



# wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 1, 2022 – 03:27 pm GMT

PDB ID : 8A19  
Title : Structure of a leucinostatin derivative determined by host lattice display :  
L1E4V1 construct  
Authors : Mittl, P.R.E.  
Deposited on : 2022-06-01  
Resolution : 2.36 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](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

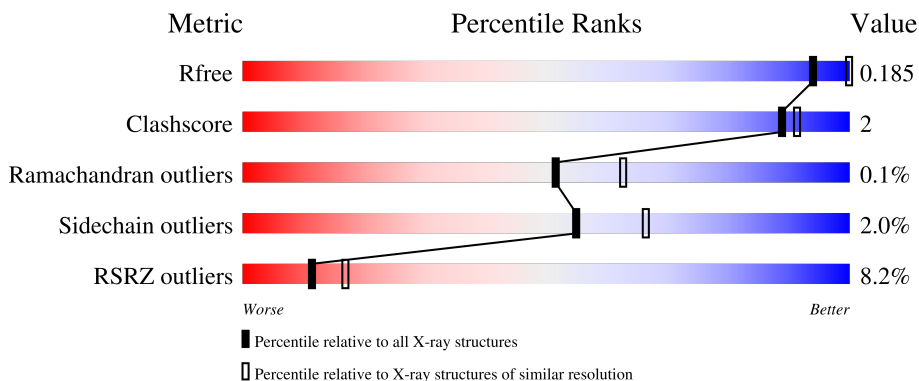
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.36 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	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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>8%</div> <div>94%</div> <div>6%</div> </div>
2	B	11	<div> <div>36%</div> <div>73%</div> <div>27%</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	HPE	B	3	-	X	-	-
4	MPD	A	1707	-	-	-	X
6	CL	A	1711	-	-	-	X
6	CL	A	1712	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11807 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 L1E4v1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1345	Total	C	N	O	S	0	10	0
			10419	6491	1792	2107	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]pentacos-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).

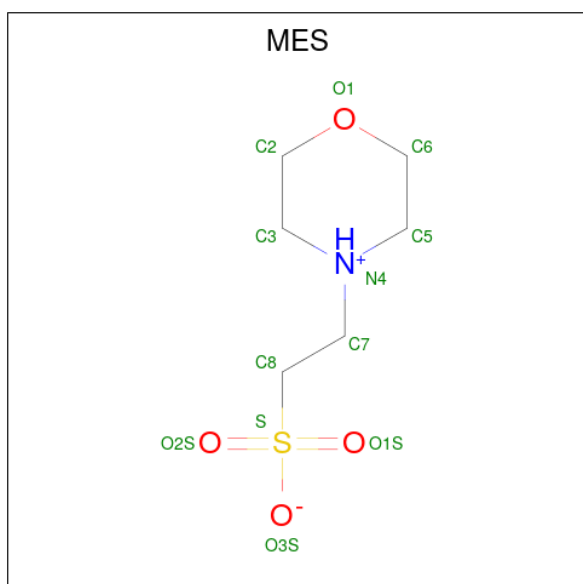
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	Mn	0	0
			4	4		

- 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	5	Total	Cl	0	0
			5	5		

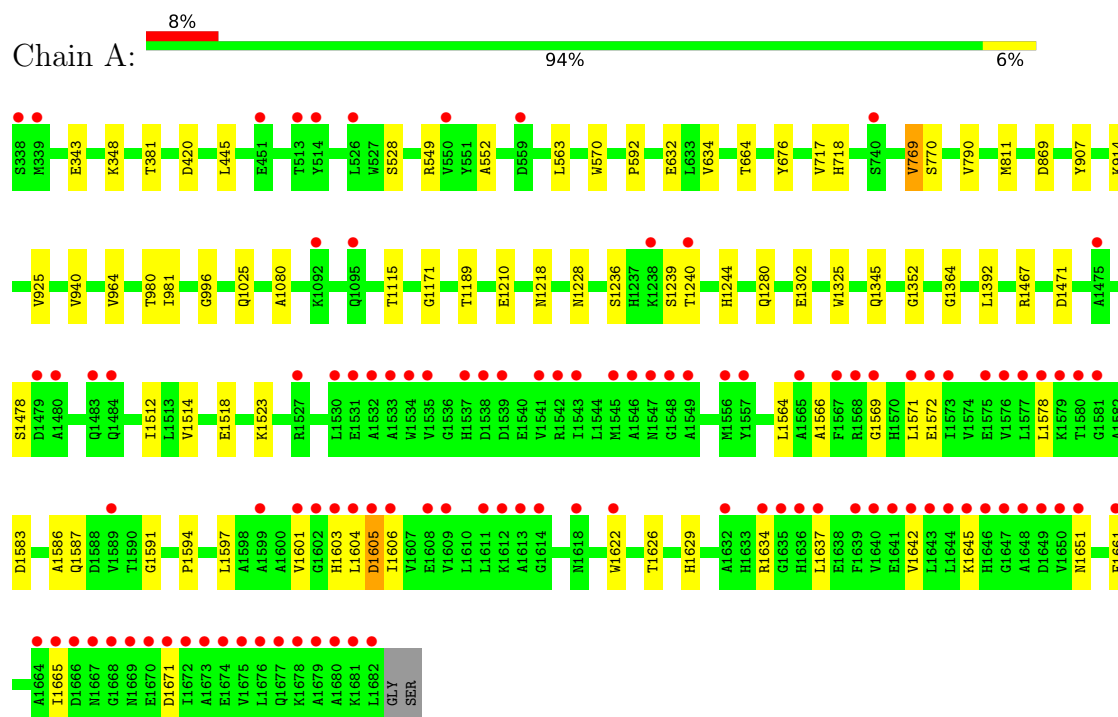
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1250	Total	O	0	0
			1250	1250		
7	B	1	Total	O	0	0
			1	1		

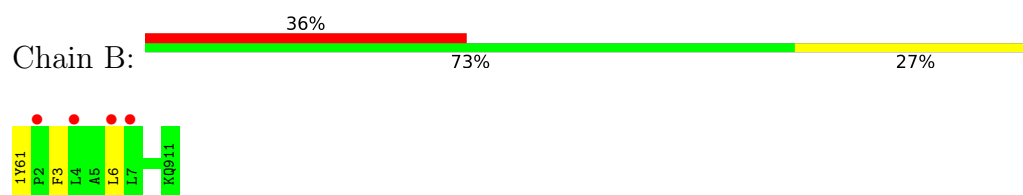
### 3 Residue-property plots

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: L1E4v1



#### • Molecule 2: 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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	192.76Å 192.76Å 122.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.52 – 2.36 34.52 – 2.36	Depositor EDS
% Data completeness (in resolution range)	90.6 (34.52-2.36) 90.6 (34.52-2.36)	Depositor EDS
$R_{merge}$	0.23	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.96 (at 2.36Å)	Xtriage
Refinement program	BUSTER 2.10.4	Depositor
R, $R_{free}$	0.163 , 0.193 0.157 , 0.185	Depositor DCC
$R_{free}$ test set	4853 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.2	Xtriage
Anisotropy	0.017	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	0.013 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	11807	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.25% 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, BAL, KQ9, MES, 1Y6, MN, AIB, HPE, 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	0.42	0/10624	0.62	0/14412
2	B	0.17	0/30	0.47	0/38
All	All	0.42	0/10654	0.62	0/14450

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

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	10419	0	9977	40	0
2	B	84	0	79	1	0
3	A	4	0	0	0	0
4	A	32	0	56	1	0
5	A	12	0	13	0	0
6	A	5	0	0	0	0
7	A	1250	0	0	1	0
7	B	1	0	0	0	0
All	All	11807	0	10125	40	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.

The worst 5 of 40 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:1569:GLY:HA2	1:A:1606:ILE:HD11	1.77	0.67
1:A:1171:GLY:HA3	1:A:1239:SER:HB2	1.77	0.67
1:A:925:VAL:HG12	1:A:940:VAL:HG12	1.78	0.65
1:A:1218:ASN:HD22	1:A:1280:GLN:NE2	1.97	0.62
1:A:1189:THR:HB	1:A:1345:GLN:HB3	1.82	0.62

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1353/1347 (100%)	1304 (96%)	48 (4%)	1 (0%)	51	63
2	B	3/11 (27%)	3 (100%)	0	0	100	100
All	All	1356/1358 (100%)	1307 (96%)	48 (4%)	1 (0%)	51	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	790	VAL

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1107/1098 (101%)	1085 (98%)	22 (2%)	55	66
2	B	4/4 (100%)	3 (75%)	1 (25%)	0	0
All	All	1111/1102 (101%)	1088 (98%)	23 (2%)	55	65

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1578	LEU
1	A	1634	ARG
1	A	1622	TRP
1	A	1637	LEU
1	A	1025	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1633	HIS
1	A	1629	HIS
1	A	1280	GLN
1	A	1244	HIS
1	A	1603	HIS

### 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	0.89	0	2,7,9	0.11	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	AIB	B	8	2	1,5,6	0.88	0	2,7,9	0.38	0
2	AIB	B	5	2	1,5,6	0.92	0	2,7,9	0.23	0
2	HPE	B	3	2	11,12,13	4.80	6 (54%)	9,14,16	4.56	8 (88%)
2	BAL	B	10	2	4,4,5	0.40	0	3,3,5	0.72	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	AIB	B	9	2	-	1/2/3/6	-
2	AIB	B	8	2	-	0/2/3/6	-
2	AIB	B	5	2	-	0/2/3/6	-
2	HPE	B	3	2	-	4/6/7/9	0/1/1/1
2	BAL	B	10	2	-	0/1/2/3	-

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3	HPE	CZ1-CE1	6.91	1.53	1.38
2	B	3	HPE	CZ2-CE2	6.90	1.53	1.38
2	B	3	HPE	CE1-CD	6.86	1.53	1.38
2	B	3	HPE	CE2-CD	6.73	1.53	1.38
2	B	3	HPE	CH-CZ2	5.75	1.53	1.38

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3	HPE	CH-CZ1-CE1	-5.55	111.73	120.19
2	B	3	HPE	CE2-CD-CE1	-5.42	109.65	118.17
2	B	3	HPE	CH-CZ2-CE2	-5.31	112.10	120.19
2	B	3	HPE	CZ2-CE2-CD	-5.28	112.53	120.63
2	B	3	HPE	CZ1-CE1-CD	-4.70	113.43	120.63

There are no chirality outliers.

All (5) torsion outliers are listed below:

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

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Mol	Chain	Res	Type	Atoms
2	B	9	AIB	O-C-CA-CB2
2	B	3	HPE	C-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 14 ligands modelled in this entry, 9 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	1708	-	7,7,7	0.71	0	9,10,10	0.29	0
4	MPD	A	1707	-	7,7,7	0.68	0	9,10,10	0.49	0
4	MPD	A	1706	-	7,7,7	0.84	1 (14%)	9,10,10	0.56	0
5	MES	A	1709	-	12,12,12	0.84	0	14,16,16	0.47	0
4	MPD	A	1705	-	7,7,7	0.58	0	9,10,10	0.19	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	1708	-	-	2/5/5/5	-
4	MPD	A	1707	-	-	3/5/5/5	-
4	MPD	A	1706	-	-	3/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MES	A	1709	-	-	4/6/14/14	0/1/1/1
4	MPD	A	1705	-	-	0/5/5/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1706	MPD	C3-C2	2.02	1.59	1.53

There are no bond angle outliers.

There are no chirality outliers.

5 of 12 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
5	A	1709	MES	C8-C7-N4-C5
5	A	1709	MES	C7-C8-S-O2S
4	A	1708	MPD	C2-C3-C4-C5

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 [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, 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%)	0.06	106 (7%) 12 19	29, 43, 110, 148	0
2	B	4/11 (36%)	4.74	4 (100%) 0 0	116, 117, 117, 119	0
All	All	1349/1358 (99%)	0.07	110 (8%) 11 17	29, 43, 110, 148	0

The worst 5 of 110 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1639	PHE	8.7
1	A	1682	LEU	8.4
1	A	1534	TRP	7.6
1	A	1667	ASN	7.0
1	A	1676	LEU	6.7

### 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	BAL	B	10	5/6	0.37	0.34	121,121,137,137	3
2	AIB	B	9	6/7	0.85	0.50	121,121,121,122	0
2	AIB	B	5	6/7	0.86	0.31	117,117,117,117	0
2	HPE	B	3	12/13	0.87	0.38	115,116,116,116	0
2	AIB	B	8	6/7	0.95	0.39	120,120,120,120	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
6	CL	A	1711	1/1	0.43	0.52	113,113,113,113	0
4	MPD	A	1705	8/8	0.70	0.26	98,99,99,99	0
6	CL	A	1712	1/1	0.73	0.42	99,99,99,99	0
4	MPD	A	1706	8/8	0.74	0.37	87,87,88,88	0
4	MPD	A	1707	8/8	0.76	0.42	83,84,85,86	0
4	MPD	A	1708	8/8	0.88	0.25	83,84,85,85	0
5	MES	A	1709	12/12	0.93	0.21	60,65,69,69	0
6	CL	A	1714	1/1	0.96	0.15	72,72,72,72	0
6	CL	A	1710	1/1	0.98	0.53	85,85,85,85	0
3	MN	A	1703	1/1	0.99	0.07	52,52,52,52	0
6	CL	A	1713	1/1	0.99	0.34	56,56,56,56	0
3	MN	A	1701	1/1	0.99	0.04	48,48,48,48	0
3	MN	A	1702	1/1	1.00	0.07	51,51,51,51	0
3	MN	A	1704	1/1	1.00	0.04	56,56,56,56	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.