



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 1, 2022 – 03:30 pm GMT

PDB ID : 8A1A  
Title : Structure of a leucinostatin derivative determined by host lattice display :  
L1F11V1 construct  
Authors : Mittl, P.R.E.  
Deposited on : 2022-06-01  
Resolution : 2.05 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 : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.31.3  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

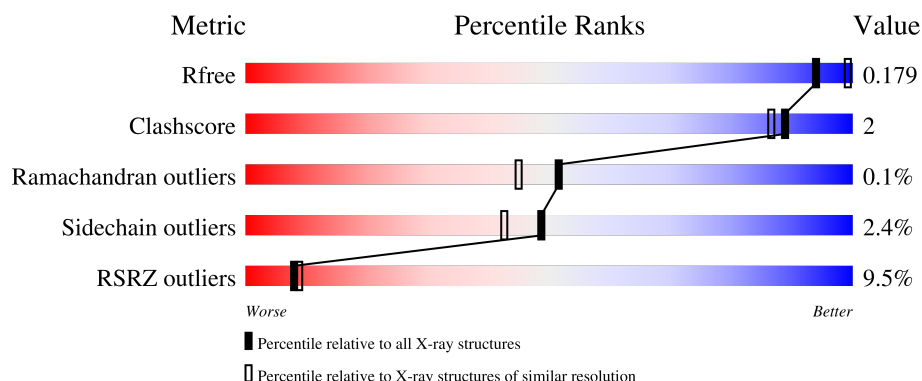
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.05 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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	1347	<div> <div>9%</div> <div>95%</div> <div>5%</div> </div>
2	B	11	<div> <div>36%</div> <div>36%</div> <div>64%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	BAL	B	10	-	-	-	X
2	HPE	B	3	-	X	-	-
2	AIB	B	5	-	-	-	X
2	AIB	B	9	-	-	-	X
4	MPD	A	1706	-	-	-	X
6	CL	A	1710	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12109 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 L1F11v1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1345	Total	C	N	O	S	0	12	0
			10435	6509	1780	2117	29			

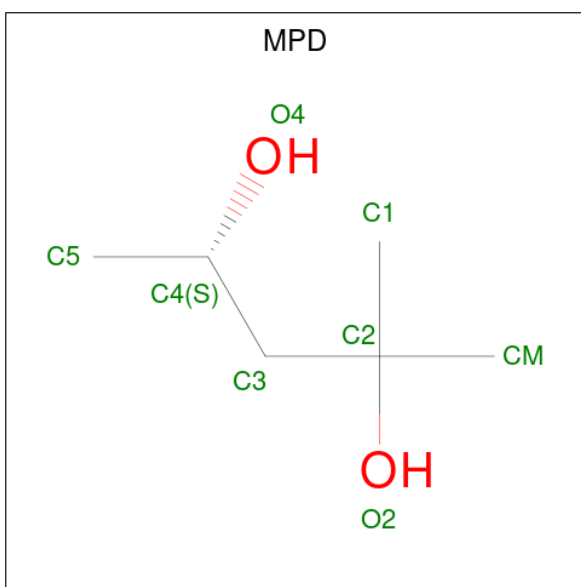
- Molecule 2 is a protein called 6-(2-methoxyethoxy)-11,15-dimethyl-8-oxa-2,11,15,19,21,23-hexazatetracyclo[15.6.1.13,7.020,24]pentacosa-1(23),3(25),4,6,17,20(24),21-heptaen-10-one.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	11	Total	C	F	N	O	12	0	0
			84	62	1	11	10			

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

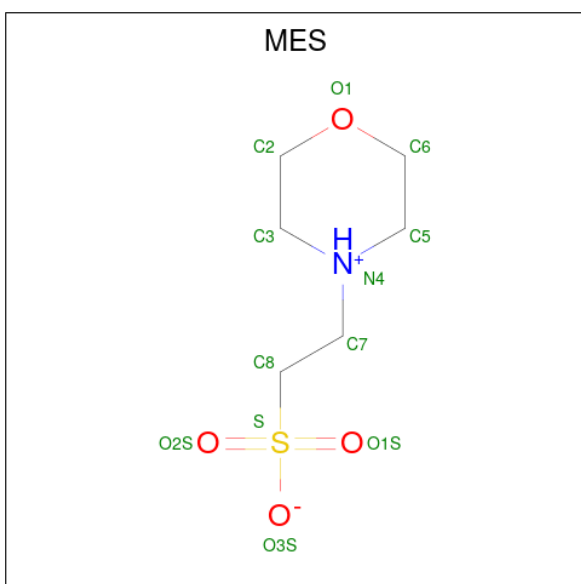
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	Mn	0	0
			4	4		

- Molecule 4 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
4	A	1	Total	C	O	0	0
			8	6	2		
4	A	1	Total	C	O	0	0
			8	6	2		
4	A	1	Total	C	O	0	0
			8	6	2		
4	A	1	Total	C	O	0	0
			8	6	2		

- Molecule 5 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula:  $C_6H_{13}NO_4S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	4	Total	Cl	0	0
			4	4		

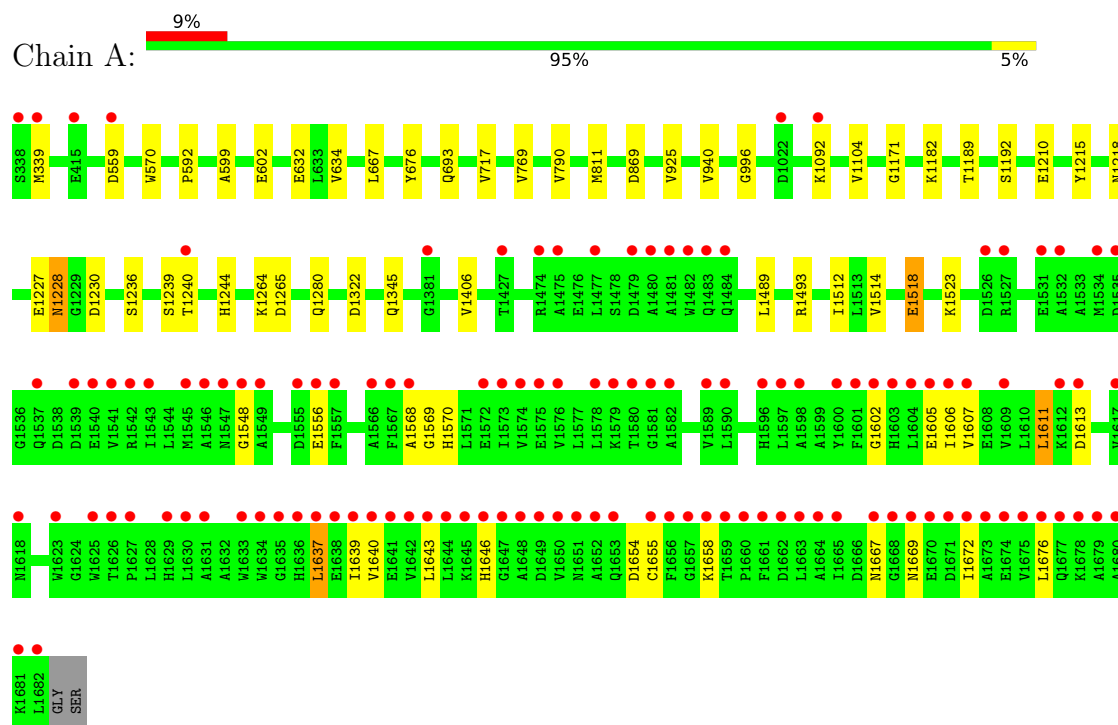
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1538	Total	O	0	0
			1538	1538		

### 3 Residue-property plots

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: L1F11v1



#### • Molecule 2: 6-(2-methoxyethoxy)-11,15-dimethyl-8-oxa-2,11,15,19,21,23-hexazatetracyclo[15.6.1.13,7.020,24]pentacos-1(23),3(25),4,6,17,20(24),21-heptaen-10-one



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	191.87Å 191.87Å 122.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.28 – 2.05 49.28 – 2.05	Depositor EDS
% Data completeness (in resolution range)	77.2 (49.28-2.05) 77.1 (49.28-2.05)	Depositor EDS
$R_{merge}$	0.29	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 2.05Å)	Xtriage
Refinement program	BUSTER 2.10.4	Depositor
R, $R_{free}$	0.161 , 0.185 0.156 , 0.179	Depositor DCC
$R_{free}$ test set	6165 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.7	Xtriage
Anisotropy	0.004	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.017 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	12109	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.17% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MPD, AIB, KQ9, HPE, CL, BAL, MES, MN, 1Y6

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	0.41	0/10643	0.61	0/14443
2	B	0.17	0/30	0.47	0/38
All	All	0.41	0/10673	0.61	0/14481

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
2	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	9	AIB	Peptide

### 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	10435	0	9967	35	0
2	B	84	0	79	4	0
3	A	4	0	0	0	0
4	A	32	0	56	1	0
5	A	12	0	13	0	0
6	A	4	0	0	0	0
7	A	1538	0	0	0	0
All	All	12109	0	10115	39	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 2.

All (39) 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:1602:GLY:HA2	1:A:1639:ILE:HD11	1.30	1.07
1:A:1171:GLY:HA3	1:A:1239:SER:HB2	1.61	0.82
1:A:1602:GLY:CA	1:A:1639:ILE:HD11	2.09	0.81
1:A:1602:GLY:HA2	1:A:1639:ILE:CD1	2.15	0.74
1:A:1637:LEU:HA	1:A:1672:ILE:HD11	1.75	0.69
2:B:1:1Y6:H26	2:B:2:PRO:CD	2.27	0.64
1:A:925:VAL:HG12	1:A:940:VAL:HG12	1.79	0.63
1:A:1189:THR:HB	1:A:1345:GLN:HB3	1.87	0.55
1:A:570:TRP:CD2	1:A:592:PRO:HB3	2.43	0.54
1:A:1210:GLU:OE1	1:A:1244:HIS:HD2	1.90	0.54
1:A:1228:ASN:HD22	1:A:1230:ASP:HB3	1.72	0.54
1:A:1569:GLY:HA2	1:A:1606:ILE:HD12	1.90	0.53
1:A:1489:LEU:O	1:A:1493:ARG:HG3	2.08	0.52
1:A:693:GLN:HB2	4:A:1707:MPD:H52	1.91	0.51
1:A:769[A]:VAL:HG23	1:A:811:MET:HB2	1.93	0.51
2:B:1:1Y6:CAP	2:B:2:PRO:CD	2.87	0.50
1:A:1568:ALA:HB3	1:A:1570:HIS:CD2	2.47	0.50
1:A:1611:LEU:HD23	1:A:1646:HIS:CE1	2.47	0.49
1:A:1171:GLY:HA3	1:A:1239:SER:CB	2.39	0.49
1:A:1514:VAL:O	1:A:1518:GLU:HG2	2.14	0.48
1:A:1218:ASN:HD22	1:A:1280:GLN:NE2	2.11	0.47
1:A:1406:VAL:HG12	1:A:1512:ILE:HD13	1.96	0.47
1:A:1669:ASN:HB3	1:A:1672:ILE:HD12	1.94	0.47
2:B:1:1Y6:CAP	2:B:2:PRO:HD3	2.45	0.47
1:A:1607:VAL:HG21	1:A:1639:ILE:HG23	1.97	0.47
1:A:1640:VAL:HG11	1:A:1672:ILE:HG23	1.98	0.45
1:A:1637:LEU:HG	1:A:1672:ILE:HG13	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:769[B]:VAL:HG23	1:A:811:MET:HB2	1.99	0.44
2:B:1:1Y6:H26	2:B:2:PRO:HD3	1.99	0.44
1:A:1192:SER:HB3	1:A:1215:TYR:HB3	2.01	0.43
1:A:869:ASP:O	1:A:996:GLY:HA3	2.19	0.42
1:A:1568:ALA:HB1	1:A:1570:HIS:NE2	2.35	0.41
1:A:676:TYR:CD1	1:A:717:VAL:HB	2.56	0.41
1:A:1640:VAL:HG21	1:A:1672:ILE:HD13	2.03	0.41
1:A:599:ALA:HB1	1:A:602:GLU:HG2	2.03	0.41
1:A:1556:GLU:H	1:A:1556:GLU:HG3	1.74	0.41
1:A:1654:ASP:HB3	1:A:1658:LYS:HB2	2.03	0.41
1:A:1611:LEU:HD23	1:A:1646:HIS:ND1	2.35	0.40
1:A:634:VAL:HG11	1:A:667:LEU:HD13	2.03	0.40

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	1355/1347 (101%)	1308 (96%)	45 (3%)	2 (0%)	51	45
2	B	3/11 (27%)	3 (100%)	0	0	100	100
All	All	1358/1358 (100%)	1311 (96%)	45 (3%)	2 (0%)	51	45

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	790	VAL
1	A	1548	GLY

### 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	1109/1098 (101%)	1086 (98%)	23 (2%)	53	48
2	B	4/4 (100%)	1 (25%)	3 (75%)	0	0
All	All	1113/1102 (101%)	1087 (98%)	26 (2%)	49	44

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	339	MET
1	A	559	ASP
1	A	632	GLU
1	A	1092	LYS
1	A	1104	VAL
1	A	1182	LYS
1	A	1227	GLU
1	A	1228	ASN
1	A	1236	SER
1	A	1240	THR
1	A	1264	LYS
1	A	1265	ASP
1	A	1322	ASP
1	A	1518	GLU
1	A	1523	LYS
1	A	1605	GLU
1	A	1611	LEU
1	A	1613	ASP
1	A	1637	LEU
1	A	1643	LEU
1	A	1655	CYS
1	A	1667	ASN
1	A	1676	LEU
2	B	4	LEU
2	B	6	LEU
2	B	7	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	897	ASN
1	A	1055	GLN
1	A	1244	HIS
1	A	1280	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

5 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	AIB	B	9	2	1,5,6	0.90	0	2,7,9	0.16	0
2	BAL	B	10	2	4,4,5	0.40	0	3,3,5	0.66	0
2	HPE	B	3	2	11,12,13	4.80	6 (54%)	9,14,16	4.56	8 (88%)
2	AIB	B	5	2	1,5,6	0.93	0	2,7,9	0.17	0
2	AIB	B	8	2	1,5,6	0.92	0	2,7,9	0.29	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	AIB	B	9	2	-	0/2/3/6	-
2	BAL	B	10	2	-	0/1/2/3	-
2	HPE	B	3	2	-	3/6/7/9	0/1/1/1
2	AIB	B	5	2	-	0/2/3/6	-
2	AIB	B	8	2	-	0/2/3/6	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3	HPE	CZ2-CE2	6.92	1.53	1.38
2	B	3	HPE	CZ1-CE1	6.92	1.53	1.38
2	B	3	HPE	CE1-CD	6.83	1.53	1.38
2	B	3	HPE	CE2-CD	6.68	1.53	1.38
2	B	3	HPE	CH-CZ2	5.75	1.53	1.38
2	B	3	HPE	CH-CZ1	5.60	1.52	1.38

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3	HPE	CH-CZ1-CE1	-5.50	111.81	120.19
2	B	3	HPE	CE2-CD-CE1	-5.40	109.67	118.17
2	B	3	HPE	CZ2-CE2-CD	-5.34	112.44	120.63
2	B	3	HPE	CH-CZ2-CE2	-5.31	112.10	120.19
2	B	3	HPE	CZ1-CE1-CD	-4.65	113.49	120.63
2	B	3	HPE	CZ2-CH-CZ1	-4.65	111.28	119.93
2	B	3	HPE	CG-CD-CE1	-4.07	110.94	121.23
2	B	3	HPE	CG-CD-CE2	-3.15	113.27	121.23

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	3	HPE	C-CA-CB-CG
2	B	3	HPE	N-CA-CB-CG
2	B	3	HPE	CE1-CD-CG-CB

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 8 are monoatomic - leaving 5 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	$\# Z  > 2$
4	MPD	A	1707	-	7,7,7	0.86	0	9,10,10	0.28	0
4	MPD	A	1706	-	7,7,7	0.67	0	9,10,10	0.53	0
5	MES	A	1709	-	12,12,12	0.83	0	14,16,16	0.44	0
4	MPD	A	1708	-	7,7,7	0.61	0	9,10,10	0.53	0
4	MPD	A	1705	-	7,7,7	0.57	0	9,10,10	0.23	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
4	MPD	A	1707	-	-	2/5/5/5	-
4	MPD	A	1706	-	-	3/5/5/5	-
5	MES	A	1709	-	-	0/6/14/14	0/1/1/1
4	MPD	A	1708	-	-	2/5/5/5	-
4	MPD	A	1705	-	-	0/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1706	MPD	C1-C2-C3-C4
4	A	1706	MPD	O2-C2-C3-C4
4	A	1708	MPD	C2-C3-C4-O4
4	A	1706	MPD	CM-C2-C3-C4
4	A	1707	MPD	C2-C3-C4-C5
4	A	1708	MPD	C2-C3-C4-C5
4	A	1707	MPD	C2-C3-C4-O4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1707	MPD	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	1345/1347 (99%)	0.10	124 (9%) <b>9</b> <b>9</b>	29, 40, 98, 165	0
2	B	4/11 (36%)	5.65	4 (100%) <b>0</b> <b>0</b>	142, 142, 143, 145	0
All	All	1349/1358 (99%)	0.11	128 (9%) <b>8</b> <b>9</b>	29, 40, 101, 165	0

All (128) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1676	LEU	13.6
1	A	1679	ALA	12.3
1	A	1672	ILE	9.9
1	A	1661	PHE	9.7
1	A	1644	LEU	9.4
1	A	1639	ILE	9.0
2	B	6	LEU	8.8
1	A	1675	VAL	8.6
1	A	1664	ALA	8.6
1	A	1680	ALA	7.9
1	A	1665	ILE	7.7
1	A	1640	VAL	7.4
1	A	1682	LEU	7.1
1	A	1634	TRP	7.1
1	A	1600	TYR	7.0
1	A	1670	GLU	6.9
1	A	1650	VAL	6.6
1	A	1671	ASP	6.6
1	A	1657	GLY	6.4
2	B	2	PRO	6.2
1	A	1649	ASP	6.2
1	A	1659	THR	6.1
1	A	1601	PHE	6.1
1	A	1630	LEU	6.0

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Mol	Chain	Res	Type	RSRZ
1	A	1667	ASN	5.9
1	A	1681	LYS	5.9
1	A	1546	ALA	5.8
1	A	1660	PRO	5.7
1	A	1604	LEU	5.6
2	B	4	LEU	5.5
1	A	1629	HIS	5.5
1	A	1534	MET	5.3
1	A	1674	GLU	5.3
1	A	1651	ASN	5.2
1	A	1539	ASP	5.2
1	A	1568	ALA	5.1
1	A	1623	TRP	5.1
1	A	1677	GLN	5.0
1	A	1663	LEU	4.9
1	A	1633	TRP	4.9
1	A	1637	LEU	4.8
1	A	338	SER	4.8
1	A	1576	VAL	4.7
1	A	1543	ILE	4.6
1	A	1475	ALA	4.5
1	A	1653	GLN	4.5
1	A	1541	VAL	4.5
1	A	1617	VAL	4.4
1	A	1669	ASN	4.3
1	A	1613	ASP	4.2
1	A	1579	LYS	4.2
1	A	1542	ARG	4.2
1	A	1545	MET	4.1
1	A	1556	GLU	4.1
1	A	1678	LYS	3.9
1	A	1590	LEU	3.8
1	A	1240	THR	3.8
1	A	1557	PHE	3.8
1	A	1646	HIS	3.7
1	A	1673	ALA	3.7
1	A	1642	VAL	3.6
1	A	1655	CYS	3.5
1	A	1662	ASP	3.5
1	A	1580	THR	3.5
1	A	1625	TRP	3.4
1	A	1548	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	1483	GLN	3.3
1	A	1609	VAL	3.2
1	A	1635	GLY	3.1
1	A	1549	ALA	3.1
1	A	1627	PRO	3.1
1	A	1477	LEU	3.1
1	A	1574	VAL	3.1
1	A	559	ASP	3.1
1	A	1652	ALA	3.1
1	A	1480	ALA	3.0
1	A	1582	ALA	3.0
1	A	1573	ILE	3.0
1	A	1607	VAL	3.0
1	A	1647	GLY	3.0
1	A	1567	PHE	3.0
1	A	1645	LYS	3.0
1	A	1631	ALA	2.9
1	A	1638	GLU	2.9
1	A	1547	ASN	2.9
1	A	1648	ALA	2.8
1	A	1479	ASP	2.8
1	A	1605	GLU	2.8
1	A	1535	ASP	2.8
1	A	1656	PHE	2.8
1	A	1575	GLU	2.8
1	A	1636	HIS	2.7
1	A	1668	GLY	2.7
1	A	1597	LEU	2.6
1	A	1589	VAL	2.6
1	A	1626	THR	2.6
1	A	1527	ARG	2.5
1	A	1092	LYS	2.5
1	A	339	MET	2.5
1	A	1612	LYS	2.5
1	A	1481	ALA	2.5
1	A	1578	LEU	2.4
1	A	1526	ASP	2.4
1	A	1603	HIS	2.4
1	A	1537	GLN	2.4
1	A	1581	GLY	2.3
1	A	1606	ILE	2.3
1	A	1641	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	1572	GLU	2.3
1	A	1598	ALA	2.3
1	A	1474	ARG	2.3
1	A	1531	GLU	2.3
1	A	1643	LEU	2.2
1	A	1596	HIS	2.2
1	A	1540	GLU	2.2
1	A	1618	ASN	2.2
1	A	1484	GLN	2.1
1	A	1566	ALA	2.1
1	A	415	GLU	2.1
2	B	7	LEU	2.1
1	A	1532	ALA	2.1
1	A	1381	GLY	2.1
1	A	1602	GLY	2.1
1	A	1555	ASP	2.1
1	A	1658	LYS	2.0
1	A	1427	THR	2.0
1	A	1482	TRP	2.0
1	A	1022	ASP	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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(Å <sup>2</sup> )	Q<0.9
2	AIB	B	9	6/7	0.23	0.62	142,142,142,143	0
2	HPE	B	3	12/13	0.30	0.28	143,143,143,144	0
2	BAL	B	10	5/6	0.73	0.87	136,137,142,143	3
2	AIB	B	5	6/7	0.75	0.40	142,142,142,142	0
2	AIB	B	8	6/7	0.86	0.45	142,142,142,142	0

## 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(Å <sup>2</sup> )	Q<0.9
4	MPD	A	1705	8/8	0.63	0.33	96,97,97,97	0
6	CL	A	1710	1/1	0.74	0.57	89,89,89,89	0
4	MPD	A	1707	8/8	0.75	0.21	68,69,70,70	0
4	MPD	A	1706	8/8	0.76	0.41	79,80,80,80	0
6	CL	A	1713	1/1	0.82	0.38	106,106,106,106	0
4	MPD	A	1708	8/8	0.84	0.20	69,70,71,71	0
6	CL	A	1711	1/1	0.92	0.20	63,63,63,63	0
5	MES	A	1709	12/12	0.92	0.19	49,57,62,63	0
6	CL	A	1712	1/1	0.98	0.28	52,52,52,52	0
3	MN	A	1701	1/1	0.99	0.04	44,44,44,44	0
3	MN	A	1702	1/1	1.00	0.07	43,43,43,43	0
3	MN	A	1703	1/1	1.00	0.04	45,45,45,45	0
3	MN	A	1704	1/1	1.00	0.04	49,49,49,49	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.