



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 4, 2016 – 05:03 AM EDT

PDB ID : 5KLB  
Title : Crystal structure of the CavAb voltage-gated calcium channel(wild-type, 2.7Å)  
Authors : Tang, L.; Gamal EL-Din, T.M.; Swanson, T.M.; Pryde, D.C.; Scheuer, T.; Zheng, N.; Catterall, W.A.  
Deposited on : 2016-06-23  
Resolution : 2.70 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

<http://wwpdb.org/validation/2016/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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027939  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027939

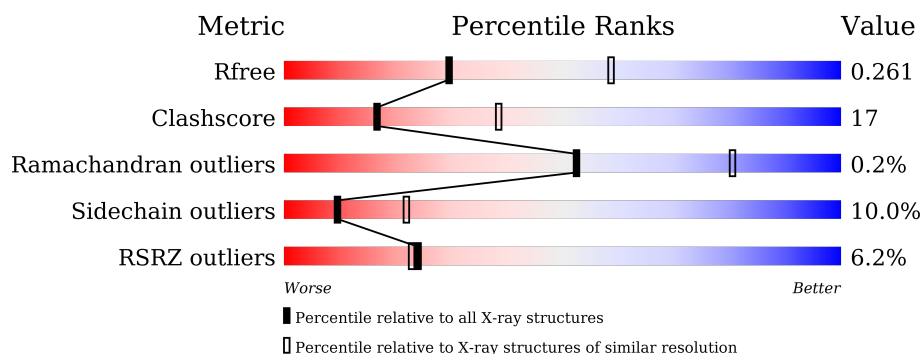
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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. 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	285	<div> <div>4%</div> <div> <div></div> <div>64%</div> <div>25%</div> <div>5%</div> <div>6%</div> </div> </div>
1	B	285	<div> <div>6%</div> <div> <div></div> <div>67%</div> <div>21%</div> <div>5%</div> <div>6%</div> </div> </div>
1	C	285	<div> <div>9%</div> <div> <div></div> <div>71%</div> <div>20%</div> <div>•</div> <div>6%</div> </div> </div>
1	D	285	<div> <div>4%</div> <div> <div></div> <div>66%</div> <div>21%</div> <div>6%</div> <div>6%</div> </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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MC3	A	1301	-	-	-	X
2	MC3	A	1303	-	-	-	X
2	MC3	B	1305	-	-	-	X
2	MC3	C	1301	-	-	-	X
3	CA	B	1301	-	-	-	X
4	CPS	A	1304	-	-	X	X
4	CPS	A	1305	-	-	X	-
4	CPS	B	1308	-	-	X	-
4	CPS	D	1308	-	-	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9684 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 Ion transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total	C	N	O	S	0	0	0
			2195	1472	337	375	11			
1	B	267	Total	C	N	O	S	0	0	0
			2195	1472	337	375	11			
1	C	267	Total	C	N	O	S	0	0	0
			2195	1472	337	375	11			
1	D	267	Total	C	N	O	S	0	0	0
			2195	1472	337	375	11			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	983	MET	-	initiating methionine	UNP A8EVM5
A	984	ASP	-	expression tag	UNP A8EVM5
A	985	TYR	-	expression tag	UNP A8EVM5
A	986	LYS	-	expression tag	UNP A8EVM5
A	987	ASP	-	expression tag	UNP A8EVM5
A	988	ASP	-	expression tag	UNP A8EVM5
A	989	ASP	-	expression tag	UNP A8EVM5
A	990	ASP	-	expression tag	UNP A8EVM5
A	991	LYS	-	expression tag	UNP A8EVM5
A	992	GLY	-	expression tag	UNP A8EVM5
A	993	SER	-	expression tag	UNP A8EVM5
A	994	LEU	-	expression tag	UNP A8EVM5
A	995	VAL	-	expression tag	UNP A8EVM5
A	996	PRO	-	expression tag	UNP A8EVM5
A	997	ARG	-	expression tag	UNP A8EVM5
A	998	GLY	-	expression tag	UNP A8EVM5
A	999	SER	-	expression tag	UNP A8EVM5
A	1000	HIS	-	expression tag	UNP A8EVM5
A	1177	ASP	GLU	conflict	UNP A8EVM5
A	1178	ASP	SER	conflict	UNP A8EVM5
A	1181	ASN	MET	conflict	UNP A8EVM5

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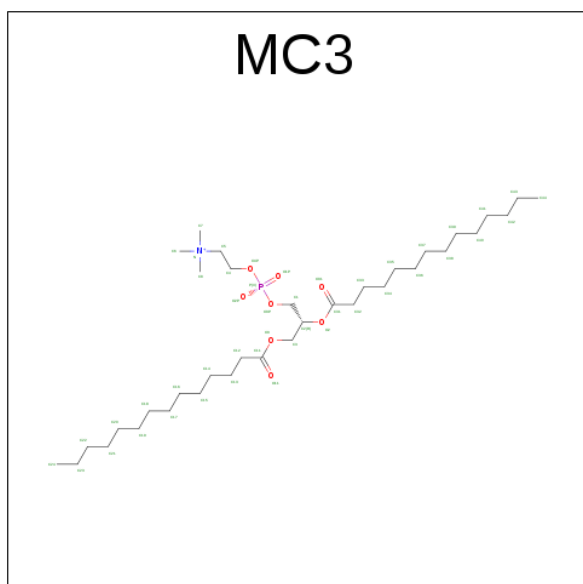
Chain	Residue	Modelled	Actual	Comment	Reference
B	983	MET	-	initiating methionine	UNP A8EVM5
B	984	ASP	-	expression tag	UNP A8EVM5
B	985	TYR	-	expression tag	UNP A8EVM5
B	986	LYS	-	expression tag	UNP A8EVM5
B	987	ASP	-	expression tag	UNP A8EVM5
B	988	ASP	-	expression tag	UNP A8EVM5
B	989	ASP	-	expression tag	UNP A8EVM5
B	990	ASP	-	expression tag	UNP A8EVM5
B	991	LYS	-	expression tag	UNP A8EVM5
B	992	GLY	-	expression tag	UNP A8EVM5
B	993	SER	-	expression tag	UNP A8EVM5
B	994	LEU	-	expression tag	UNP A8EVM5
B	995	VAL	-	expression tag	UNP A8EVM5
B	996	PRO	-	expression tag	UNP A8EVM5
B	997	ARG	-	expression tag	UNP A8EVM5
B	998	GLY	-	expression tag	UNP A8EVM5
B	999	SER	-	expression tag	UNP A8EVM5
B	1000	HIS	-	expression tag	UNP A8EVM5
B	1177	ASP	GLU	conflict	UNP A8EVM5
B	1178	ASP	SER	conflict	UNP A8EVM5
B	1181	ASN	MET	conflict	UNP A8EVM5
C	983	MET	-	initiating methionine	UNP A8EVM5
C	984	ASP	-	expression tag	UNP A8EVM5
C	985	TYR	-	expression tag	UNP A8EVM5
C	986	LYS	-	expression tag	UNP A8EVM5
C	987	ASP	-	expression tag	UNP A8EVM5
C	988	ASP	-	expression tag	UNP A8EVM5
C	989	ASP	-	expression tag	UNP A8EVM5
C	990	ASP	-	expression tag	UNP A8EVM5
C	991	LYS	-	expression tag	UNP A8EVM5
C	992	GLY	-	expression tag	UNP A8EVM5
C	993	SER	-	expression tag	UNP A8EVM5
C	994	LEU	-	expression tag	UNP A8EVM5
C	995	VAL	-	expression tag	UNP A8EVM5
C	996	PRO	-	expression tag	UNP A8EVM5
C	997	ARG	-	expression tag	UNP A8EVM5
C	998	GLY	-	expression tag	UNP A8EVM5
C	999	SER	-	expression tag	UNP A8EVM5
C	1000	HIS	-	expression tag	UNP A8EVM5
C	1177	ASP	GLU	conflict	UNP A8EVM5
C	1178	ASP	SER	conflict	UNP A8EVM5
C	1181	ASN	MET	conflict	UNP A8EVM5

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Chain	Residue	Modelled	Actual	Comment	Reference
D	983	MET	-	initiating methionine	UNP A8EVM5
D	984	ASP	-	expression tag	UNP A8EVM5
D	985	TYR	-	expression tag	UNP A8EVM5
D	986	LYS	-	expression tag	UNP A8EVM5
D	987	ASP	-	expression tag	UNP A8EVM5
D	988	ASP	-	expression tag	UNP A8EVM5
D	989	ASP	-	expression tag	UNP A8EVM5
D	990	ASP	-	expression tag	UNP A8EVM5
D	991	LYS	-	expression tag	UNP A8EVM5
D	992	GLY	-	expression tag	UNP A8EVM5
D	993	SER	-	expression tag	UNP A8EVM5
D	994	LEU	-	expression tag	UNP A8EVM5
D	995	VAL	-	expression tag	UNP A8EVM5
D	996	PRO	-	expression tag	UNP A8EVM5
D	997	ARG	-	expression tag	UNP A8EVM5
D	998	GLY	-	expression tag	UNP A8EVM5
D	999	SER	-	expression tag	UNP A8EVM5
D	1000	HIS	-	expression tag	UNP A8EVM5
D	1177	ASP	GLU	conflict	UNP A8EVM5
D	1178	ASP	SER	conflict	UNP A8EVM5
D	1181	ASN	MET	conflict	UNP A8EVM5

- Molecule 2 is 1,2-DIMYRISTOYL-RAC-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: MC3) (formula:  $C_{36}H_{72}NO_8P$ ).

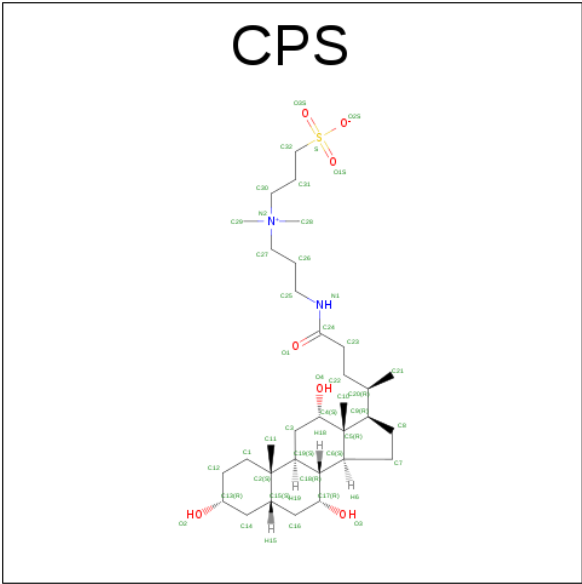


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O P 21 13 7 1	0	0
2	A	1	Total C N O P 46 36 1 8 1	0	0
2	B	1	Total C O P 21 13 7 1	0	0
2	B	1	Total C O P 41 32 8 1	0	0
2	B	1	Total C N O P 41 31 1 8 1	0	0
2	B	1	Total C N O P 46 36 1 8 1	0	0
2	B	1	Total C 8 8	0	0
2	C	1	Total C O P 21 13 7 1	0	0
2	C	1	Total C O P 41 32 8 1	0	0
2	C	1	Total C N O P 40 30 1 8 1	0	0
2	C	1	Total C N O P 46 36 1 8 1	0	0
2	C	1	Total C 9 9	0	0
2	C	1	Total C 9 9	0	0
2	C	1	Total C O P 41 32 8 1	0	0
2	D	1	Total C O P 21 13 7 1	0	0
2	D	1	Total C O P 41 32 8 1	0	0
2	D	1	Total C N O P 43 33 1 8 1	0	0
2	D	1	Total C N O P 42 32 1 8 1	0	0
2	D	1	Total C N O P 46 36 1 8 1	0	0
2	D	1	Total C 8 8	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Ca 1 1	0	0
3	A	1	Total Ca 1 1	0	0
3	D	1	Total Ca 1 1	0	0

- Molecule 4 is 3-[(3-CHOLAMIDOPROPYL)DIMETHYLAMMONIO]-1-PROPANESULFO NATE (three-letter code: CPS) (formula: C<sub>32</sub>H<sub>58</sub>N<sub>2</sub>O<sub>7</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O S 42 32 2 7 1	0	0
4	A	1	Total C N O S 42 32 2 7 1	0	0
4	A	1	Total C N O S 42 32 2 7 1	0	0
4	B	1	Total C N O S 42 32 2 7 1	0	0
4	B	1	Total C N O S 42 32 2 7 1	0	0
4	D	1	Total C N O S 42 32 2 7 1	0	0

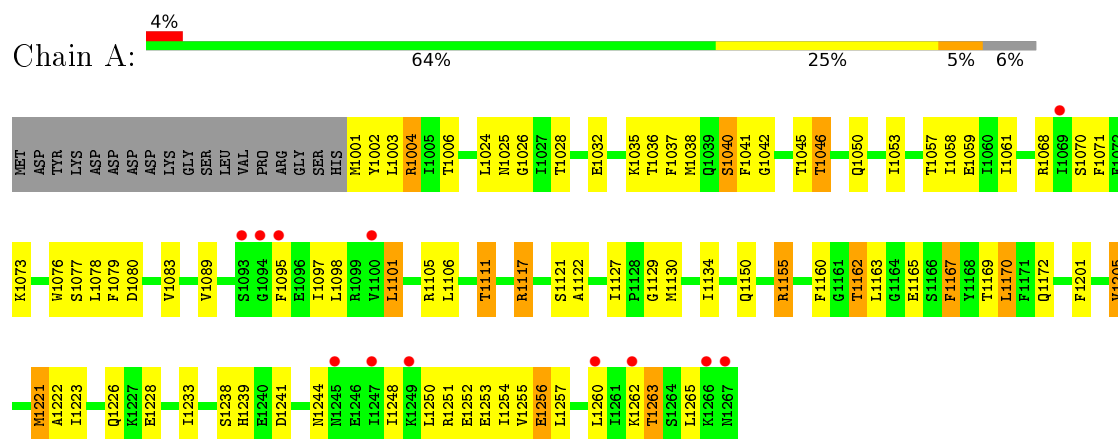
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total 3	O 3	0	0
5	B	6	Total 6	O 6	0	0
5	C	3	Total 3	O 3	0	0
5	D	5	Total 5	O 5	0	0

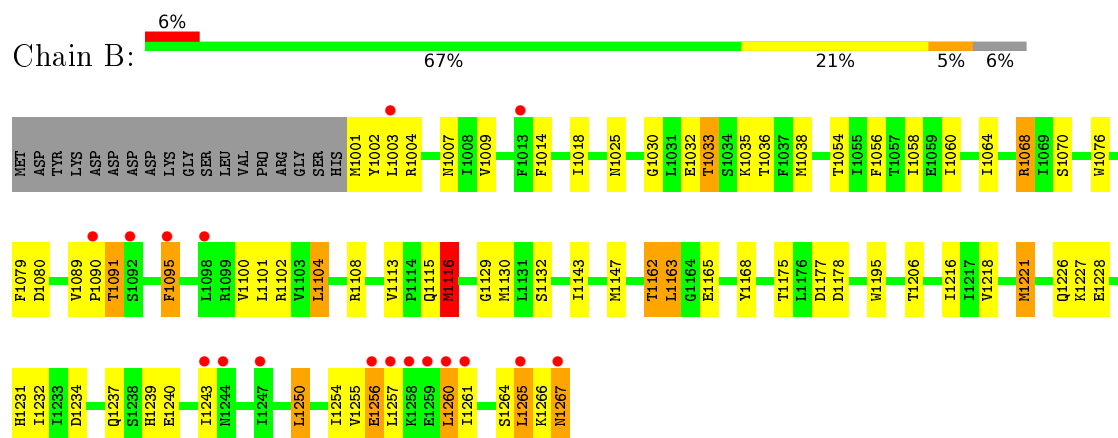
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

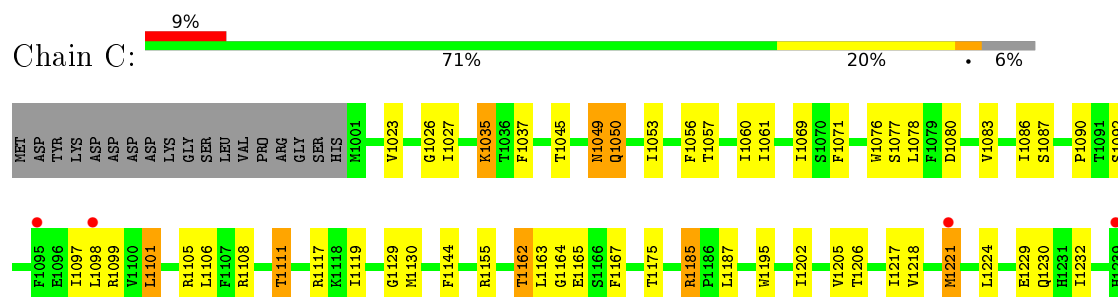
#### • Molecule 1: Ion transport protein

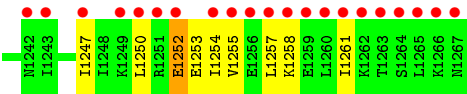


#### • Molecule 1: Ion transport protein

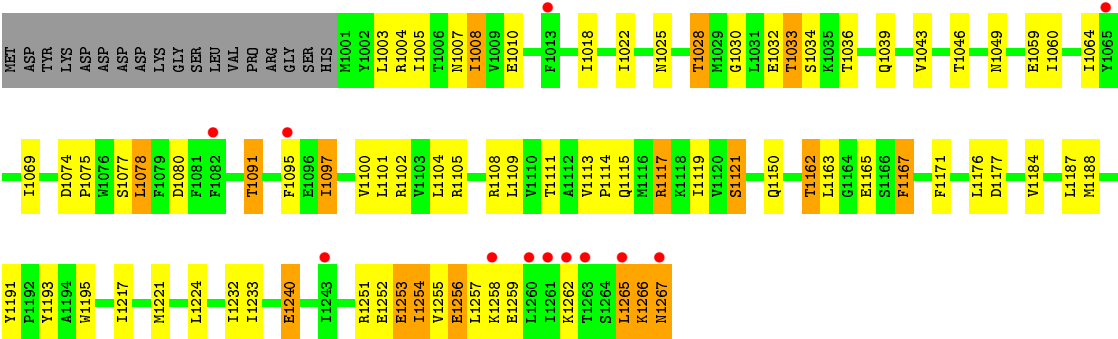


#### • Molecule 1: Ion transport protein





● Molecule 1: Ion transport protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	124.90Å 125.70Å 191.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.93 – 2.70 29.93 – 2.70	Depositor EDS
% Data completeness (in resolution range)	92.5 (29.93-2.70) 91.8 (29.93-2.70)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.08 (at 2.68Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1839)	Depositor
R, $R_{free}$	0.219 , 0.260 0.219 , 0.261	Depositor DCC
$R_{free}$ test set	3784 reflections (4.95%)	DCC
Wilson B-factor (Å <sup>2</sup> )	58.8	Xtriage
Anisotropy	0.569	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 56.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.055 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	9684	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.83% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, CPS, MC3

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	0.60	0/2248	0.65	0/3053
1	B	0.58	0/2248	0.63	1/3053 (0.0%)
1	C	0.58	0/2248	0.64	0/3053
1	D	0.61	0/2248	0.67	0/3053
All	All	0.59	0/8992	0.65	1/12212 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1116	MET	CG-SD-CE	-5.29	91.73	100.20

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	2195	0	2274	54	0
1	B	2195	0	2274	60	0
1	C	2195	0	2274	55	0
1	D	2195	0	2274	53	0
2	A	67	0	91	4	0
2	B	157	0	218	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	207	0	291	22	0
2	D	201	0	283	9	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
4	A	126	0	135	65	0
4	B	84	0	89	39	0
4	D	42	0	45	23	0
5	A	3	0	0	0	0
5	B	6	0	0	0	0
5	C	3	0	0	0	0
5	D	5	0	0	1	0
All	All	9684	0	10248	329	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 17.

All (329) 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)
4:A:1305:CPS:O3	4:A:1305:CPS:C17	1.69	1.39
4:D:1308:CPS:C17	4:D:1308:CPS:O3	1.70	1.39
4:A:1306:CPS:O3	4:A:1306:CPS:C17	1.70	1.39
4:B:1307:CPS:C17	4:B:1307:CPS:O3	1.69	1.38
4:A:1304:CPS:C10	4:A:1304:CPS:C4	2.02	1.37
4:A:1306:CPS:C13	4:A:1306:CPS:O2	1.73	1.36
4:A:1304:CPS:O3	4:A:1304:CPS:C17	1.71	1.36
4:A:1305:CPS:O2	4:A:1305:CPS:C13	1.73	1.36
4:B:1307:CPS:O2	4:B:1307:CPS:C13	1.73	1.36
4:B:1308:CPS:C17	4:B:1308:CPS:O3	1.71	1.35
4:D:1308:CPS:C4	4:D:1308:CPS:C10	2.05	1.34
4:D:1308:CPS:C13	4:D:1308:CPS:O2	1.73	1.34
4:A:1305:CPS:C4	4:A:1305:CPS:C10	2.06	1.34
4:A:1306:CPS:C4	4:A:1306:CPS:O4	1.76	1.33
4:B:1308:CPS:C13	4:B:1308:CPS:O2	1.75	1.33
4:A:1304:CPS:O2	4:A:1304:CPS:C13	1.74	1.32
4:A:1305:CPS:C9	4:A:1305:CPS:C4	2.05	1.32
4:D:1308:CPS:C4	4:D:1308:CPS:C9	2.08	1.32
4:A:1305:CPS:O4	4:A:1305:CPS:C4	1.77	1.31
4:D:1308:CPS:C4	4:D:1308:CPS:O4	1.78	1.31
4:A:1304:CPS:O4	4:A:1304:CPS:C4	1.77	1.31

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1308:CPS:C4	4:B:1308:CPS:C9	2.08	1.31
4:B:1308:CPS:C4	4:B:1308:CPS:O4	1.78	1.30
4:A:1304:CPS:C9	4:A:1304:CPS:C4	2.08	1.30
4:B:1307:CPS:O4	4:B:1307:CPS:C4	1.78	1.30
4:B:1308:CPS:C4	4:B:1308:CPS:C10	2.08	1.29
4:D:1308:CPS:C3	4:D:1308:CPS:C5	2.13	1.16
4:D:1308:CPS:C4	4:D:1308:CPS:C6	2.09	1.14
4:A:1305:CPS:C3	4:A:1305:CPS:C5	2.13	1.13
4:A:1304:CPS:C5	4:A:1304:CPS:C3	2.11	1.10
4:A:1304:CPS:C6	4:A:1304:CPS:C4	2.12	1.09
4:B:1308:CPS:C3	4:B:1308:CPS:C5	2.14	1.08
4:B:1308:CPS:C4	4:B:1308:CPS:C6	2.05	1.08
4:A:1305:CPS:C4	4:A:1305:CPS:C6	2.10	1.05
4:D:1308:CPS:C4	4:D:1308:CPS:C5	0.94	0.94
4:A:1304:CPS:C5	4:A:1304:CPS:C4	0.93	0.93
4:A:1305:CPS:C4	4:A:1305:CPS:C5	0.93	0.92
4:B:1308:CPS:C4	4:B:1308:CPS:C5	0.93	0.92
4:B:1308:CPS:O4	4:B:1308:CPS:C5	2.22	0.88
4:A:1306:CPS:O4	4:A:1306:CPS:C5	2.23	0.83
4:A:1305:CPS:O4	4:A:1305:CPS:C5	2.25	0.83
1:A:1257:LEU:HD21	1:C:1257:LEU:HD21	1.61	0.82
1:B:1162:THR:HG22	1:B:1165:GLU:H	1.44	0.82
4:B:1307:CPS:C14	4:B:1307:CPS:O2	2.25	0.81
1:D:1162:THR:HG22	1:D:1165:GLU:H	1.45	0.81
4:A:1304:CPS:C5	4:A:1304:CPS:O4	2.26	0.81
4:A:1305:CPS:O2	4:A:1305:CPS:C14	2.27	0.80
4:D:1308:CPS:C5	4:D:1308:CPS:O4	2.29	0.80
4:B:1307:CPS:O4	4:B:1307:CPS:C5	2.27	0.78
4:B:1308:CPS:C3	4:B:1308:CPS:C10	2.60	0.77
2:C:1304:MC3:H161	2:C:1304:MC3:H381	1.67	0.76
1:A:1122:ALA:HB1	4:A:1305:CPS:H25A	1.69	0.75
1:B:1265:LEU:HD12	1:B:1265:LEU:O	1.86	0.74
4:A:1306:CPS:C14	4:A:1306:CPS:O2	2.29	0.74
1:C:1247:ILE:HA	1:C:1250:LEU:HB2	1.72	0.71
1:A:1162:THR:HG22	1:A:1165:GLU:H	1.55	0.70
4:D:1308:CPS:C3	4:D:1308:CPS:C10	2.63	0.70
4:A:1304:CPS:O2	4:A:1304:CPS:C14	2.31	0.70
1:B:1254:ILE:HG12	1:D:1254:ILE:HD13	1.75	0.69
1:C:1162:THR:HG22	1:C:1165:GLU:H	1.57	0.69
2:C:1302:MC3:H121	2:C:1302:MC3:H342	1.74	0.68
1:A:1163:LEU:HB2	1:D:1033:THR:HG21	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1206:THR:HG21	2:C:1306:MC3:H332	1.76	0.67
1:A:1025:ASN:OD1	1:A:1105:ARG:NH1	2.26	0.67
1:A:1026:GLY:HA3	2:C:1307:MC3:H231	1.77	0.67
1:A:1073:LYS:NZ	4:A:1304:CPS:H3	2.09	0.67
1:A:1127:ILE:HA	1:A:1130:MET:HE2	1.77	0.66
4:D:1308:CPS:H3A	4:D:1308:CPS:H10A	1.76	0.66
4:D:1308:CPS:C12	4:D:1308:CPS:O2	2.44	0.65
1:B:1030:GLY:O	1:B:1033:THR:HB	1.97	0.65
4:B:1308:CPS:C3	4:B:1308:CPS:H10A	2.27	0.64
1:C:1252:GLU:HA	1:C:1255:VAL:HB	1.79	0.64
1:C:1026:GLY:HA3	2:C:1302:MC3:H231	1.79	0.64
4:B:1308:CPS:H3A	4:B:1308:CPS:H10A	1.79	0.63
1:D:1003:LEU:O	1:D:1007:ASN:ND2	2.30	0.63
4:D:1308:CPS:C14	4:D:1308:CPS:O2	2.31	0.63
1:D:1265:LEU:O	1:D:1267:ASN:N	2.31	0.63
4:A:1305:CPS:C18	4:A:1305:CPS:O3	2.37	0.63
1:B:1132:SER:HB2	1:C:1119:ILE:HD11	1.80	0.63
4:A:1306:CPS:O4	4:A:1306:CPS:C3	2.47	0.62
1:A:1221:MET:HE1	1:C:1218:VAL:HA	1.80	0.62
4:B:1308:CPS:H10B	4:B:1308:CPS:H21A	1.82	0.62
2:B:1303:MC3:H402	2:B:1303:MC3:H182	1.81	0.62
1:D:1259:GLU:HA	1:D:1262:LYS:HB2	1.80	0.61
1:B:1254:ILE:HD12	1:C:1250:LEU:HD22	1.83	0.61
1:D:1251:ARG:O	1:D:1255:VAL:HG13	2.01	0.61
4:A:1305:CPS:O4	4:A:1305:CPS:H9	2.01	0.61
1:C:1202:ILE:O	1:C:1206:THR:HG22	2.00	0.60
4:A:1304:CPS:C10	4:A:1304:CPS:C3	2.68	0.60
1:B:1129:GLY:HA3	4:B:1307:CPS:O3	2.00	0.60
1:C:1037:PHE:HE1	1:C:1045:THR:HG21	1.64	0.60
1:D:1171:PHE:HB2	2:D:1304:MC3:H142	1.83	0.60
1:D:1091:THR:HA	1:D:1102:ARG:HH22	1.66	0.60
4:D:1308:CPS:C16	4:D:1308:CPS:O3	2.48	0.60
4:B:1308:CPS:C18	4:B:1308:CPS:O3	2.39	0.60
1:A:1070:SER:OG	4:A:1304:CPS:O4	2.13	0.60
1:D:1177:ASP:OD1	5:D:1401:HOH:O	2.17	0.59
1:A:1254:ILE:HD13	1:D:1253:GLU:HG2	1.83	0.59
4:D:1308:CPS:H30	4:D:1308:CPS:O2S	2.03	0.59
1:B:1001:MET:N	4:B:1308:CPS:H29B	2.17	0.59
1:A:1003:LEU:HA	1:A:1006:THR:HB	1.85	0.59
1:A:1257:LEU:HD11	1:C:1257:LEU:HD11	1.84	0.59
4:A:1304:CPS:H3A	4:A:1304:CPS:H10A	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1057:THR:O	1:C:1061:ILE:HG12	2.03	0.58
1:C:1258:LYS:O	1:C:1258:LYS:HD2	2.03	0.58
4:D:1308:CPS:C3	4:D:1308:CPS:H10A	2.31	0.58
4:A:1306:CPS:O3	4:A:1306:CPS:C16	2.49	0.58
1:A:1050:GLN:O	1:A:1053:ILE:HG22	2.05	0.57
1:C:1080:ASP:OD1	1:C:1111:THR:HG21	2.05	0.57
1:B:1076:TRP:CH2	2:B:1302:MC3:H121	2.41	0.56
1:B:1033:THR:HG21	1:D:1163:LEU:HB2	1.88	0.56
4:A:1305:CPS:C4	4:A:1305:CPS:H9	2.29	0.56
2:B:1304:MC3:H122	1:C:1167:PHE:HB3	1.88	0.56
1:A:1130:MET:HE3	1:A:1134:ILE:HD11	1.88	0.55
4:B:1308:CPS:C6	4:B:1308:CPS:O4	2.54	0.55
4:A:1305:CPS:O4	4:A:1305:CPS:C9	2.54	0.55
4:A:1306:CPS:H29B	4:A:1306:CPS:O2S	2.07	0.55
1:D:1255:VAL:O	1:D:1258:LYS:HG2	2.07	0.55
1:A:1253:GLU:HB3	1:C:1254:ILE:HG21	1.87	0.55
1:B:1206:THR:HG21	2:C:1305:MC3:H332	1.89	0.55
1:A:1032:GLU:HG2	1:A:1038:MET:HE3	1.89	0.54
4:A:1304:CPS:H10A	4:A:1304:CPS:C3	2.37	0.54
1:B:1162:THR:HG22	1:B:1165:GLU:N	2.19	0.54
1:D:1030:GLY:O	1:D:1033:THR:HB	2.08	0.54
1:B:1032:GLU:HG2	1:B:1038:MET:HE1	1.88	0.54
1:C:1080:ASP:OD1	1:C:1108:ARG:NE	2.39	0.54
1:B:1239:HIS:HB3	1:D:1240:GLU:HG2	1.90	0.54
4:B:1307:CPS:O3	4:B:1307:CPS:C16	2.52	0.54
2:C:1302:MC3:H352	2:D:1305:MC3:O31	2.07	0.54
4:A:1305:CPS:O2	4:A:1305:CPS:C12	2.50	0.54
1:B:1004:ARG:NH1	4:B:1308:CPS:O1S	2.41	0.53
1:A:1252:GLU:HA	1:A:1255:VAL:HG12	1.89	0.53
4:D:1308:CPS:C3	4:D:1308:CPS:O4	2.54	0.53
4:A:1306:CPS:HO3	4:A:1306:CPS:C17	2.13	0.53
4:D:1308:CPS:C10	4:D:1308:CPS:H3A	2.36	0.53
4:B:1308:CPS:H3A	4:B:1308:CPS:C10	2.34	0.53
1:B:1035:LYS:HG3	1:B:1036:THR:N	2.24	0.52
1:A:1076:TRP:CD2	1:A:1117:ARG:HD2	2.44	0.52
1:B:1002:TYR:HD2	1:B:1003:LEU:HD23	1.74	0.52
1:A:1001:MET:HA	1:A:1004:ARG:HD3	1.92	0.52
1:A:1073:LYS:HZ3	4:A:1304:CPS:H3	1.73	0.52
1:B:1101:LEU:O	1:B:1104:LEU:HB2	2.10	0.52
1:D:1060:ILE:O	1:D:1064:ILE:HG13	2.09	0.52
1:B:1264:SER:O	1:B:1265:LEU:HB3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1305:MC3:H182	2:B:1305:MC3:H402	1.91	0.52
2:C:1303:MC3:H321	2:D:1303:MC3:H352	1.92	0.51
1:B:1091:THR:HG23	1:B:1102:ARG:HH21	1.74	0.51
1:B:1056:PHE:O	1:B:1060:ILE:HG12	2.10	0.51
1:A:1040:SER:HB3	1:A:1041:PHE:CD2	2.45	0.51
1:D:1117:ARG:O	1:D:1121:SER:HB2	2.11	0.51
4:B:1308:CPS:C14	4:B:1308:CPS:O2	2.36	0.51
1:B:1221:MET:HE2	1:D:1221:MET:HB3	1.93	0.51
1:B:1254:ILE:CG1	1:D:1254:ILE:HD13	2.39	0.51
1:B:1227:LYS:O	1:B:1231:HIS:ND1	2.44	0.51
1:D:1025:ASN:OD1	1:D:1105:ARG:HD2	2.11	0.51
4:D:1308:CPS:C4	4:D:1308:CPS:H9	2.30	0.51
2:B:1304:MC3:H321	2:B:1304:MC3:H121	1.93	0.51
1:B:1221:MET:HG2	1:D:1221:MET:HE3	1.92	0.51
1:A:1042:GLY:O	1:A:1046:THR:OG1	2.29	0.50
1:B:1163:LEU:HD12	2:C:1302:MC3:H351	1.93	0.50
1:B:1175:THR:HG22	2:B:1306:MC3:H161	1.93	0.50
1:D:1074:ASP:OD2	1:D:1077:SER:OG	2.22	0.50
1:B:1221:MET:CE	1:D:1221:MET:HB3	2.42	0.50
4:A:1305:CPS:O3	1:C:1129:GLY:HA3	2.12	0.50
1:B:1079:PHE:CD1	2:B:1302:MC3:H162	2.47	0.50
1:B:1227:LYS:HE2	1:B:1231:HIS:CE1	2.46	0.50
1:D:1115:GLN:N	1:D:1115:GLN:OE1	2.40	0.50
1:B:1143:ILE:HD11	1:C:1106:LEU:HB2	1.92	0.50
1:C:1087:SER:OG	1:C:1105:ARG:NH1	2.45	0.50
1:C:1050:GLN:HA	1:C:1053:ILE:HG22	1.94	0.50
1:C:1217:ILE:O	1:C:1221:MET:HG2	2.12	0.50
1:D:1075:PRO:HB2	2:D:1302:MC3:H121	1.93	0.50
1:C:1098:LEU:HD23	1:C:1101:LEU:HD23	1.94	0.49
1:D:1043:VAL:HA	1:D:1046:THR:HG22	1.94	0.49
1:B:1018:ILE:HD13	1:B:1108:ARG:HH21	1.76	0.49
1:C:1076:TRP:CZ2	1:C:1117:ARG:HG2	2.47	0.49
1:A:1150:GLN:OE1	1:D:1100:VAL:HG22	2.12	0.49
1:A:1221:MET:SD	1:D:1221:MET:SD	3.11	0.49
1:B:1218:VAL:HA	1:C:1221:MET:HE1	1.95	0.49
1:A:1080:ASP:OD1	1:A:1111:THR:HG21	2.12	0.49
2:A:1303:MC3:H362	1:D:1097:ILE:HD12	1.94	0.49
1:B:1267:ASN:N	1:B:1267:ASN:OD1	2.45	0.49
1:A:1106:LEU:HB3	2:C:1307:MC3:H241	1.95	0.49
4:A:1305:CPS:O3	4:A:1305:CPS:C16	2.52	0.49
1:B:1240:GLU:HA	1:B:1243:ILE:HG12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1262:LYS:HD2	1:A:1265:LEU:HB2	1.95	0.49
1:B:1113:VAL:O	1:B:1116:MET:HB2	2.13	0.49
4:A:1304:CPS:HO3	4:A:1304:CPS:C17	2.14	0.48
1:C:1056:PHE:O	1:C:1060:ILE:HG12	2.12	0.48
4:B:1308:CPS:O1	4:B:1308:CPS:H272	2.13	0.48
2:D:1306:MC3:H161	2:D:1306:MC3:H381	1.94	0.48
1:A:1155:ARG:HH21	2:A:1303:MC3:H61	1.78	0.48
1:A:1076:TRP:CZ2	2:A:1301:MC3:H2	2.48	0.48
4:A:1306:CPS:C12	4:A:1306:CPS:O2	2.54	0.48
1:A:1129:GLY:HA3	4:A:1306:CPS:O3	2.14	0.48
1:A:1244:ASN:O	1:A:1248:ILE:HG13	2.13	0.48
4:B:1307:CPS:HO3	4:B:1307:CPS:C17	2.13	0.48
1:A:1089:VAL:HG21	1:A:1098:LEU:HD13	1.96	0.47
1:C:1106:LEU:HB3	2:C:1302:MC3:H241	1.97	0.47
1:C:1023:VAL:O	1:C:1027:ILE:HG13	2.14	0.47
1:A:1079:PHE:O	1:A:1083:VAL:HB	2.15	0.47
1:C:1035:LYS:HA	1:C:1035:LYS:HD3	1.71	0.47
1:D:1080:ASP:OD2	1:D:1111:THR:HG21	2.15	0.47
1:B:1195:TRP:NE1	2:B:1304:MC3:H42	2.30	0.47
2:B:1304:MC3:O2P	1:C:1164:GLY:HA3	2.15	0.47
4:A:1305:CPS:H28	4:A:1305:CPS:H31	1.44	0.46
1:A:1172:GLN:OE1	1:C:1185:ARG:NH1	2.48	0.46
1:C:1195:TRP:CZ2	2:C:1303:MC3:H12	2.51	0.46
1:B:1100:VAL:HG22	1:D:1150:GLN:OE1	2.15	0.46
4:B:1308:CPS:C17	4:B:1308:CPS:HO3	2.14	0.46
1:C:1097:ILE:HG13	1:C:1101:LEU:HD22	1.96	0.46
4:A:1304:CPS:C13	4:A:1304:CPS:HO2	2.17	0.46
1:B:1130:MET:HE1	1:B:1216:ILE:HD11	1.97	0.46
1:D:1188:MET:HA	1:D:1191:TYR:O	2.15	0.46
1:A:1076:TRP:CZ2	1:A:1117:ARG:HG3	2.51	0.46
1:B:1009:VAL:HA	1:B:1014:PHE:CD2	2.50	0.46
4:B:1308:CPS:C6	4:B:1308:CPS:O3	2.62	0.46
1:C:1071:PHE:CE2	1:C:1077:SER:HB3	2.51	0.46
4:D:1308:CPS:H23	4:D:1308:CPS:H21	1.78	0.46
1:D:1036:THR:O	1:D:1039:GLN:HG2	2.16	0.46
1:D:1115:GLN:O	1:D:1119:ILE:HG12	2.16	0.46
1:A:1035:LYS:HA	1:A:1035:LYS:HD2	1.75	0.46
1:C:1050:GLN:O	1:C:1053:ILE:HG22	2.16	0.46
1:A:1037:PHE:HD1	1:A:1038:MET:HE2	1.80	0.45
1:D:1018:ILE:O	1:D:1022:ILE:HG13	2.16	0.45
1:A:1071:PHE:CE1	1:A:1077:SER:HB3	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1305:CPS:C3	4:A:1305:CPS:C10	2.78	0.45
1:B:1256:GLU:O	1:B:1260:LEU:HB2	2.17	0.45
4:A:1306:CPS:H31A	4:A:1306:CPS:H29	1.67	0.45
1:B:1266:LYS:HE3	1:B:1266:LYS:HB3	1.76	0.45
4:B:1307:CPS:HO2	4:B:1307:CPS:C13	2.16	0.45
4:B:1308:CPS:H21B	4:B:1308:CPS:N1	2.31	0.45
1:C:1195:TRP:CH2	2:C:1303:MC3:H12	2.51	0.45
1:B:1232:ILE:HD13	1:D:1232:ILE:HG21	1.99	0.45
4:B:1308:CPS:C3	4:B:1308:CPS:O4	2.58	0.45
1:A:1058:ILE:HA	1:A:1061:ILE:HD12	1.97	0.45
1:A:1222:ALA:O	1:A:1226:GLN:HG2	2.16	0.45
4:A:1304:CPS:O2	4:A:1304:CPS:C12	2.57	0.45
1:D:1113:VAL:HA	1:D:1114:PRO:HD3	1.76	0.45
1:C:1130:MET:HE2	1:C:1130:MET:HB2	1.69	0.45
4:B:1308:CPS:C9	4:B:1308:CPS:O4	2.65	0.45
4:D:1308:CPS:C13	4:D:1308:CPS:HO2	2.16	0.45
4:A:1305:CPS:H23	4:A:1305:CPS:H21	1.60	0.45
1:B:1250:LEU:HD13	1:C:1250:LEU:HD13	1.99	0.44
1:C:1078:LEU:HA	1:C:1078:LEU:HD23	1.74	0.44
1:A:1170:LEU:HA	1:A:1170:LEU:HD12	1.86	0.44
4:A:1304:CPS:H9	4:A:1304:CPS:O4	2.18	0.44
1:D:1167:PHE:CE2	2:D:1304:MC3:H341	2.53	0.44
2:D:1306:MC3:H41	2:D:1306:MC3:H83	1.66	0.44
2:D:1306:MC3:H362	2:D:1306:MC3:H141	1.99	0.44
4:A:1304:CPS:C9	4:A:1304:CPS:O4	2.66	0.44
1:B:1195:TRP:CZ3	2:B:1304:MC3:H32	2.53	0.44
4:B:1307:CPS:H11B	4:B:1307:CPS:H3A	1.76	0.44
1:C:1108:ARG:O	1:C:1111:THR:HG22	2.17	0.44
1:B:1261:ILE:HD12	1:B:1261:ILE:HA	1.82	0.44
1:C:1090:PRO:O	1:C:1092:SER:N	2.49	0.44
4:A:1306:CPS:O4	4:A:1306:CPS:H9	2.18	0.44
1:B:1089:VAL:HA	1:B:1090:PRO:HD3	1.89	0.44
1:A:1221:MET:SD	1:C:1221:MET:HG3	2.58	0.44
2:C:1303:MC3:H73	2:C:1303:MC3:H41	1.53	0.44
4:A:1305:CPS:H261	4:A:1305:CPS:H29B	1.73	0.43
1:D:1256:GLU:HG3	1:D:1257:LEU:N	2.33	0.43
2:C:1303:MC3:H332	2:D:1303:MC3:H372	2.00	0.43
1:C:1049:ASN:OD1	1:C:1105:ARG:NH2	2.51	0.43
4:D:1308:CPS:HO3	4:D:1308:CPS:C17	2.13	0.43
1:C:1069:ILE:HA	1:C:1069:ILE:HD12	1.83	0.43
4:A:1305:CPS:HO3	4:A:1305:CPS:C17	2.12	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1306:CPS:O4	4:A:1306:CPS:C6	2.66	0.43
1:B:1003:LEU:O	1:B:1007:ASN:N	2.46	0.43
1:B:1250:LEU:O	1:B:1254:ILE:HG13	2.19	0.43
1:A:1053:ILE:HD12	1:A:1053:ILE:HA	1.79	0.43
4:A:1305:CPS:O3	4:A:1305:CPS:C6	2.67	0.43
1:C:1250:LEU:HD23	1:C:1250:LEU:HA	1.81	0.43
1:D:1255:VAL:HA	1:D:1258:LYS:HD2	2.01	0.43
4:D:1308:CPS:O3	4:D:1308:CPS:C18	2.43	0.43
1:C:1257:LEU:HD13	1:C:1261:ILE:HD12	2.00	0.43
1:B:1080:ASP:OD2	1:B:1108:ARG:HG2	2.19	0.43
4:B:1307:CPS:H29	4:B:1307:CPS:H31A	1.82	0.43
1:D:1101:LEU:HD22	1:D:1104:LEU:HD11	2.00	0.43
4:B:1308:CPS:C13	4:B:1308:CPS:HO2	2.18	0.42
1:C:1076:TRP:CH2	1:C:1117:ARG:HG2	2.54	0.42
1:D:1028:THR:O	1:D:1032:GLU:HG3	2.19	0.42
1:D:1162:THR:HG22	1:D:1165:GLU:N	2.24	0.42
4:B:1307:CPS:O4	4:B:1307:CPS:H9	2.19	0.42
1:B:1168:TYR:OH	1:D:1184:VAL:HG22	2.20	0.42
4:A:1305:CPS:HO2	4:A:1305:CPS:C13	2.16	0.42
1:D:1193:TYR:HA	1:D:1195:TRP:NE1	2.35	0.42
1:A:1097:ILE:HG13	1:A:1101:LEU:CD2	2.50	0.42
1:B:1101:LEU:HA	1:B:1101:LEU:HD23	1.79	0.42
2:C:1304:MC3:H42	2:C:1304:MC3:H72	1.81	0.42
1:A:1252:GLU:O	1:A:1256:GLU:HB2	2.20	0.42
1:B:1143:ILE:O	1:B:1147:MET:HG3	2.20	0.41
1:B:1234:ASP:HA	1:B:1237:GLN:HB3	2.01	0.41
2:B:1305:MC3:H322	2:B:1305:MC3:H351	1.57	0.41
1:D:1059:GLU:OE1	1:D:1108:ARG:NH2	2.53	0.41
1:A:1260:LEU:HA	1:A:1263:THR:OG1	2.20	0.41
1:A:1130:MET:HB2	1:A:1130:MET:HE2	1.74	0.41
1:B:1195:TRP:CE3	2:B:1304:MC3:H32	2.55	0.41
1:D:1005:ILE:O	1:D:1008:ILE:HG23	2.20	0.41
1:A:1250:LEU:HD23	1:A:1250:LEU:HA	1.87	0.41
4:A:1306:CPS:H11B	4:A:1306:CPS:H3A	1.85	0.41
1:C:1101:LEU:HA	1:C:1101:LEU:HD12	1.89	0.41
1:D:1060:ILE:HD13	1:D:1060:ILE:HA	1.93	0.41
1:B:1265:LEU:CD1	1:B:1265:LEU:O	2.64	0.41
4:A:1304:CPS:H10	4:A:1304:CPS:H8A	1.58	0.41
1:B:1095:PHE:HD2	1:B:1095:PHE:HA	1.77	0.41
4:B:1307:CPS:O4	4:B:1307:CPS:C9	2.69	0.41
1:D:1217:ILE:HG22	1:D:1221:MET:HE2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1303:MC3:O31	2:A:1303:MC3:H131	2.21	0.41
1:C:1163:LEU:HD22	2:C:1307:MC3:H122	2.02	0.41
1:A:1201:PHE:O	1:A:1205:VAL:HB	2.20	0.41
4:A:1304:CPS:C18	4:A:1304:CPS:O3	2.46	0.41
1:B:1143:ILE:CD1	1:C:1106:LEU:HB2	2.50	0.41
1:C:1175:THR:HG22	2:C:1305:MC3:H342	2.02	0.41
1:D:1004:ARG:O	1:D:1008:ILE:HG22	2.21	0.41
1:D:1224:LEU:HD23	1:D:1224:LEU:HA	1.84	0.41
1:A:1053:ILE:O	1:A:1057:THR:OG1	2.34	0.40
1:C:1144:PHE:HZ	2:C:1304:MC3:H202	1.86	0.40
2:C:1303:MC3:H392	2:C:1303:MC3:H181	2.04	0.40
4:A:1304:CPS:H261	4:A:1304:CPS:H28A	1.53	0.40
1:D:1069:ILE:HA	1:D:1069:ILE:HD12	1.78	0.40
1:B:1177:ASP:O	1:B:1178:ASP:C	2.59	0.40
1:A:1160:PHE:CZ	1:A:1169:THR:HG21	2.56	0.40
1:B:1064:ILE:O	1:B:1068:ARG:N	2.44	0.40
1:C:1163:LEU:CD2	2:C:1307:MC3:H122	2.52	0.40
4:A:1306:CPS:O3	4:A:1306:CPS:C18	2.43	0.40
1:A:1221:MET:CE	1:C:1221:MET:HG3	2.52	0.40
1:A:1167:PHE:HB3	2:C:1303:MC3:H121	2.03	0.40
1:D:1078:LEU:HD12	1:D:1078:LEU:HA	1.96	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	265/285 (93%)	251 (95%)	14 (5%)	0	100	100
1	B	265/285 (93%)	254 (96%)	10 (4%)	1 (0%)	39	69
1	C	265/285 (93%)	254 (96%)	11 (4%)	0	100	100
1	D	265/285 (93%)	252 (95%)	12 (4%)	1 (0%)	39	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1060/1140 (93%)	1011 (95%)	47 (4%)	2 (0%)	52 80

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	1266	LYS
1	B	1255	VAL

### 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	248/264 (94%)	217 (88%)	31 (12%)	6 13
1	B	248/264 (94%)	226 (91%)	22 (9%)	12 27
1	C	248/264 (94%)	228 (92%)	20 (8%)	15 33
1	D	248/264 (94%)	222 (90%)	26 (10%)	8 19
All	All	992/1056 (94%)	893 (90%)	99 (10%)	9 22

All (99) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1002	TYR
1	A	1004	ARG
1	A	1024	LEU
1	A	1028	THR
1	A	1036	THR
1	A	1040	SER
1	A	1045	THR
1	A	1046	THR
1	A	1059	GLU
1	A	1068	ARG
1	A	1078	LEU
1	A	1095	PHE
1	A	1101	LEU

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Mol	Chain	Res	Type
1	A	1111	THR
1	A	1117	ARG
1	A	1121	SER
1	A	1155	ARG
1	A	1162	THR
1	A	1167	PHE
1	A	1170	LEU
1	A	1205	VAL
1	A	1221	MET
1	A	1223	ILE
1	A	1228	GLU
1	A	1233	ILE
1	A	1238	SER
1	A	1239	HIS
1	A	1241	ASP
1	A	1251	ARG
1	A	1256	GLU
1	A	1263	THR
1	B	1025	ASN
1	B	1033	THR
1	B	1054	THR
1	B	1058	ILE
1	B	1068	ARG
1	B	1070	SER
1	B	1091	THR
1	B	1095	PHE
1	B	1104	LEU
1	B	1115	GLN
1	B	1116	MET
1	B	1162	THR
1	B	1163	LEU
1	B	1221	MET
1	B	1226	GLN
1	B	1228	GLU
1	B	1250	LEU
1	B	1256	GLU
1	B	1257	LEU
1	B	1260	LEU
1	B	1265	LEU
1	B	1267	ASN
1	C	1035	LYS
1	C	1049	ASN

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Mol	Chain	Res	Type
1	C	1050	GLN
1	C	1083	VAL
1	C	1086	ILE
1	C	1099	ARG
1	C	1101	LEU
1	C	1111	THR
1	C	1155	ARG
1	C	1162	THR
1	C	1185	ARG
1	C	1187	LEU
1	C	1205	VAL
1	C	1221	MET
1	C	1224	LEU
1	C	1229	GLU
1	C	1230	GLN
1	C	1232	ILE
1	C	1252	GLU
1	C	1253	GLU
1	D	1008	ILE
1	D	1010	GLU
1	D	1028	THR
1	D	1033	THR
1	D	1034	SER
1	D	1049	ASN
1	D	1078	LEU
1	D	1091	THR
1	D	1095	PHE
1	D	1097	ILE
1	D	1109	LEU
1	D	1117	ARG
1	D	1121	SER
1	D	1162	THR
1	D	1167	PHE
1	D	1176	LEU
1	D	1187	LEU
1	D	1233	ILE
1	D	1240	GLU
1	D	1252	GLU
1	D	1253	GLU
1	D	1254	ILE
1	D	1256	GLU
1	D	1265	LEU

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Mol	Chain	Res	Type
1	D	1266	LYS
1	D	1267	ASN

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 ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 29 ligands modelled in this entry, 3 are monoatomic - leaving 26 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	MC3	A	1301	-	20,20,45	1.81	3 (15%)	21,24,53	1.44	2 (9%)
2	MC3	A	1303	-	45,45,45	1.55	3 (6%)	49,53,53	1.68	6 (12%)
4	CPS	A	1304	-	45,45,45	11.16	30 (66%)	69,70,70	4.04	41 (59%)
4	CPS	A	1305	-	45,45,45	11.22	31 (68%)	69,70,70	4.05	39 (56%)
4	CPS	A	1306	-	45,45,45	11.10	29 (64%)	69,70,70	3.98	43 (62%)
2	MC3	B	1302	-	20,20,45	1.76	3 (15%)	21,24,53	1.96	3 (14%)
2	MC3	B	1303	-	40,40,45	1.69	5 (12%)	42,45,53	1.57	4 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	MC3	B	1304	-	40,40,45	1.75	4 (10%)	44,48,53	1.75	5 (11%)
2	MC3	B	1305	-	45,45,45	1.61	6 (13%)	49,53,53	1.59	5 (10%)
2	MC3	B	1306	-	7,7,45	0.68	0	6,6,53	0.25	0
4	CPS	B	1307	-	45,45,45	11.16	28 (62%)	69,70,70	4.80	43 (62%)
4	CPS	B	1308	-	45,45,45	11.10	30 (66%)	69,70,70	3.96	41 (59%)
2	MC3	C	1301	-	20,20,45	1.77	2 (10%)	21,24,53	1.63	2 (9%)
2	MC3	C	1302	-	40,40,45	1.71	5 (12%)	42,45,53	1.57	5 (11%)
2	MC3	C	1303	-	39,39,45	1.64	5 (12%)	43,47,53	1.75	7 (16%)
2	MC3	C	1304	-	45,45,45	1.70	7 (15%)	49,53,53	1.65	6 (12%)
2	MC3	C	1305	-	8,8,45	0.72	0	7,7,53	0.35	0
2	MC3	C	1306	-	8,8,45	0.62	0	7,7,53	0.43	0
2	MC3	C	1307	-	40,40,45	1.71	5 (12%)	42,45,53	1.58	5 (11%)
2	MC3	D	1302	-	20,20,45	1.77	2 (10%)	21,24,53	1.65	3 (14%)
2	MC3	D	1303	-	40,40,45	1.75	6 (15%)	42,45,53	1.52	5 (11%)
2	MC3	D	1304	-	42,42,45	1.68	5 (11%)	46,50,53	1.74	6 (13%)
2	MC3	D	1305	-	41,41,45	1.66	4 (9%)	45,49,53	1.80	6 (13%)
2	MC3	D	1306	-	45,45,45	1.64	6 (13%)	49,53,53	1.57	5 (10%)
2	MC3	D	1307	-	7,7,45	0.70	0	6,6,53	0.20	0
4	CPS	D	1308	-	45,45,45	11.12	31 (68%)	69,70,70	4.49	43 (62%)

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	MC3	A	1301	-	-	0/22/22/49	0/0/0/0
2	MC3	A	1303	-	-	0/49/49/49	0/0/0/0
4	CPS	A	1304	-	-	0/25/90/90	0/4/4/4
4	CPS	A	1305	-	-	0/25/90/90	0/4/4/4
4	CPS	A	1306	-	-	0/25/90/90	0/4/4/4
2	MC3	B	1302	-	-	0/22/22/49	0/0/0/0
2	MC3	B	1303	-	-	0/44/44/49	0/0/0/0
2	MC3	B	1304	-	-	0/44/44/49	0/0/0/0
2	MC3	B	1305	-	-	0/49/49/49	0/0/0/0
2	MC3	B	1306	-	-	0/5/5/49	0/0/0/0
4	CPS	B	1307	-	-	0/25/90/90	0/4/4/4
4	CPS	B	1308	-	-	0/25/90/90	0/4/4/4
2	MC3	C	1301	-	-	0/22/22/49	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	C	1302	-	-	0/44/44/49	0/0/0/0
2	MC3	C	1303	-	-	0/43/43/49	0/0/0/0
2	MC3	C	1304	-	-	0/49/49/49	0/0/0/0
2	MC3	C	1305	-	-	0/6/6/49	0/0/0/0
2	MC3	C	1306	-	-	0/6/6/49	0/0/0/0
2	MC3	C	1307	-	-	0/44/44/49	0/0/0/0
2	MC3	D	1302	-	-	0/22/22/49	0/0/0/0
2	MC3	D	1303	-	-	0/44/44/49	0/0/0/0
2	MC3	D	1304	-	-	1/46/46/49	0/0/0/0
2	MC3	D	1305	-	-	1/45/45/49	0/0/0/0
2	MC3	D	1306	-	-	0/49/49/49	0/0/0/0
2	MC3	D	1307	-	-	0/5/5/49	0/0/0/0
4	CPS	D	1308	-	-	0/25/90/90	0/4/4/4

All (250) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1304	CPS	C5-C4	-39.81	0.93	1.54
4	B	1308	CPS	C5-C4	-39.76	0.93	1.54
4	A	1305	CPS	C5-C4	-39.73	0.93	1.54
4	D	1308	CPS	C5-C4	-39.27	0.94	1.54
4	A	1306	CPS	C5-C4	-39.03	0.94	1.54
4	B	1307	CPS	C5-C4	-38.93	0.94	1.54
4	B	1307	CPS	C14-C13	-26.29	1.02	1.51
4	B	1308	CPS	C14-C13	-26.02	1.02	1.51
4	A	1306	CPS	C14-C13	-25.85	1.02	1.51
4	A	1305	CPS	C14-C13	-25.82	1.02	1.51
4	D	1308	CPS	C14-C13	-25.73	1.03	1.51
4	A	1304	CPS	C14-C13	-25.47	1.03	1.51
4	B	1307	CPS	C16-C15	-23.23	1.14	1.53
4	B	1308	CPS	C16-C15	-22.38	1.15	1.53
4	A	1305	CPS	C16-C15	-22.35	1.15	1.53
4	A	1304	CPS	C16-C15	-22.33	1.15	1.53
4	A	1305	CPS	C18-C17	-22.15	1.15	1.53
4	A	1306	CPS	C16-C15	-22.10	1.15	1.53
4	D	1308	CPS	C16-C15	-21.82	1.16	1.53
4	B	1308	CPS	C18-C17	-21.70	1.16	1.53
4	B	1307	CPS	C18-C17	-21.57	1.16	1.53
4	A	1306	CPS	C18-C17	-21.52	1.16	1.53
4	D	1308	CPS	C18-C17	-21.40	1.16	1.53
4	A	1304	CPS	C18-C17	-21.18	1.16	1.53
4	D	1308	CPS	C1-C2	-19.43	1.17	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1306	CPS	C1-C2	-19.40	1.17	1.54
4	A	1304	CPS	C1-C2	-19.11	1.17	1.54
4	A	1305	CPS	C1-C2	-18.92	1.18	1.54
4	B	1308	CPS	C1-C2	-18.74	1.18	1.54
4	B	1307	CPS	C1-C2	-18.59	1.18	1.54
4	B	1307	CPS	C2-C15	-18.47	1.23	1.55
4	D	1308	CPS	C2-C15	-18.31	1.24	1.55
4	A	1306	CPS	C2-C15	-18.10	1.24	1.55
4	A	1305	CPS	C2-C15	-18.06	1.24	1.55
4	A	1304	CPS	C2-C15	-18.06	1.24	1.55
4	B	1308	CPS	C2-C15	-17.15	1.26	1.55
4	B	1307	CPS	C18-C19	-16.61	1.21	1.53
4	A	1305	CPS	C18-C19	-16.60	1.21	1.53
4	A	1304	CPS	C18-C19	-16.42	1.21	1.53
4	D	1308	CPS	C18-C19	-16.26	1.21	1.53
4	A	1306	CPS	C18-C19	-16.13	1.22	1.53
4	B	1308	CPS	C18-C19	-15.81	1.22	1.53
4	A	1306	CPS	C18-C6	-12.82	1.28	1.53
4	A	1304	CPS	C18-C6	-12.76	1.28	1.53
4	B	1307	CPS	C18-C6	-12.49	1.29	1.53
4	A	1305	CPS	C18-C6	-12.05	1.30	1.53
4	D	1308	CPS	C18-C6	-11.89	1.30	1.53
4	B	1308	CPS	C18-C6	-11.83	1.30	1.53
4	A	1305	CPS	C32-S	-11.78	1.59	1.77
4	A	1306	CPS	C32-S	-11.28	1.60	1.77
4	A	1304	CPS	C32-S	-10.47	1.61	1.77
4	B	1307	CPS	C32-S	-10.43	1.61	1.77
4	A	1305	CPS	C3-C19	-10.39	1.36	1.53
4	D	1308	CPS	C3-C19	-9.77	1.37	1.53
4	B	1307	CPS	C3-C19	-9.57	1.37	1.53
4	A	1304	CPS	C5-C9	-9.53	1.38	1.55
4	A	1304	CPS	C3-C19	-9.39	1.38	1.53
4	D	1308	CPS	C32-S	-9.34	1.63	1.77
4	A	1306	CPS	C3-C19	-9.25	1.38	1.53
4	B	1308	CPS	C32-S	-8.93	1.64	1.77
4	B	1307	CPS	C5-C9	-8.89	1.39	1.55
4	B	1308	CPS	C3-C19	-8.86	1.39	1.53
4	A	1305	CPS	C5-C9	-8.80	1.40	1.55
4	D	1308	CPS	C5-C9	-8.79	1.40	1.55
4	A	1306	CPS	C5-C9	-8.65	1.40	1.55
4	B	1308	CPS	C5-C9	-7.97	1.41	1.55
4	B	1307	CPS	C2-C19	-7.21	1.42	1.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1304	CPS	C2-C19	-7.10	1.42	1.56
4	A	1306	CPS	C2-C19	-7.05	1.42	1.56
4	D	1308	CPS	C2-C19	-6.99	1.42	1.56
4	A	1305	CPS	C2-C19	-6.73	1.43	1.56
4	B	1308	CPS	C2-C19	-6.63	1.43	1.56
4	D	1308	CPS	C1-C12	-4.37	1.43	1.53
4	A	1305	CPS	C1-C12	-4.35	1.43	1.53
4	A	1306	CPS	C1-C12	-4.34	1.43	1.53
4	A	1304	CPS	C1-C12	-3.88	1.44	1.53
4	B	1307	CPS	C16-C17	-3.80	1.46	1.52
4	B	1308	CPS	C1-C12	-3.78	1.45	1.53
4	B	1307	CPS	C1-C12	-3.64	1.45	1.53
4	B	1308	CPS	C16-C17	-3.34	1.47	1.52
2	B	1304	MC3	O2-C2	-3.33	1.37	1.46
4	A	1306	CPS	C16-C17	-3.27	1.47	1.52
4	B	1308	CPS	C8-C7	-3.11	1.45	1.54
4	D	1308	CPS	C16-C17	-3.10	1.47	1.52
4	A	1304	CPS	C8-C7	-3.06	1.45	1.54
2	D	1304	MC3	O2-C2	-3.03	1.38	1.46
4	A	1305	CPS	C16-C17	-3.03	1.47	1.52
4	A	1304	CPS	C16-C17	-2.94	1.48	1.52
4	A	1306	CPS	C8-C7	-2.84	1.45	1.54
2	D	1305	MC3	O2-C2	-2.79	1.39	1.46
4	B	1307	CPS	C8-C7	-2.71	1.46	1.54
2	C	1304	MC3	O2-C2	-2.55	1.39	1.46
2	C	1307	MC3	O2-C2	-2.54	1.39	1.46
2	C	1303	MC3	O2-C2	-2.54	1.39	1.46
2	B	1305	MC3	O2-C2	-2.54	1.39	1.46
4	A	1306	CPS	C12-C13	-2.51	1.45	1.51
4	D	1308	CPS	C12-C13	-2.48	1.45	1.51
4	A	1305	CPS	C12-C13	-2.41	1.45	1.51
4	D	1308	CPS	C8-C7	-2.39	1.47	1.54
2	D	1306	MC3	O2-C2	-2.38	1.40	1.46
2	C	1302	MC3	O2-C2	-2.38	1.40	1.46
2	B	1303	MC3	O2-C2	-2.38	1.40	1.46
4	A	1305	CPS	C8-C7	-2.29	1.47	1.54
2	D	1306	MC3	O3-C3	-2.17	1.40	1.45
4	B	1308	CPS	C12-C13	-2.12	1.46	1.51
2	D	1303	MC3	O2-C2	-2.06	1.41	1.46
2	C	1304	MC3	O3-C3	-2.04	1.40	1.45
4	A	1304	CPS	C12-C13	-2.02	1.46	1.51
4	A	1305	CPS	C25-N1	2.02	1.50	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1304	MC3	C12-C11	2.04	1.56	1.50
2	B	1305	MC3	P-O4P	2.06	1.67	1.59
2	B	1305	MC3	O2-C31	2.11	1.40	1.34
4	A	1305	CPS	C22-C23	2.14	1.59	1.52
2	D	1304	MC3	O3-C11	2.18	1.39	1.33
2	D	1303	MC3	P-O4P	2.19	1.67	1.59
4	D	1308	CPS	C31-C32	2.20	1.58	1.52
4	D	1308	CPS	C25-N1	2.22	1.51	1.46
2	C	1307	MC3	O2-C31	2.22	1.40	1.34
2	C	1303	MC3	O2-C31	2.23	1.40	1.34
2	B	1302	MC3	P-O4P	2.23	1.67	1.59
2	B	1303	MC3	O2-C31	2.23	1.40	1.34
4	B	1307	CPS	C22-C23	2.24	1.60	1.52
2	B	1305	MC3	O3-C11	2.26	1.40	1.33
2	C	1302	MC3	O2-C31	2.27	1.41	1.34
2	D	1306	MC3	O2-C31	2.30	1.41	1.34
2	A	1301	MC3	P-O4P	2.31	1.68	1.59
2	D	1306	MC3	O3-C11	2.31	1.40	1.33
2	A	1303	MC3	O2-C31	2.31	1.41	1.34
4	A	1304	CPS	C22-C23	2.33	1.60	1.52
4	B	1308	CPS	C22-C23	2.33	1.60	1.52
2	D	1305	MC3	O2-C31	2.38	1.41	1.34
2	C	1307	MC3	O3-C11	2.42	1.40	1.33
2	B	1302	MC3	O3-C11	2.43	1.40	1.33
4	A	1305	CPS	C7-C6	2.44	1.59	1.54
4	D	1308	CPS	C22-C23	2.44	1.60	1.52
4	B	1308	CPS	C7-C6	2.48	1.59	1.54
2	D	1303	MC3	O2-C31	2.50	1.41	1.34
2	C	1304	MC3	O2-C31	2.50	1.41	1.34
4	A	1306	CPS	C11-C2	2.54	1.59	1.54
2	B	1303	MC3	O3-C11	2.55	1.40	1.33
4	A	1306	CPS	C22-C23	2.55	1.61	1.52
4	D	1308	CPS	C11-C2	2.56	1.59	1.54
4	A	1304	CPS	C7-C6	2.57	1.59	1.54
2	C	1303	MC3	O3-C11	2.58	1.41	1.33
2	C	1304	MC3	O3-C11	2.59	1.41	1.33
2	B	1304	MC3	O3-C11	2.59	1.41	1.33
2	C	1301	MC3	O3-C11	2.64	1.41	1.33
2	D	1304	MC3	O2-C31	2.72	1.42	1.34
2	D	1302	MC3	O3-C11	2.77	1.41	1.33
4	B	1307	CPS	C11-C2	2.81	1.59	1.54
2	D	1303	MC3	O3-C11	2.90	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1301	MC3	O3-C11	2.91	1.42	1.33
4	D	1308	CPS	C10-C5	2.98	1.59	1.54
4	A	1304	CPS	C11-C2	3.00	1.59	1.54
4	B	1307	CPS	C10-C5	3.05	1.59	1.54
2	C	1302	MC3	O3-C11	3.07	1.42	1.33
4	A	1305	CPS	C11-C2	3.12	1.60	1.54
4	A	1305	CPS	C10-C5	3.17	1.59	1.54
4	A	1304	CPS	C23-C24	3.26	1.57	1.51
4	A	1304	CPS	C20-C9	3.30	1.60	1.54
4	B	1308	CPS	C11-C2	3.34	1.60	1.54
4	A	1304	CPS	C10-C5	3.37	1.59	1.54
4	A	1306	CPS	C10-C5	3.50	1.60	1.54
4	B	1308	CPS	C23-C24	3.52	1.58	1.51
4	A	1305	CPS	C23-C24	3.62	1.58	1.51
4	B	1307	CPS	C23-C24	3.76	1.58	1.51
4	B	1308	CPS	C10-C5	3.78	1.60	1.54
4	A	1306	CPS	C20-C9	4.13	1.61	1.54
4	B	1307	CPS	C20-C9	4.18	1.62	1.54
4	B	1308	CPS	C20-C9	4.26	1.62	1.54
4	A	1305	CPS	C20-C9	4.27	1.62	1.54
4	B	1307	CPS	C14-C15	4.41	1.61	1.53
4	A	1306	CPS	C23-C24	4.43	1.60	1.51
4	A	1306	CPS	C8-C9	4.43	1.63	1.54
4	B	1307	CPS	C8-C9	4.48	1.63	1.54
4	D	1308	CPS	C23-C24	4.52	1.60	1.51
4	D	1308	CPS	C20-C9	4.63	1.62	1.54
4	D	1308	CPS	C8-C9	4.74	1.64	1.54
4	A	1305	CPS	C14-C15	4.88	1.62	1.53
4	A	1306	CPS	C14-C15	4.90	1.62	1.53
4	A	1305	CPS	C8-C9	5.05	1.65	1.54
4	A	1304	CPS	C8-C9	5.05	1.65	1.54
4	D	1308	CPS	C14-C15	5.27	1.62	1.53
4	B	1308	CPS	C8-C9	5.27	1.65	1.54
2	C	1303	MC3	O11-C11	5.39	1.38	1.22
2	C	1302	MC3	O31-C31	5.46	1.38	1.22
4	A	1304	CPS	C14-C15	5.52	1.63	1.53
4	B	1308	CPS	C14-C15	5.54	1.63	1.53
2	D	1304	MC3	O11-C11	5.66	1.39	1.22
2	D	1303	MC3	O31-C31	5.67	1.39	1.22
2	A	1303	MC3	O31-C31	5.67	1.39	1.22
2	B	1305	MC3	O31-C31	5.68	1.39	1.22
2	B	1304	MC3	O11-C11	5.71	1.39	1.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1303	MC3	O11-C11	5.76	1.39	1.22
2	D	1305	MC3	O11-C11	5.80	1.39	1.22
2	A	1303	MC3	O11-C11	5.89	1.40	1.22
2	B	1304	MC3	O31-C31	5.92	1.40	1.22
2	D	1302	MC3	O11-C11	5.92	1.40	1.22
2	C	1307	MC3	O31-C31	5.92	1.40	1.22
2	D	1306	MC3	O31-C31	5.95	1.40	1.22
2	B	1303	MC3	O31-C31	5.95	1.40	1.22
2	C	1304	MC3	O31-C31	5.97	1.40	1.22
2	B	1302	MC3	O11-C11	5.98	1.40	1.22
2	C	1301	MC3	O11-C11	6.03	1.40	1.22
2	C	1303	MC3	O31-C31	6.06	1.40	1.22
2	C	1307	MC3	O11-C11	6.07	1.40	1.22
2	C	1304	MC3	O11-C11	6.08	1.40	1.22
2	B	1305	MC3	O11-C11	6.09	1.40	1.22
2	D	1306	MC3	O11-C11	6.10	1.40	1.22
2	D	1305	MC3	O31-C31	6.15	1.40	1.22
2	A	1301	MC3	O11-C11	6.16	1.40	1.22
2	C	1302	MC3	O11-C11	6.16	1.40	1.22
2	D	1303	MC3	O11-C11	6.18	1.40	1.22
2	D	1304	MC3	O31-C31	6.25	1.41	1.22
4	A	1304	CPS	C24-N1	6.37	1.48	1.33
4	A	1306	CPS	O3S-S	6.87	1.65	1.45
4	A	1305	CPS	O3S-S	6.95	1.65	1.45
4	B	1308	CPS	C24-N1	6.97	1.50	1.33
4	B	1307	CPS	C24-N1	7.00	1.50	1.33
4	B	1307	CPS	O1S-S	7.19	1.66	1.45
4	A	1306	CPS	O1S-S	7.28	1.66	1.45
4	D	1308	CPS	O3S-S	7.29	1.66	1.45
4	B	1307	CPS	O3S-S	7.34	1.66	1.45
4	A	1304	CPS	O3S-S	7.34	1.66	1.45
4	A	1304	CPS	O1S-S	7.36	1.66	1.45
4	B	1308	CPS	O3S-S	7.37	1.66	1.45
4	A	1306	CPS	C24-N1	7.43	1.51	1.33
4	D	1308	CPS	O1S-S	7.47	1.66	1.45
4	B	1308	CPS	O1S-S	7.51	1.67	1.45
4	A	1305	CPS	O1S-S	7.61	1.67	1.45
4	A	1305	CPS	C24-N1	7.63	1.51	1.33
4	D	1308	CPS	C24-N1	7.76	1.52	1.33
4	D	1308	CPS	O2-C13	10.27	1.73	1.43
4	B	1307	CPS	O2-C13	10.28	1.73	1.43
4	A	1306	CPS	O2-C13	10.30	1.73	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1305	CPS	O2-C13	10.35	1.73	1.43
4	A	1304	CPS	O2-C13	10.71	1.74	1.43
4	B	1308	CPS	O2-C13	10.86	1.75	1.43
4	A	1305	CPS	O3-C17	11.68	1.69	1.43
4	B	1307	CPS	O3-C17	11.88	1.69	1.43
4	D	1308	CPS	O3-C17	11.96	1.70	1.43
4	A	1306	CPS	O3-C17	12.03	1.70	1.43
4	B	1308	CPS	O3-C17	12.43	1.71	1.43
4	A	1304	CPS	O3-C17	12.59	1.71	1.43
4	A	1306	CPS	O4-C4	19.30	1.76	1.43
4	A	1304	CPS	O4-C4	19.36	1.77	1.43
4	A	1305	CPS	O4-C4	19.61	1.77	1.43
4	B	1307	CPS	O4-C4	19.96	1.78	1.43
4	B	1308	CPS	O4-C4	19.99	1.78	1.43
4	D	1308	CPS	O4-C4	20.14	1.78	1.43

All (325) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1307	CPS	O1S-S-C32	-21.95	91.36	106.87
4	A	1305	CPS	O1S-S-C32	-12.76	97.85	106.87
4	D	1308	CPS	O1S-S-C32	-11.36	98.85	106.87
4	A	1306	CPS	O1S-S-C32	-8.04	101.19	106.87
4	A	1304	CPS	O1S-S-C32	-7.93	101.27	106.87
4	B	1308	CPS	C8-C9-C20	-7.14	100.71	112.12
2	B	1302	MC3	O3-C11-O11	-6.93	105.34	123.51
2	D	1305	MC3	O3-C11-O11	-6.90	105.43	123.51
2	B	1304	MC3	O2-C31-O31	-6.68	105.49	123.67
2	B	1304	MC3	O3-C11-O11	-6.68	106.00	123.51
4	B	1308	CPS	C11-C2-C19	-6.65	102.40	111.20
2	C	1304	MC3	O3-C11-O11	-6.44	106.64	123.51
4	A	1304	CPS	C10-C5-C9	-6.37	101.17	111.20
2	A	1303	MC3	O3-C11-O11	-6.15	107.39	123.51
2	C	1302	MC3	O2-C31-O31	-6.12	107.01	123.67
4	A	1305	CPS	C11-C2-C1	-6.12	97.87	108.23
4	D	1308	CPS	C11-C2-C1	-6.07	97.95	108.23
2	C	1301	MC3	O3-C11-O11	-6.06	107.63	123.51
4	A	1304	CPS	C10-C5-C4	-6.02	103.07	109.09
2	A	1303	MC3	O2-C31-O31	-6.01	107.31	123.67
4	D	1308	CPS	O1S-S-O3S	-6.01	96.99	113.96
4	A	1304	CPS	O2S-S-O1S	-5.93	98.13	111.26
4	A	1305	CPS	C10-C5-C9	-5.90	101.90	111.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1307	MC3	O3-C11-O11	-5.86	108.16	123.51
4	A	1304	CPS	C11-C2-C1	-5.85	98.33	108.23
2	B	1305	MC3	O3-C11-O11	-5.82	108.25	123.51
2	D	1302	MC3	O3-C11-O11	-5.78	108.35	123.51
4	A	1306	CPS	O4-C4-C3	-5.71	97.26	109.09
2	D	1304	MC3	O3-C11-O11	-5.68	108.61	123.51
2	B	1305	MC3	O2-C31-O31	-5.59	108.47	123.67
2	B	1303	MC3	O3-C11-O11	-5.58	108.88	123.51
4	A	1306	CPS	O1S-S-O3S	-5.58	98.20	113.96
2	C	1303	MC3	O11-C11-C12	-5.51	102.65	123.76
4	B	1308	CPS	O1S-S-O3S	-5.41	98.67	113.96
4	A	1305	CPS	O1S-S-O3S	-5.41	98.67	113.96
2	C	1307	MC3	O2-C31-O31	-5.39	109.02	123.67
2	B	1303	MC3	O2-C31-O31	-5.36	109.10	123.67
4	B	1307	CPS	C10-C5-C9	-5.34	102.78	111.20
4	D	1308	CPS	C10-C5-C9	-5.28	102.88	111.20
4	B	1308	CPS	O2S-S-O1S	-5.20	99.75	111.26
4	B	1308	CPS	C10-C5-C6	-5.16	103.07	111.20
2	C	1303	MC3	O2-C31-O31	-5.09	109.82	123.67
4	B	1308	CPS	C27-C26-C25	-5.04	100.99	111.34
2	D	1303	MC3	O2-C31-O31	-5.01	110.05	123.67
2	D	1303	MC3	O3-C11-O11	-4.91	110.64	123.51
2	C	1304	MC3	O2-C31-O31	-4.88	110.40	123.67
2	D	1306	MC3	O2-C31-O31	-4.87	110.41	123.67
2	C	1303	MC3	O3-C11-O11	-4.86	110.76	123.51
4	A	1306	CPS	C10-C5-C6	-4.85	103.56	111.20
2	D	1305	MC3	O2-C31-O31	-4.82	110.56	123.67
2	D	1304	MC3	O2-C31-O31	-4.81	110.59	123.67
4	A	1304	CPS	O1S-S-O3S	-4.78	100.46	113.96
2	D	1306	MC3	O3-C11-O11	-4.78	110.99	123.51
4	A	1306	CPS	C10-C5-C9	-4.77	103.69	111.20
4	A	1306	CPS	C11-C2-C15	-4.72	101.91	110.28
4	A	1306	CPS	C11-C2-C1	-4.72	100.24	108.23
4	A	1305	CPS	C21-C20-C22	-4.68	102.72	110.33
2	A	1301	MC3	O11-C11-C12	-4.60	106.14	123.76
4	B	1307	CPS	O2S-S-O1S	-4.57	101.15	111.26
2	B	1303	MC3	O11-C11-C12	-4.48	106.59	123.76
2	B	1305	MC3	O31-C31-C32	-4.48	106.61	123.76
2	D	1304	MC3	O31-C31-C32	-4.47	106.64	123.76
4	A	1306	CPS	O2S-S-O1S	-4.45	101.42	111.26
2	A	1301	MC3	O3-C11-O11	-4.40	111.98	123.51
2	C	1304	MC3	C3-C2-C1	-4.39	101.85	112.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1302	MC3	O11-C11-C12	-4.32	107.22	123.76
4	D	1308	CPS	O4-C4-C3	-4.30	100.18	109.09
4	B	1307	CPS	C11-C2-C15	-4.29	102.68	110.28
4	D	1308	CPS	C29-N2-C30	-4.28	98.17	109.42
4	B	1307	CPS	C16-C15-C14	-4.26	106.50	111.07
4	A	1305	CPS	C10-C5-C6	-4.24	104.52	111.20
2	D	1306	MC3	O31-C31-C32	-4.22	107.59	123.76
4	D	1308	CPS	O2-C13-C12	-4.21	99.87	110.04
4	B	1307	CPS	C10-C5-C6	-4.17	104.62	111.20
4	D	1308	CPS	O2S-S-O1S	-4.16	102.06	111.26
2	C	1304	MC3	O31-C31-C32	-4.12	107.98	123.76
4	B	1307	CPS	C21-C20-C22	-4.08	103.71	110.33
2	D	1305	MC3	O11-C11-C12	-4.04	108.28	123.76
4	D	1308	CPS	C21-C20-C22	-4.01	103.81	110.33
4	A	1306	CPS	C28-N2-C30	-4.01	98.89	109.42
4	D	1308	CPS	C11-C2-C15	-3.95	103.28	110.28
2	D	1305	MC3	O31-C31-C32	-3.92	108.74	123.76
4	A	1306	CPS	C21-C20-C22	-3.91	103.98	110.33
2	D	1306	MC3	O11-C11-C12	-3.90	108.82	123.76
2	D	1304	MC3	O11-C11-C12	-3.90	108.84	123.76
2	B	1302	MC3	O11-C11-C12	-3.89	108.87	123.76
2	C	1302	MC3	O3-C11-O11	-3.89	113.33	123.51
4	A	1304	CPS	C8-C9-C20	-3.84	105.98	112.12
2	D	1303	MC3	O11-C11-C12	-3.77	109.33	123.76
4	A	1304	CPS	C25-N1-C24	-3.73	115.40	122.79
4	D	1308	CPS	C10-C5-C6	-3.71	105.36	111.20
4	B	1307	CPS	C11-C2-C1	-3.70	101.97	108.23
4	B	1308	CPS	C16-C15-C14	-3.69	107.11	111.07
2	A	1303	MC3	O31-C31-C32	-3.68	109.67	123.76
4	A	1305	CPS	C31-C30-N2	-3.67	107.80	115.54
4	A	1305	CPS	C11-C2-C15	-3.64	103.84	110.28
2	D	1302	MC3	O11-C11-C12	-3.60	109.98	123.76
2	C	1303	MC3	O31-C31-C32	-3.60	109.99	123.76
4	A	1304	CPS	O1-C24-N1	-3.58	115.85	122.96
2	C	1302	MC3	O31-C31-C32	-3.55	110.18	123.76
2	C	1307	MC3	O31-C31-C32	-3.52	110.28	123.76
2	C	1307	MC3	O11-C11-C12	-3.52	110.29	123.76
2	B	1304	MC3	O11-C11-C12	-3.52	110.30	123.76
4	B	1308	CPS	C28-N2-C27	-3.50	100.22	109.42
4	B	1308	CPS	C21-C20-C22	-3.44	104.74	110.33
4	B	1307	CPS	O1S-S-O3S	-3.37	104.44	113.96
2	D	1303	MC3	O31-C31-C32	-3.33	111.02	123.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1308	CPS	O4-C4-C5	-3.27	105.65	111.12
2	C	1301	MC3	O11-C11-C12	-3.26	111.29	123.76
4	B	1308	CPS	O4-C4-C3	-3.24	102.37	109.09
4	D	1308	CPS	C10-C5-C4	-3.19	105.90	109.09
2	B	1305	MC3	O11-C11-C12	-3.14	111.75	123.76
2	A	1303	MC3	O11-C11-C12	-3.11	111.86	123.76
4	A	1305	CPS	O2S-S-O1S	-3.06	104.49	111.26
2	C	1304	MC3	O11-C11-C12	-3.04	112.12	123.76
2	B	1304	MC3	O31-C31-C32	-3.03	112.17	123.76
4	A	1306	CPS	C26-C27-N2	-2.99	109.24	115.54
4	D	1308	CPS	O3-C17-C16	-2.98	102.76	110.02
4	A	1304	CPS	C11-C2-C19	-2.97	107.27	111.20
2	B	1303	MC3	O31-C31-C32	-2.92	112.58	123.76
4	B	1307	CPS	O1-C24-N1	-2.91	117.18	122.96
4	B	1307	CPS	C26-C27-N2	-2.90	109.42	115.54
4	B	1307	CPS	O4-C4-C3	-2.85	103.17	109.09
2	C	1303	MC3	C2-O2-C31	-2.78	111.03	117.91
4	B	1308	CPS	C11-C2-C15	-2.77	105.37	110.28
4	B	1308	CPS	O1S-S-C32	-2.77	104.91	106.87
2	B	1302	MC3	C3-C2-C1	-2.76	103.63	112.42
4	A	1306	CPS	O3-C17-C16	-2.76	103.29	110.02
4	A	1305	CPS	C28-N2-C30	-2.75	102.20	109.42
4	A	1305	CPS	O2-C13-C12	-2.75	103.40	110.04
4	A	1305	CPS	C10-C5-C4	-2.74	106.35	109.09
4	A	1306	CPS	C21-C20-C9	-2.73	108.78	112.99
4	A	1305	CPS	O1-C24-C23	-2.71	117.27	121.97
4	A	1305	CPS	C26-C27-N2	-2.68	109.89	115.54
4	A	1304	CPS	C31-C30-N2	-2.63	109.98	115.54
2	D	1305	MC3	C2-O2-C31	-2.52	111.69	117.91
4	A	1304	CPS	C8-C9-C5	-2.48	101.19	103.59
4	B	1307	CPS	C10-C5-C4	-2.41	106.69	109.09
2	D	1304	MC3	C3-C2-C1	-2.39	106.51	112.08
4	B	1307	CPS	C11-C2-C19	-2.36	108.07	111.20
4	A	1304	CPS	C16-C15-C14	-2.35	108.54	111.07
4	B	1307	CPS	C28-N2-C30	-2.32	103.31	109.42
2	D	1303	MC3	C3-O3-C11	-2.32	110.08	117.00
4	A	1306	CPS	O4-C4-C5	-2.30	107.27	111.12
2	D	1302	MC3	C3-C2-C1	-2.29	105.14	112.42
4	A	1305	CPS	C16-C15-C14	-2.19	108.71	111.07
4	A	1305	CPS	C3-C19-C2	-2.18	111.50	113.77
2	A	1303	MC3	C3-C2-C1	-2.16	107.04	112.08
2	B	1304	MC3	C2-O2-C31	-2.15	112.59	117.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1303	MC3	C4-C5-N	-2.13	109.08	116.04
4	B	1308	CPS	C10-C5-C9	-2.11	107.88	111.20
2	C	1307	MC3	C2-O2-C31	-2.09	112.75	117.91
4	A	1304	CPS	C28-N2-C27	-2.05	104.03	109.42
4	B	1307	CPS	C31-C30-N2	-2.01	111.30	115.54
4	A	1306	CPS	C7-C6-C18	2.00	121.31	118.34
2	C	1302	MC3	O3-C3-C2	2.05	114.24	108.70
4	B	1308	CPS	C7-C6-C18	2.09	121.44	118.34
4	B	1307	CPS	C7-C6-C18	2.11	121.47	118.34
4	A	1306	CPS	C22-C23-C24	2.12	118.10	113.26
4	B	1307	CPS	C22-C23-C24	2.14	118.15	113.26
4	A	1304	CPS	C29-N2-C28	2.14	115.23	108.83
4	A	1304	CPS	C7-C6-C5	2.19	105.70	103.59
4	A	1306	CPS	O2S-S-C32	2.20	109.56	104.99
4	A	1306	CPS	C9-C5-C6	2.20	102.31	100.08
4	A	1305	CPS	C15-C16-C17	2.25	117.00	114.44
4	B	1308	CPS	O2-C13-C14	2.30	114.51	109.86
4	A	1305	CPS	C26-C25-N1	2.33	118.87	112.29
4	A	1304	CPS	O2S-S-C32	2.41	110.00	104.99
4	A	1304	CPS	C15-C16-C17	2.48	117.26	114.44
4	A	1305	CPS	C19-C18-C6	2.51	113.16	109.63
4	A	1304	CPS	C15-C14-C13	2.52	116.62	112.88
4	A	1306	CPS	C23-C22-C20	2.53	119.16	114.46
4	A	1304	CPS	C5-C9-C20	2.57	122.57	119.44
4	A	1306	CPS	O3-C17-C18	2.57	115.14	109.28
4	B	1307	CPS	C15-C16-C17	2.63	117.43	114.44
4	A	1305	CPS	C19-C18-C17	2.63	115.07	111.89
4	D	1308	CPS	C15-C14-C13	2.63	116.78	112.88
4	D	1308	CPS	C5-C9-C20	2.64	122.66	119.44
4	A	1306	CPS	C29-N2-C28	2.66	116.79	108.83
4	B	1308	CPS	C1-C12-C13	2.70	114.01	110.41
4	D	1308	CPS	O3-C17-C18	2.73	115.50	109.28
4	D	1308	CPS	C19-C18-C6	2.73	113.48	109.63
4	B	1307	CPS	C23-C24-N1	2.76	121.26	116.46
4	A	1306	CPS	C19-C18-C6	2.76	113.53	109.63
4	B	1308	CPS	C2-C19-C18	2.77	114.86	111.86
4	B	1307	CPS	C5-C9-C20	2.79	122.83	119.44
4	B	1308	CPS	C14-C15-C2	2.83	115.70	112.66
4	A	1305	CPS	C15-C14-C13	2.84	117.09	112.88
4	B	1308	CPS	C29-N2-C30	2.94	117.16	109.42
4	A	1304	CPS	O3-C17-C18	2.97	116.03	109.28
4	A	1306	CPS	C22-C20-C9	3.01	116.58	110.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1308	CPS	C6-C18-C17	3.04	116.12	111.77
4	B	1307	CPS	C14-C13-C12	3.05	114.44	110.53
4	A	1306	CPS	C15-C16-C17	3.14	118.01	114.44
2	C	1304	MC3	C8-N-C6	3.16	117.14	108.96
4	A	1306	CPS	C6-C18-C17	3.21	116.36	111.77
4	B	1308	CPS	C29-N2-C28	3.23	118.48	108.83
2	C	1303	MC3	C8-N-C6	3.24	117.34	108.96
4	B	1308	CPS	C8-C9-C5	3.28	106.75	103.59
4	D	1308	CPS	C29-N2-C28	3.32	118.76	108.83
4	B	1307	CPS	C1-C12-C13	3.37	114.89	110.41
4	A	1305	CPS	C23-C24-N1	3.37	122.32	116.46
4	A	1304	CPS	C2-C19-C18	3.40	115.54	111.86
4	B	1307	CPS	O3-C17-C18	3.41	117.05	109.28
2	D	1305	MC3	C8-N-C6	3.43	117.84	108.96
4	A	1306	CPS	C1-C12-C13	3.46	115.01	110.41
4	B	1308	CPS	C31-C30-N2	3.51	122.94	115.54
4	D	1308	CPS	C25-N1-C24	3.54	129.81	122.79
4	A	1305	CPS	C19-C2-C15	3.54	113.72	108.68
4	B	1307	CPS	C29-N2-C28	3.55	119.44	108.83
2	B	1305	MC3	C8-N-C6	3.57	118.20	108.96
4	A	1305	CPS	C6-C18-C17	3.60	116.91	111.77
4	A	1304	CPS	C19-C2-C15	3.60	113.81	108.68
4	D	1308	CPS	C22-C20-C9	3.63	117.88	110.24
4	B	1307	CPS	C31-C32-S	3.64	119.08	113.15
4	D	1308	CPS	C15-C16-C17	3.65	118.60	114.44
4	A	1304	CPS	C22-C23-C24	3.67	121.65	113.26
4	B	1307	CPS	O2S-S-C32	3.68	112.64	104.99
4	D	1308	CPS	C7-C6-C18	3.74	123.89	118.34
4	B	1308	CPS	O2S-S-C32	3.78	112.84	104.99
4	B	1308	CPS	C12-C1-C2	3.80	119.63	112.81
4	B	1307	CPS	O2S-S-O3S	3.81	119.69	111.26
4	B	1307	CPS	C22-C20-C9	3.83	118.31	110.24
4	D	1308	CPS	O2S-S-C32	3.84	112.96	104.99
4	A	1304	CPS	C19-C18-C6	3.84	115.05	109.63
4	A	1305	CPS	C29-N2-C28	3.85	120.35	108.83
4	A	1306	CPS	C5-C9-C20	3.87	124.15	119.44
4	D	1308	CPS	C22-C23-C24	3.87	122.11	113.26
4	A	1306	CPS	C14-C13-C12	3.89	115.51	110.53
4	A	1304	CPS	C23-C24-N1	3.91	123.25	116.46
4	B	1308	CPS	C21-C20-C9	3.98	119.12	112.99
4	B	1307	CPS	C6-C18-C17	4.01	117.51	111.77
4	B	1307	CPS	C2-C19-C18	4.02	116.21	111.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1304	CPS	C6-C18-C17	4.02	117.52	111.77
4	D	1308	CPS	O2S-S-O3S	4.10	120.33	111.26
4	D	1308	CPS	C6-C5-C4	4.10	111.08	107.37
2	A	1303	MC3	C8-N-C6	4.11	119.60	108.96
4	A	1306	CPS	C26-C25-N1	4.11	123.93	112.29
4	A	1306	CPS	C2-C19-C18	4.13	116.32	111.86
4	A	1306	CPS	C12-C1-C2	4.16	120.27	112.81
4	A	1306	CPS	C31-C32-S	4.21	120.02	113.15
4	A	1304	CPS	C16-C17-C18	4.24	115.95	111.46
4	B	1308	CPS	O2S-S-O3S	4.25	120.67	111.26
4	B	1308	CPS	C19-C2-C15	4.26	114.75	108.68
4	B	1307	CPS	C25-N1-C24	4.27	131.26	122.79
4	B	1307	CPS	C19-C18-C6	4.30	115.69	109.63
4	D	1308	CPS	C16-C15-C2	4.31	117.28	112.66
4	D	1308	CPS	C19-C18-C17	4.32	117.11	111.89
4	B	1307	CPS	C12-C1-C2	4.36	120.62	112.81
4	B	1308	CPS	C9-C5-C6	4.37	104.50	100.08
4	A	1304	CPS	C14-C13-C12	4.37	116.12	110.53
2	D	1306	MC3	C8-N-C6	4.37	120.26	108.96
4	B	1307	CPS	C16-C17-C18	4.38	116.11	111.46
4	B	1307	CPS	C19-C2-C15	4.39	114.93	108.68
4	D	1308	CPS	C1-C12-C13	4.40	116.27	110.41
4	A	1304	CPS	C16-C15-C2	4.41	117.39	112.66
4	D	1308	CPS	C26-C27-N2	4.41	124.84	115.54
4	A	1305	CPS	C7-C6-C18	4.43	124.91	118.34
4	A	1305	CPS	C12-C1-C2	4.47	120.82	112.81
2	D	1304	MC3	C8-N-C6	4.49	120.56	108.96
4	A	1305	CPS	C16-C15-C2	4.55	117.54	112.66
4	A	1304	CPS	C12-C1-C2	4.55	120.97	112.81
4	D	1308	CPS	C6-C18-C17	4.56	118.29	111.77
4	B	1308	CPS	C19-C18-C17	4.57	117.41	111.89
4	A	1304	CPS	C1-C12-C13	4.60	116.53	110.41
4	D	1308	CPS	C19-C2-C15	4.61	115.25	108.68
4	A	1306	CPS	C19-C2-C15	4.66	115.32	108.68
4	A	1305	CPS	C1-C12-C13	4.73	116.71	110.41
4	A	1306	CPS	C19-C18-C17	4.74	117.61	111.89
4	A	1304	CPS	C31-C32-S	4.77	120.93	113.15
4	D	1308	CPS	C9-C5-C6	4.88	105.02	100.08
4	A	1306	CPS	C16-C17-C18	4.92	116.67	111.46
4	B	1308	CPS	C16-C17-C18	4.97	116.72	111.46
4	B	1307	CPS	C16-C15-C2	5.02	118.04	112.66
4	D	1308	CPS	C14-C13-C12	5.05	117.00	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1306	CPS	C6-C5-C4	5.06	111.95	107.37
4	A	1305	CPS	C14-C13-C12	5.06	117.01	110.53
4	D	1308	CPS	C12-C1-C2	5.34	122.38	112.81
4	A	1305	CPS	C2-C19-C18	5.39	117.69	111.86
4	A	1305	CPS	C16-C17-C18	5.40	117.19	111.46
4	B	1308	CPS	C25-N1-C24	5.46	133.62	122.79
4	A	1304	CPS	C23-C22-C20	5.49	124.67	114.46
4	A	1304	CPS	C3-C4-C5	5.49	116.76	111.22
4	A	1304	CPS	C19-C18-C17	5.50	118.53	111.89
4	B	1308	CPS	C19-C18-C6	5.58	117.50	109.63
4	B	1307	CPS	C19-C18-C17	5.63	118.69	111.89
4	A	1305	CPS	C9-C5-C4	5.73	122.71	117.68
4	B	1308	CPS	C16-C15-C2	5.73	118.81	112.66
4	D	1308	CPS	C16-C17-C18	5.81	117.61	111.46
4	B	1307	CPS	C6-C5-C4	5.89	112.70	107.37
4	A	1306	CPS	C16-C15-C2	5.91	119.00	112.66
4	A	1304	CPS	O2S-S-O3S	5.95	124.43	111.26
4	A	1305	CPS	C9-C5-C6	5.98	106.13	100.08
4	D	1308	CPS	C2-C19-C18	5.99	118.33	111.86
4	B	1307	CPS	C3-C4-C5	6.03	117.30	111.22
4	D	1308	CPS	C3-C4-C5	6.35	117.62	111.22
4	A	1306	CPS	O2S-S-O3S	6.40	125.42	111.26
4	A	1305	CPS	C6-C5-C4	6.49	113.24	107.37
4	D	1308	CPS	C31-C32-S	6.53	123.81	113.15
4	A	1306	CPS	C3-C4-C5	6.77	118.05	111.22
4	D	1308	CPS	C27-C26-C25	6.86	125.45	111.34
4	A	1304	CPS	C1-C2-C15	7.00	115.48	107.76
4	B	1308	CPS	C9-C5-C4	7.01	123.83	117.68
4	A	1304	CPS	C6-C5-C4	7.19	113.88	107.37
4	A	1305	CPS	O2S-S-O3S	7.31	127.44	111.26
4	B	1308	CPS	C3-C4-C5	7.35	118.64	111.22
4	A	1306	CPS	C25-N1-C24	7.36	137.38	122.79
4	B	1307	CPS	C1-C2-C15	7.58	116.11	107.76
4	B	1308	CPS	C1-C2-C15	7.71	116.25	107.76
4	B	1308	CPS	C5-C9-C20	7.76	128.89	119.44
4	D	1308	CPS	C9-C5-C4	8.19	124.86	117.68
4	B	1308	CPS	C31-C32-S	8.19	126.51	113.15
4	A	1306	CPS	C9-C5-C4	8.33	124.98	117.68
4	A	1305	CPS	C3-C4-C5	8.97	120.27	111.22
4	A	1306	CPS	C1-C2-C15	9.18	117.88	107.76
4	D	1308	CPS	C1-C2-C15	9.39	118.11	107.76
4	A	1305	CPS	C1-C2-C15	9.40	118.12	107.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1307	CPS	C9-C5-C4	9.48	126.00	117.68
4	A	1304	CPS	C9-C5-C4	10.60	126.97	117.68
4	A	1305	CPS	O3S-S-C32	11.30	114.85	106.87
4	A	1306	CPS	O3S-S-C32	12.51	115.71	106.87
4	B	1308	CPS	O3S-S-C32	12.57	115.75	106.87
4	A	1304	CPS	O3S-S-C32	13.99	116.75	106.87
4	D	1308	CPS	O3S-S-C32	17.27	119.07	106.87
4	B	1307	CPS	O3S-S-C32	18.86	120.20	106.87

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1304	MC3	C2-O2-C31-O31
2	D	1305	MC3	C2-O2-C31-O31

There are no ring outliers.

24 monomers are involved in 171 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1301	MC3	1	0
2	A	1303	MC3	3	0
4	A	1304	CPS	24	0
4	A	1305	CPS	25	0
4	A	1306	CPS	16	0
2	B	1302	MC3	2	0
2	B	1303	MC3	1	0
2	B	1304	MC3	6	0
2	B	1305	MC3	2	0
2	B	1306	MC3	1	0
4	B	1307	CPS	13	0
4	B	1308	CPS	26	0
2	C	1302	MC3	5	0
2	C	1303	MC3	7	0
2	C	1304	MC3	3	0
2	C	1305	MC3	2	0
2	C	1306	MC3	1	0
2	C	1307	MC3	4	0
2	D	1302	MC3	1	0
2	D	1303	MC3	2	0
2	D	1304	MC3	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1305	MC3	1	0
2	D	1306	MC3	3	0
4	D	1308	CPS	23	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	267/285 (93%)	0.41	12 (4%) 37 36	33, 73, 160, 168	0
1	B	267/285 (93%)	0.48	17 (6%) 23 21	35, 69, 162, 181	0
1	C	267/285 (93%)	0.63	25 (9%) 11 8	35, 70, 180, 206	0
1	D	267/285 (93%)	0.42	12 (4%) 37 36	35, 70, 151, 164	0
All	All	1068/1140 (93%)	0.48	66 (6%) 24 23	33, 71, 161, 206	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1265	LEU	8.8
1	D	1261	ILE	7.1
1	C	1259	GLU	7.0
1	B	1258	LYS	6.9
1	C	1261	ILE	6.8
1	B	1259	GLU	6.4
1	B	1260	LEU	5.9
1	C	1260	LEU	5.6
1	C	1256	GLU	5.5
1	C	1263	THR	5.3
1	C	1264	SER	5.1
1	D	1265	LEU	5.1
1	C	1266	LYS	5.0
1	C	1267	ASN	4.9
1	C	1247	ILE	4.7
1	D	1262	LYS	4.6
1	B	1257	LEU	4.5
1	A	1260	LEU	4.2
1	C	1258	LYS	4.1
1	C	1255	VAL	4.1
1	B	1243	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
1	C	1095	PHE	3.8
1	A	1249	LYS	3.8
1	A	1247	ILE	3.8
1	B	1247	ILE	3.8
1	D	1267	ASN	3.6
1	B	1090	PRO	3.5
1	D	1263	THR	3.3
1	D	1243	ILE	3.3
1	C	1257	LEU	3.2
1	B	1261	ILE	3.1
1	C	1254	ILE	3.1
1	D	1095	PHE	3.1
1	D	1260	LEU	2.9
1	C	1239	HIS	2.9
1	C	1262	LYS	2.9
1	A	1266	LYS	2.8
1	A	1093	SER	2.8
1	B	1092	SER	2.8
1	C	1250	LEU	2.8
1	D	1258	LYS	2.8
1	A	1262	LYS	2.7
1	B	1265	LEU	2.7
1	D	1082	PHE	2.7
1	B	1095	PHE	2.7
1	B	1098	LEU	2.7
1	A	1095	PHE	2.6
1	D	1013	PHE	2.6
1	A	1245	ASN	2.6
1	C	1242	ASN	2.6
1	C	1098	LEU	2.5
1	C	1249	LYS	2.5
1	C	1243	ILE	2.4
1	A	1094	GLY	2.4
1	C	1221	MET	2.3
1	B	1003	LEU	2.3
1	B	1244	ASN	2.3
1	D	1065	TYR	2.3
1	C	1251	ARG	2.2
1	A	1267	ASN	2.2
1	B	1267	ASN	2.2
1	B	1013	PHE	2.2
1	C	1252	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	1069	ILE	2.1
1	A	1100	VAL	2.0
1	B	1256	GLU	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	CA	B	1301	1/1	0.92	0.53	14.36	103,103,103,103	0
2	MC3	A	1303	46/46	0.93	0.35	6.24	52,69,84,93	0
2	MC3	C	1301	21/46	0.86	0.27	4.24	64,81,101,115	0
2	MC3	A	1301	21/46	0.89	0.28	3.16	54,79,94,104	0
2	MC3	B	1305	46/46	0.92	0.32	3.14	51,70,88,99	0
4	CPS	A	1304	42/42	0.65	0.31	2.19	83,108,131,133	2
2	MC3	C	1304	46/46	0.92	0.29	1.64	51,71,83,90	0
2	MC3	C	1303	40/46	0.97	0.22	1.34	49,59,72,78	0
2	MC3	C	1302	41/46	0.92	0.23	1.05	50,66,89,93	0
2	MC3	C	1307	41/46	0.94	0.24	0.95	58,71,88,96	0
2	MC3	D	1306	46/46	0.95	0.24	0.91	54,68,77,82	0
2	MC3	D	1303	41/46	0.93	0.24	0.88	53,67,92,103	0
2	MC3	D	1304	43/46	0.97	0.22	0.84	44,56,70,77	0
2	MC3	B	1306	8/46	0.91	0.21	0.66	43,47,54,60	0
2	MC3	D	1302	21/46	0.83	0.21	0.52	57,80,121,128	0
4	CPS	A	1306	42/42	0.85	0.21	0.42	54,77,81,83	2
4	CPS	B	1308	42/42	0.74	0.25	0.12	90,108,122,124	2
4	CPS	A	1305	42/42	0.85	0.19	0.06	60,78,87,91	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MC3	B	1303	41/46	0.94	0.21	0.04	58,68,93,98	0
2	MC3	B	1304	41/46	0.96	0.21	0.03	46,60,75,77	0
2	MC3	D	1305	42/46	0.96	0.20	0.02	45,60,73,77	0
4	CPS	D	1308	42/42	0.85	0.18	-0.02	53,71,78,86	2
4	CPS	B	1307	42/42	0.91	0.16	-0.59	55,72,79,81	1
2	MC3	C	1306	9/46	0.91	0.19	-0.86	44,50,54,55	0
2	MC3	C	1305	9/46	0.90	0.18	-1.06	42,48,60,60	0
2	MC3	B	1302	21/46	0.89	0.14	-1.42	56,78,93,104	0
2	MC3	D	1307	8/46	0.92	0.16	-2.94	42,49,51,54	0
3	CA	D	1301	1/1	0.98	0.12	-4.13	70,70,70,70	0
3	CA	A	1302	1/1	0.99	0.19	-	79,79,79,79	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.