



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 11:44 AM BST

PDB ID : 4KNL  
Title : Crystal structure of Staphylococcus aureus hydrolase AmiA in complex with its ligand  
Authors : Buettner, F.M.; Stehle, T.  
Deposited on : 2013-05-10  
Resolution : 1.55 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

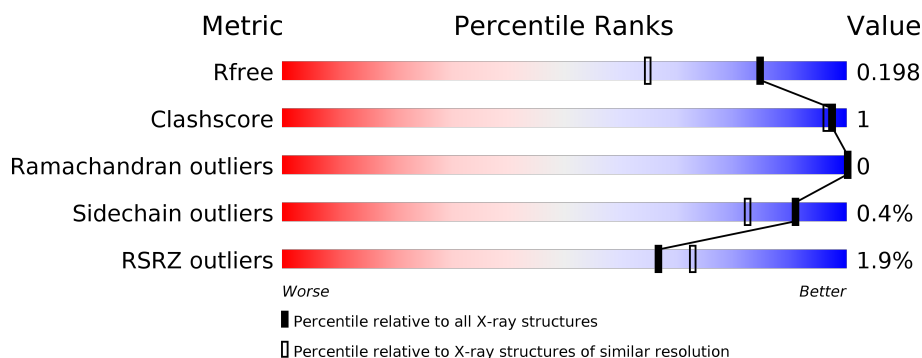
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.55 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	1483 (1.56-1.56)
Clashscore	141614	1529 (1.56-1.56)
Ramachandran outliers	138981	1498 (1.56-1.56)
Sidechain outliers	138945	1495 (1.56-1.56)
RSRZ outliers	127900	1465 (1.56-1.56)

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	225	<div> <div style="width: 89%;"></div> <div>89%</div> <div style="width: 9%; background-color: grey;"></div> <div>9%</div> </div>
1	B	225	<div> <div style="width: 90%;"></div> <div>90%</div> <div style="width: 9%; background-color: grey;"></div> <div>9%</div> </div>
1	C	225	<div> <div style="width: 90%;"></div> <div>90%</div> <div style="width: 8%; background-color: grey;"></div> <div>8%</div> </div>
1	D	225	<div> <div style="width: 5%; background-color: red;"></div> <div>5%</div> <div style="width: 88%;"></div> <div>88%</div> <div style="width: 9%; background-color: grey;"></div> <div>9%</div> </div>
2	F	6	<div> <div style="width: 17%; background-color: red;"></div> <div>17%</div> <div style="width: 50%;"></div> <div>50%</div> <div style="width: 50%; background-color: yellow;"></div> <div>50%</div> </div>
2	G	6	<div> <div style="width: 50%;"></div> <div>50%</div> <div style="width: 33%; background-color: yellow;"></div> <div>33%</div> <div style="width: 17%; background-color: orange;"></div> <div>17%</div> </div>

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 7321 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 Bifunctional autolysin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	0	0	0
			1631	1039	270	318	4			
1	B	205	Total	C	N	O	S	0	0	0
			1630	1038	270	318	4			
1	C	207	Total	C	N	O	S	0	1	0
			1648	1048	274	322	4			
1	D	204	Total	C	N	O	S	0	0	0
			1622	1033	269	316	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	197	GLY	-	expression tag	UNP Q2FZK7
B	197	GLY	-	expression tag	UNP Q2FZK7
C	197	GLY	-	expression tag	UNP Q2FZK7
D	197	GLY	-	expression tag	UNP Q2FZK7

- Molecule 2 is a protein called Muramyl tetrapeptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	F	6	Total	C	N	O	0	0	1
			51	30	8	13			
2	G	6	Total	C	N	O	0	0	1
			51	30	8	13			

- Molecule 3 is IMIDAZOLE (three-letter code: IMD) (formula: C<sub>3</sub>H<sub>5</sub>N<sub>2</sub>).



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

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

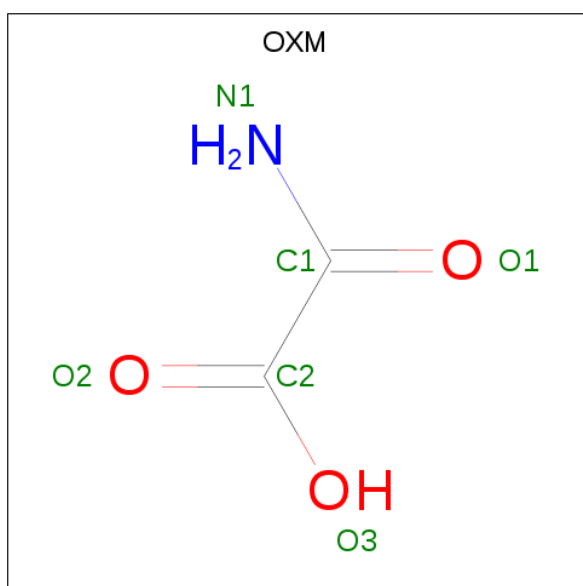
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Na	0	0
			2	2		
4	A	2	Total	Na	0	0
			2	2		
4	D	2	Total	Na	0	0
			2	2		
4	C	2	Total	Na	0	0
			2	2		

- Molecule 5 is FORMIC ACID (three-letter code: FMT) (formula: CH<sub>2</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			3	1	2		
5	B	1	Total	C	O	0	0
			3	1	2		

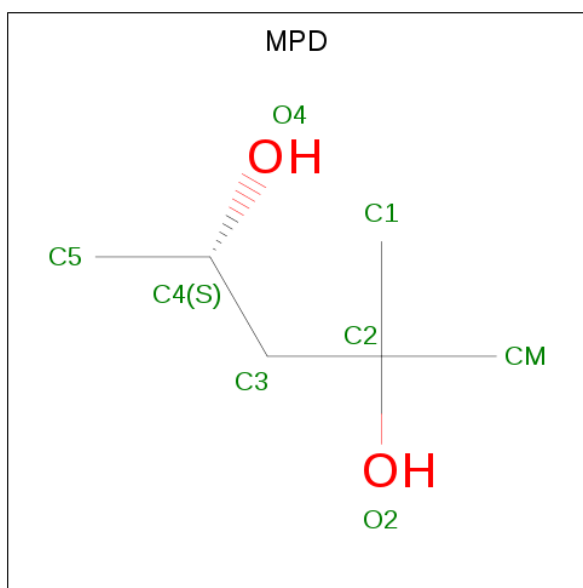
- Molecule 6 is OXAMIC ACID (three-letter code: OXM) (formula:  $C_2H_3NO_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			6	2	1	3		

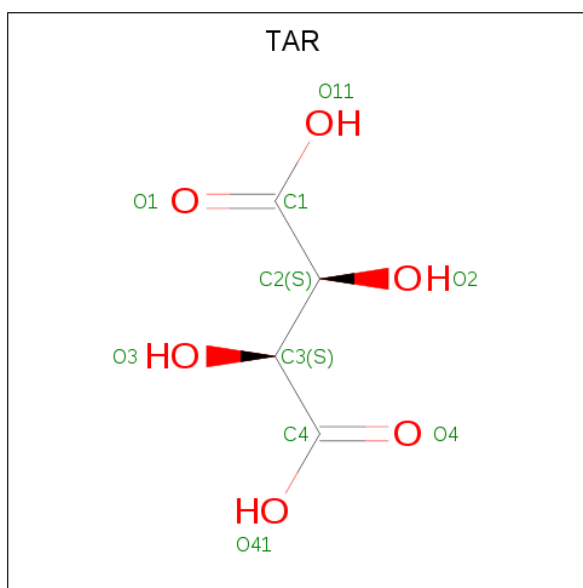
- Molecule 7 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula:

C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			8	6	2		

- Molecule 8 is D(-)-TARTARIC ACID (three-letter code: TAR) (formula: C<sub>4</sub>H<sub>6</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			10	4	6		

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	169	Total 169	O 169	0	0
9	B	134	Total 134	O 134	0	0
9	C	174	Total 174	O 174	0	0
9	D	144	Total 144	O 144	0	0
9	F	5	Total 5	O 5	0	0
9	G	4	Total 4	O 4	0	0

### 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.

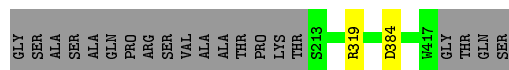
- Molecule 1: Bifunctional autolysin

Chain A: 




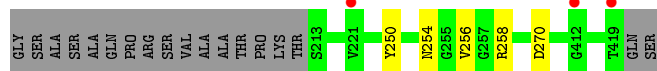
- Molecule 1: Bifunctional autolysin

Chain B: 



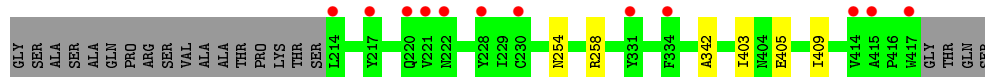
- Molecule 1: Bifunctional autolysin

Chain C: 



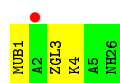
- Molecule 1: Bifunctional autolysin

Chain D: 



- Molecule 2: Muramyl tetrapeptide

Chain F: 



- Molecule 2: Muramyl tetrapeptide





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.81Å 82.83Å 77.43Å 90.00° 96.18° 90.00°	Depositor
Resolution (Å)	48.21 – 1.55 48.21 – 1.55	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.21-1.55) 99.5 (48.21-1.55)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.94 (at 1.55Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, $R_{free}$	0.171 , 0.198 0.172 , 0.198	Depositor DCC
$R_{free}$ test set	6137 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.0	Xtriage
Anisotropy	0.588	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 57.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7321	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	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 62.56 % 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 1.1055e-05. 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: MPD, IMD, TAR, DAL, NA, FMT, NH2, MUB, OXM, ZGL, ALY

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	0.65	1/1681 (0.1%)	0.72	0/2297
1	B	0.54	0/1680	0.66	0/2296
1	C	0.60	0/1701	0.70	0/2324
1	D	0.56	0/1672	0.64	0/2286
2	F	0.57	0/4	1.28	0/4
2	G	0.66	0/4	0.73	0/4
All	All	0.59	1/6742 (0.0%)	0.68	0/9211

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	309	SER	CB-OG	5.18	1.49	1.42

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	1631	0	1482	3	0
1	B	1630	0	1480	1	0
1	C	1648	0	1503	3	0
1	D	1622	0	1471	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	51	0	47	0	0
2	G	51	0	47	1	0
3	A	5	0	5	1	0
3	B	5	0	5	0	0
3	C	5	0	5	0	0
3	D	5	0	5	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
5	A	3	0	1	1	0
5	B	3	0	1	1	0
6	B	6	0	2	0	0
7	C	8	0	14	2	0
8	C	10	0	4	0	0
9	A	169	0	0	0	0
9	B	134	0	0	0	0
9	C	174	0	0	0	0
9	D	144	0	0	0	0
9	F	5	0	0	0	0
9	G	4	0	0	0	0
All	All	7321	0	6072	10	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 1.

All (10) 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:319:ARG:NH1	5:A:503:FMT:O1	2.30	0.61
1:B:319:ARG:NH1	5:B:503:FMT:O1	2.36	0.56
1:C:254:ASN:O	1:C:258:ARG:HD2	2.08	0.54
1:A:405:GLU:OE1	3:A:501:IMD:H5	2.09	0.51
1:C:250:TYR:CE2	7:C:503:MPD:H11	2.51	0.46
7:C:503:MPD:H4	2:G:4:ALY:HH32	1.99	0.45
1:D:254:ASN:O	1:D:258:ARG:HD2	2.17	0.45
1:A:256:VAL:HG11	1:C:256:VAL:HG11	1.98	0.44
1:D:405:GLU:O	1:D:409:ILE:HG13	2.19	0.43
1:D:342:ALA:HA	1:D:403:ILE:HG12	2.02	0.41

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	203/225 (90%)	196 (97%)	7 (3%)	0	100	100
1	B	203/225 (90%)	198 (98%)	5 (2%)	0	100	100
1	C	206/225 (92%)	202 (98%)	4 (2%)	0	100	100
1	D	202/225 (90%)	198 (98%)	4 (2%)	0	100	100
All	All	814/900 (90%)	794 (98%)	20 (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	167/188 (89%)	166 (99%)	1 (1%)	86	73
1	B	167/188 (89%)	166 (99%)	1 (1%)	86	73
1	C	170/188 (90%)	169 (99%)	1 (1%)	86	73
1	D	166/188 (88%)	166 (100%)	0	100	100
All	All	670/752 (89%)	667 (100%)	3 (0%)	91	82

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	384	ASP
1	B	384	ASP
1	C	270	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	ZGL	G	3	2	8,8,9	0.47	0	7,9,11	0.93	1 (14%)
2	ALY	G	4	2	10,11,12	2.24	3 (30%)	7,12,14	0.89	0
2	ALY	F	4	2	10,11,12	2.11	3 (30%)	7,12,14	0.87	0
2	ZGL	F	3	2	8,8,9	0.53	0	7,9,11	1.20	1 (14%)
2	MUB	F	1	2	19,19,20	1.42	3 (15%)	23,26,28	1.52	4 (17%)
2	MUB	G	1	2	19,19,20	1.49	4 (21%)	23,26,28	1.39	3 (13%)

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	ZGL	G	3	2	-	0/7/8/9	-
2	ALY	G	4	2	-	2/9/10/12	-
2	ALY	F	4	2	-	2/9/10/12	-
2	ZGL	F	3	2	-	0/7/8/9	-
2	MUB	F	1	2	-	6/12/32/34	0/1/1/1
2	MUB	G	1	2	-	2/12/32/34	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	4	ALY	OH-CH	5.11	1.34	1.23
2	F	4	ALY	OH-CH	5.04	1.34	1.23
2	G	1	MUB	O11-C10	-4.48	1.23	1.42
2	F	1	MUB	O11-C10	-4.42	1.23	1.42
2	G	4	ALY	CH-NZ	-3.32	1.24	1.34
2	F	4	ALY	CH-NZ	-3.24	1.24	1.34
2	G	4	ALY	CB-CA	-3.04	1.49	1.53
2	G	1	MUB	O3-C9	-2.71	1.41	1.44
2	F	1	MUB	O3-C9	-2.57	1.41	1.44
2	G	1	MUB	O5-C5	-2.39	1.38	1.44
2	F	4	ALY	CB-CA	-2.32	1.50	1.53
2	F	1	MUB	O5-C5	-2.25	1.38	1.44
2	G	1	MUB	O4-C4	-2.05	1.38	1.43

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	MUB	O11-C10-C9	3.44	120.92	111.78
2	G	1	MUB	O11-C10-C9	3.36	120.70	111.78
2	F	3	ZGL	CB-CG-CD	-2.59	104.92	112.29
2	F	1	MUB	C1-C2-N2	2.43	113.54	110.73
2	G	3	ZGL	CB-CG-CD	-2.30	105.75	112.29
2	G	1	MUB	C3-C4-C5	2.21	114.37	109.66
2	G	1	MUB	O5-C5-C4	2.03	113.38	109.69
2	F	1	MUB	O5-C1-C2	2.01	111.54	109.52
2	F	1	MUB	O7-C7-N2	2.01	125.64	121.95

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	4	ALY	OH-CH-NZ-CE
2	G	4	ALY	CH3-CH-NZ-CE
2	F	1	MUB	O11-C10-C9-C11
2	F	1	MUB	O11-C10-C9-O3
2	G	1	MUB	O11-C10-C9-C11
2	G	1	MUB	O11-C10-C9-O3
2	F	4	ALY	OH-CH-NZ-CE
2	F	4	ALY	CH3-CH-NZ-CE
2	F	1	MUB	C4-C5-C6-O6
2	F	1	MUB	O5-C5-C6-O6
2	F	1	MUB	C8-C7-N2-C2
2	F	1	MUB	O7-C7-N2-C2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	4	ALY	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 8 are monoatomic - leaving 9 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	MPD	C	503	-	7,7,7	0.25	0	9,10,10	0.84	0
5	FMT	A	503	-	0,2,2	0.00	-	0,1,1	0.00	-
3	IMD	A	501	-	3,5,5	0.38	0	4,5,5	0.68	0
3	IMD	D	501	-	3,5,5	0.43	0	4,5,5	0.58	0
3	IMD	B	501	-	3,5,5	0.38	0	4,5,5	0.71	0
5	FMT	B	503	-	0,2,2	0.00	-	0,1,1	0.00	-
3	IMD	C	501	-	3,5,5	0.43	0	4,5,5	0.68	0
8	TAR	C	504	-	3,9,9	1.82	1 (33%)	6,12,12	0.79	0
6	OXM	B	505	-	2,5,5	3.79	1 (50%)	2,6,6	2.10	1 (50%)

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	MPD	C	503	-	-	1/5/5/5	-
3	IMD	A	501	-	-	-	0/1/1/1
3	IMD	D	501	-	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	IMD	B	501	-	-	-	0/1/1/1
3	IMD	C	501	-	-	-	0/1/1/1
8	TAR	C	504	-	-	0/4/12/12	-
6	OXM	B	505	-	-	0/0/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	505	OXM	C1-N1	5.34	1.43	1.33
8	C	504	TAR	O2-C2	-2.37	1.38	1.42

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	505	OXM	C2-C1-N1	2.65	120.26	115.85

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	503	MPD	O2-C2-C3-C4

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	503	MPD	2	0
5	A	503	FMT	1	0
3	A	501	IMD	1	0
5	B	503	FMT	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	205/225 (91%)	-0.26	0 100 100	14, 19, 32, 50	0
1	B	205/225 (91%)	-0.05	0 100 100	16, 27, 44, 53	0
1	C	207/225 (92%)	-0.05	3 (1%) 75 80	14, 20, 36, 51	0
1	D	204/225 (90%)	0.28	12 (5%) 22 26	16, 25, 45, 59	0
2	F	1/6 (16%)	2.37	1 (100%) 0 0	35, 35, 35, 35	0
2	G	1/6 (16%)	0.29	0 100 100	39, 39, 39, 39	0
All	All	823/912 (90%)	-0.02	16 (1%) 66 73	14, 23, 42, 59	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	417	TRP	5.2
1	D	222	ASN	3.6
1	D	221	VAL	3.4
1	D	415	ALA	3.4
1	D	214	LEU	3.3
1	C	221	VAL	3.2
1	D	414	VAL	2.9
1	D	228	TYR	2.6
1	C	412	GLY	2.4
2	F	2	ALA	2.4
1	D	334	PHE	2.2
1	D	220	GLN	2.2
1	D	217	TYR	2.2
1	D	230	CYS	2.1
1	D	331	TYR	2.1
1	C	419	THR	2.1

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

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(Å <sup>2</sup> )	Q<0.9
2	MUB	G	1	19/20	0.63	0.32	39,54,60,61	0
2	MUB	F	1	19/20	0.66	0.28	31,40,46,47	0
2	ALY	G	4	12/13	0.92	0.10	19,25,48,55	0
2	ZGL	G	3	9/10	0.93	0.10	17,25,36,37	0
2	ZGL	F	3	9/10	0.93	0.10	19,26,33,35	0
2	ALY	F	4	12/13	0.94	0.09	18,23,41,44	0
2	DAL	G	5	5/6	0.95	0.10	27,28,31,34	0
2	DAL	F	5	5/6	0.96	0.08	26,27,29,30	0

## 6.3 Carbohydrates ⓘ

There are no monosaccharides 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, 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(Å <sup>2</sup> )	Q<0.9
3	IMD	D	501	5/5	0.83	0.29	44,45,47,48	0
8	TAR	C	504	10/10	0.84	0.16	18,32,37,41	10
7	MPD	C	503	8/8	0.85	0.18	32,37,48,52	0
3	IMD	B	501	5/5	0.88	0.28	36,37,40,42	0
3	IMD	A	501	5/5	0.90	0.19	29,33,35,37	0
5	FMT	A	503	3/3	0.90	0.18	36,36,41,44	0
6	OXM	B	505	6/6	0.90	0.18	28,39,51,53	0
5	FMT	B	503	3/3	0.91	0.23	38,38,40,44	0
3	IMD	C	501	5/5	0.91	0.25	36,36,39,40	0
4	NA	B	504	1/1	0.94	0.09	33,33,33,33	0
4	NA	A	504	1/1	0.97	0.07	27,27,27,27	0
4	NA	D	503	1/1	0.98	0.07	22,22,22,22	0
4	NA	C	502	1/1	0.98	0.06	24,24,24,24	0
4	NA	B	502	1/1	0.98	0.05	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	NA	D	502	1/1	0.98	0.04	29,29,29,29	0
4	NA	A	502	1/1	0.99	0.04	22,22,22,22	0
4	NA	C	505	1/1	0.99	0.07	19,19,19,19	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.