\# Z  > 2$
2	IMD	B	301	-	3,5,5	0.91	0	4,5,5	0.51	0
2	IMD	D	301	-	3,5,5	0.96	0	4,5,5	0.51	0
2	IMD	A	301	-	3,5,5	0.88	0	4,5,5	0.52	0
2	IMD	C	301	-	3,5,5	0.94	0	4,5,5	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
2	IMD	B	301	-	-	-	0/1/1/1
2	IMD	D	301	-	-	-	0/1/1/1
2	IMD	A	301	-	-	-	0/1/1/1
2	IMD	C	301	-	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	271/279 (97%)	-0.15	3 (1%) 77 81	18, 29, 49, 91	0
1	B	266/279 (95%)	0.18	15 (5%) 31 31	19, 34, 72, 107	0
1	C	260/279 (93%)	0.21	8 (3%) 51 52	19, 34, 73, 98	0
1	D	269/279 (96%)	0.01	7 (2%) 57 57	19, 31, 50, 81	0
All	All	1066/1116 (95%)	0.06	33 (3%) 51 52	18, 32, 63, 107	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	195	GLY	4.5
1	B	271	LEU	4.4
1	C	234	TRP	3.9
1	C	265	VAL	3.7
1	A	199	THR	3.4
1	B	270	ALA	3.1
1	B	274	HIS	3.1
1	D	275	HIS	3.0
1	C	264	ALA	3.0
1	B	273	HIS	2.8
1	C	201	PRO	2.7
1	D	269	ALA	2.7
1	B	193	THR	2.6
1	D	191	PHE	2.6
1	C	266	GLU	2.5
1	B	269	ALA	2.5
1	B	265	VAL	2.4
1	C	30	GLN	2.4
1	B	201	PRO	2.4
1	C	55	SER	2.3
1	B	200	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	192	GLY	2.3
1	B	267	THR	2.2
1	D	193	THR	2.2
1	D	266	GLU	2.2
1	B	55	SER	2.1
1	D	201	PRO	2.1
1	A	194	GLU	2.1
1	B	264	ALA	2.1
1	A	200	ASN	2.1
1	B	191	PHE	2.1
1	D	271	LEU	2.0
1	B	245	ARG	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 oligosaccharides 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
2	IMD	D	301	5/5	0.78	0.16	38,50,60,65	0
2	IMD	B	301	5/5	0.81	0.16	35,42,51,61	0
2	IMD	A	301	5/5	0.82	0.14	26,31,36,37	0
2	IMD	C	301	5/5	0.83	0.16	41,50,60,64	0
3	CL	A	303	1/1	0.98	0.10	36,36,36,36	0
3	CL	A	302	1/1	0.99	0.05	23,23,23,23	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.