



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 3, 2024 – 03:46 am GMT

PDB ID : 4XC5  
Title : CRYSTAL STRUCTURE OF THE T1L REOVIRUS ATTACHMENT PROTEIN SIGMA1  
Authors : Reiss, K.; Stehle, T.  
Deposited on : 2014-12-17  
Resolution : 2.20 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>.

---

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 : 2.36  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

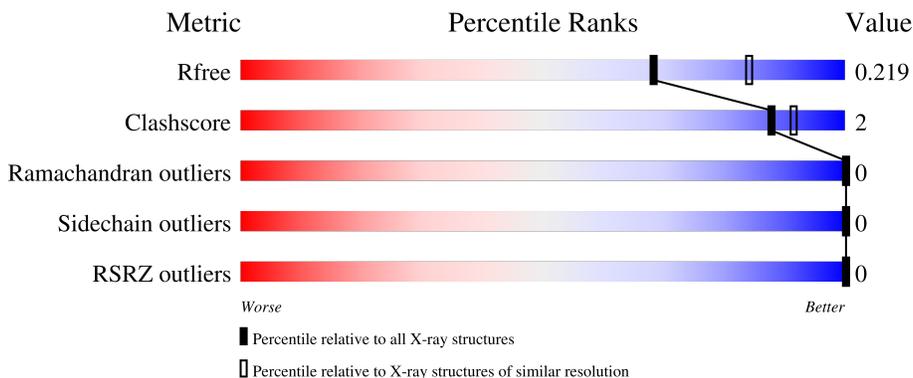
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	218	 69% 5% 26%
1	B	218	 71% 26%
1	C	218	 71% 26%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3951 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 Outer capsid protein sigma-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	162	1274	811	213	243	7	0	0	0
1	B	161	1260	801	211	241	7	0	0	0
1	C	162	1263	802	212	242	7	0	0	0

There are 165 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	253	HIS	-	expression tag	UNP P04506
A	254	HIS	-	expression tag	UNP P04506
A	255	HIS	-	expression tag	UNP P04506
A	256	HIS	-	expression tag	UNP P04506
A	257	HIS	-	expression tag	UNP P04506
A	258	HIS	-	expression tag	UNP P04506
A	259	GLY	-	expression tag	UNP P04506
A	260	SER	-	expression tag	UNP P04506
A	261	SER	-	expression tag	UNP P04506
A	262	ASN	-	expression tag	UNP P04506
A	263	SER	-	expression tag	UNP P04506
A	264	GLY	-	expression tag	UNP P04506
A	265	LYS	-	expression tag	UNP P04506
A	266	GLN	-	expression tag	UNP P04506
A	267	ILE	-	expression tag	UNP P04506
A	268	GLU	-	expression tag	UNP P04506
A	269	ASP	-	expression tag	UNP P04506
A	270	LYS	-	expression tag	UNP P04506
A	271	ILE	-	expression tag	UNP P04506
A	272	GLU	-	expression tag	UNP P04506
A	273	GLU	-	expression tag	UNP P04506
A	274	ILE	-	expression tag	UNP P04506
A	275	LEU	-	expression tag	UNP P04506

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	276	SER	-	expression tag	UNP P04506
A	277	LYS	-	expression tag	UNP P04506
A	278	ILE	-	expression tag	UNP P04506
A	279	TYR	-	expression tag	UNP P04506
A	280	HIS	-	expression tag	UNP P04506
A	281	ILE	-	expression tag	UNP P04506
A	282	GLU	-	expression tag	UNP P04506
A	283	ASN	-	expression tag	UNP P04506
A	284	GLU	-	expression tag	UNP P04506
A	285	ILE	-	expression tag	UNP P04506
A	286	ALA	-	expression tag	UNP P04506
A	287	ARG	-	expression tag	UNP P04506
A	288	ILE	-	expression tag	UNP P04506
A	289	LYS	-	expression tag	UNP P04506
A	290	LYS	-	expression tag	UNP P04506
A	291	LEU	-	expression tag	UNP P04506
A	292	ILE	-	expression tag	UNP P04506
A	293	GLY	-	expression tag	UNP P04506
A	294	GLU	-	expression tag	UNP P04506
A	295	GLY	-	expression tag	UNP P04506
A	296	SER	-	expression tag	UNP P04506
A	297	GLY	-	expression tag	UNP P04506
A	298	ARG	-	expression tag	UNP P04506
A	299	GLY	-	expression tag	UNP P04506
A	300	VAL	-	expression tag	UNP P04506
A	301	LEU	-	expression tag	UNP P04506
A	302	ASN	-	expression tag	UNP P04506
A	303	GLN	-	expression tag	UNP P04506
A	304	GLY	-	expression tag	UNP P04506
A	305	VAL	-	expression tag	UNP P04506
A	306	THR	-	expression tag	UNP P04506
A	307	SER	-	expression tag	UNP P04506
B	253	HIS	-	expression tag	UNP P04506
B	254	HIS	-	expression tag	UNP P04506
B	255	HIS	-	expression tag	UNP P04506
B	256	HIS	-	expression tag	UNP P04506
B	257	HIS	-	expression tag	UNP P04506
B	258	HIS	-	expression tag	UNP P04506
B	259	GLY	-	expression tag	UNP P04506
B	260	SER	-	expression tag	UNP P04506
B	261	SER	-	expression tag	UNP P04506
B	262	ASN	-	expression tag	UNP P04506

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	263	SER	-	expression tag	UNP P04506
B	264	GLY	-	expression tag	UNP P04506
B	265	LYS	-	expression tag	UNP P04506
B	266	GLN	-	expression tag	UNP P04506
B	267	ILE	-	expression tag	UNP P04506
B	268	GLU	-	expression tag	UNP P04506
B	269	ASP	-	expression tag	UNP P04506
B	270	LYS	-	expression tag	UNP P04506
B	271	ILE	-	expression tag	UNP P04506
B	272	GLU	-	expression tag	UNP P04506
B	273	GLU	-	expression tag	UNP P04506
B	274	ILE	-	expression tag	UNP P04506
B	275	LEU	-	expression tag	UNP P04506
B	276	SER	-	expression tag	UNP P04506
B	277	LYS	-	expression tag	UNP P04506
B	278	ILE	-	expression tag	UNP P04506
B	279	TYR	-	expression tag	UNP P04506
B	280	HIS	-	expression tag	UNP P04506
B	281	ILE	-	expression tag	UNP P04506
B	282	GLU	-	expression tag	UNP P04506
B	283	ASN	-	expression tag	UNP P04506
B	284	GLU	-	expression tag	UNP P04506
B	285	ILE	-	expression tag	UNP P04506
B	286	ALA	-	expression tag	UNP P04506
B	287	ARG	-	expression tag	UNP P04506
B	288	ILE	-	expression tag	UNP P04506
B	289	LYS	-	expression tag	UNP P04506
B	290	LYS	-	expression tag	UNP P04506
B	291	LEU	-	expression tag	UNP P04506
B	292	ILE	-	expression tag	UNP P04506
B	293	GLY	-	expression tag	UNP P04506
B	294	GLU	-	expression tag	UNP P04506
B	295	GLY	-	expression tag	UNP P04506
B	296	SER	-	expression tag	UNP P04506
B	297	GLY	-	expression tag	UNP P04506
B	298	ARG	-	expression tag	UNP P04506
B	299	GLY	-	expression tag	UNP P04506
B	300	VAL	-	expression tag	UNP P04506
B	301	LEU	-	expression tag	UNP P04506
B	302	ASN	-	expression tag	UNP P04506
B	303	GLN	-	expression tag	UNP P04506
B	304	GLY	-	expression tag	UNP P04506

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	305	VAL	-	expression tag	UNP P04506
B	306	THR	-	expression tag	UNP P04506
B	307	SER	-	expression tag	UNP P04506
C	253	HIS	-	expression tag	UNP P04506
C	254	HIS	-	expression tag	UNP P04506
C	255	HIS	-	expression tag	UNP P04506
C	256	HIS	-	expression tag	UNP P04506
C	257	HIS	-	expression tag	UNP P04506
C	258	HIS	-	expression tag	UNP P04506
C	259	GLY	-	expression tag	UNP P04506
C	260	SER	-	expression tag	UNP P04506
C	261	SER	-	expression tag	UNP P04506
C	262	ASN	-	expression tag	UNP P04506
C	263	SER	-	expression tag	UNP P04506
C	264	GLY	-	expression tag	UNP P04506
C	265	LYS	-	expression tag	UNP P04506
C	266	GLN	-	expression tag	UNP P04506
C	267	ILE	-	expression tag	UNP P04506
C	268	GLU	-	expression tag	UNP P04506
C	269	ASP	-	expression tag	UNP P04506
C	270	LYS	-	expression tag	UNP P04506
C	271	ILE	-	expression tag	UNP P04506
C	272	GLU	-	expression tag	UNP P04506
C	273	GLU	-	expression tag	UNP P04506
C	274	ILE	-	expression tag	UNP P04506
C	275	LEU	-	expression tag	UNP P04506
C	276	SER	-	expression tag	UNP P04506
C	277	LYS	-	expression tag	UNP P04506
C	278	ILE	-	expression tag	UNP P04506
C	279	TYR	-	expression tag	UNP P04506
C	280	HIS	-	expression tag	UNP P04506
C	281	ILE	-	expression tag	UNP P04506
C	282	GLU	-	expression tag	UNP P04506
C	283	ASN	-	expression tag	UNP P04506
C	284	GLU	-	expression tag	UNP P04506
C	285	ILE	-	expression tag	UNP P04506
C	286	ALA	-	expression tag	UNP P04506
C	287	ARG	-	expression tag	UNP P04506
C	288	ILE	-	expression tag	UNP P04506
C	289	LYS	-	expression tag	UNP P04506
C	290	LYS	-	expression tag	UNP P04506
C	291	LEU	-	expression tag	UNP P04506

*Continued on next page...*

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	292	ILE	-	expression tag	UNP P04506
C	293	GLY	-	expression tag	UNP P04506
C	294	GLU	-	expression tag	UNP P04506
C	295	GLY	-	expression tag	UNP P04506
C	296	SER	-	expression tag	UNP P04506
C	297	GLY	-	expression tag	UNP P04506
C	298	ARG	-	expression tag	UNP P04506
C	299	GLY	-	expression tag	UNP P04506
C	300	VAL	-	expression tag	UNP P04506
C	301	LEU	-	expression tag	UNP P04506
C	302	ASN	-	expression tag	UNP P04506
C	303	GLN	-	expression tag	UNP P04506
C	304	GLY	-	expression tag	UNP P04506
C	305	VAL	-	expression tag	UNP P04506
C	306	THR	-	expression tag	UNP P04506
C	307	SER	-	expression tag	UNP P04506

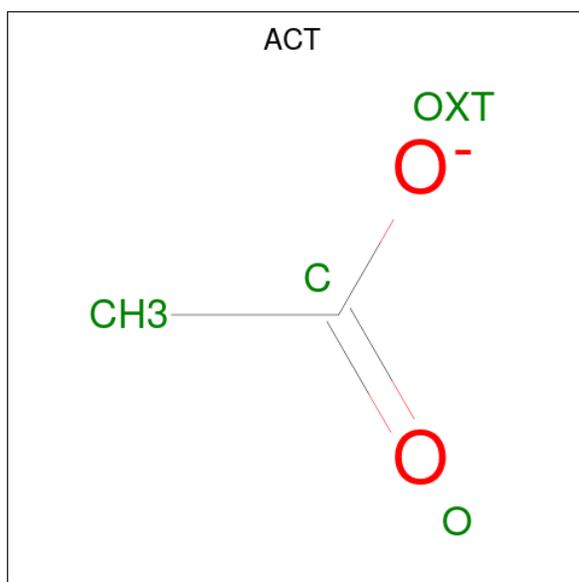
- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl 1 1	0	0
2	B	1	Total Cl 1 1	0	0
2	C	1	Total Cl 1 1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

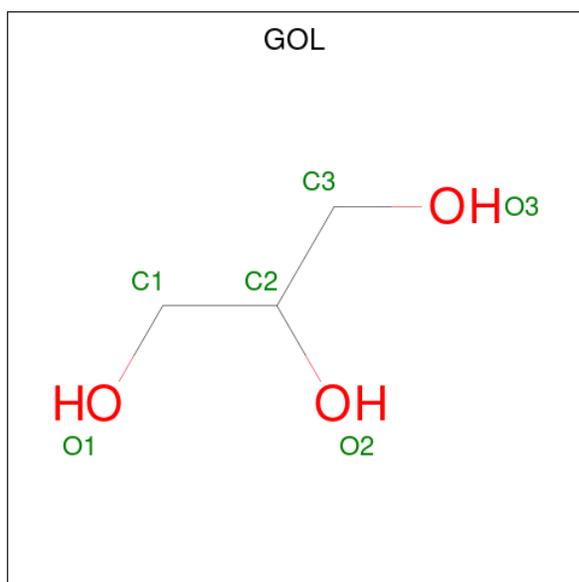
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 6	C 3	O 3	0	0
5	B	1	Total 6	C 3	O 3	0	0
5	B	1	Total 6	C 3	O 3	0	0
5	B	1	Total 6	C 3	O 3	0	0
5	C	1	Total 6	C 3	O 3	0	0
5	C	1	Total 6	C 3	O 3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	29	Total 29	O 29	0	0
6	B	32	Total 32	O 32	0	0
6	C	33	Total 33	O 33	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	112.93Å 112.96Å 113.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.32 – 2.20 46.18 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (42.32-2.20) 98.5 (46.18-2.00)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.38 (at 2.00Å)	Xtrriage
Refinement program	BUSTER 2.10.0	Depositor
R, $R_{free}$	0.190 , 0.223 0.189 , 0.219	Depositor DCC
$R_{free}$ test set	4835 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.1	Xtrriage
Anisotropy	0.081	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 38.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.048 for -h,-l,-k 0.045 for l,-k,h 0.045 for -k,-h,-l 0.447 for k,-l,-h 0.447 for -l,h,-k	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3951	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.29% 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: CL, ACT, GOL, MG

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	0.52	0/1309	0.68	0/1789
1	B	0.51	0/1295	0.68	0/1770
1	C	0.51	0/1298	0.69	0/1776
All	All	0.51	0/3902	0.68	0/5335

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	1274	0	1204	6	0
1	B	1260	0	1180	5	0
1	C	1263	0	1172	4	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	4	0	3	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	4	0	3	0	0
4	C	4	0	3	0	0
5	A	12	0	16	1	0
5	B	18	0	24	3	0
5	C	12	0	16	0	0
6	A	29	0	0	0	0
6	B	32	0	0	0	0
6	C	33	0	0	0	0
All	All	3951	0	3621	15	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 15 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:B:355:THR:H	5:B:504:GOL:H32	1.54	0.70
1:A:419:LEU:HD22	1:A:424:ARG:HG2	1.87	0.57
1:A:420:ASN:O	1:A:423:GLN:HG2	2.09	0.53
1:A:333:ARG:NH2	1:A:394:GLY:O	2.44	0.51
1:C:412:THR:HG22	1:C:463:ILE:HD12	1.94	0.49

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	160/218 (73%)	157 (98%)	3 (2%)	0	100	100
1	B	159/218 (73%)	155 (98%)	4 (2%)	0	100	100
1	C	160/218 (73%)	156 (98%)	4 (2%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	479/654 (73%)	468 (98%)	11 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	137/189 (72%)	137 (100%)	0	100	100
1	B	134/189 (71%)	134 (100%)	0	100	100
1	C	133/189 (70%)	133 (100%)	0	100	100
All	All	404/567 (71%)	404 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	357	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

Of 16 ligands modelled in this entry, 6 are monoatomic - leaving 10 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
5	GOL	B	505	-	5,5,5	0.05	0	5,5,5	0.09	0
5	GOL	A	505	-	5,5,5	0.11	0	5,5,5	0.16	0
5	GOL	C	505	-	5,5,5	0.19	0	5,5,5	0.35	0
4	ACT	A	503	-	3,3,3	1.29	0	3,3,3	0.70	0
5	GOL	B	504	-	5,5,5	0.16	0	5,5,5	0.56	0
5	GOL	B	506	-	5,5,5	0.11	0	5,5,5	0.17	0
4	ACT	B	503	-	3,3,3	1.17	0	3,3,3	0.84	0
5	GOL	A	504	-	5,5,5	0.22	0	5,5,5	0.45	0
4	ACT	C	503	-	3,3,3	1.22	0	3,3,3	0.76	0
5	GOL	C	504	-	5,5,5	0.04	0	5,5,5	0.35	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
5	GOL	B	505	-	-	0/4/4/4	-
5	GOL	A	505	-	-	2/4/4/4	-
5	GOL	C	505	-	-	0/4/4/4	-
5	GOL	B	504	-	-	2/4/4/4	-
5	GOL	B	506	-	-	0/4/4/4	-
5	GOL	A	504	-	-	0/4/4/4	-
5	GOL	C	504	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	504	GOL	C1-C2-C3-O3
5	A	505	GOL	C1-C2-C3-O3
5	A	505	GOL	O2-C2-C3-O3
5	B	504	GOL	O2-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	505	GOL	1	0
5	A	505	GOL	1	0
5	B	504	GOL	2	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	162/218 (74%)	0.13	0 100 100	26, 36, 55, 69	0
1	B	161/218 (73%)	0.12	0 100 100	23, 35, 53, 69	0
1	C	162/218 (74%)	0.10	0 100 100	25, 36, 55, 70	0
All	All	485/654 (74%)	0.12	0 100 100	23, 36, 55, 70	0

There are no RSRZ outliers to report.

### 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 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	ACT	C	503	4/4	0.78	0.20	63,65,66,73	0
5	GOL	A	505	6/6	0.83	0.26	46,51,58,61	0
5	GOL	B	506	6/6	0.83	0.23	49,52,61,65	0
5	GOL	B	505	6/6	0.85	0.17	52,57,61,64	0
5	GOL	C	505	6/6	0.86	0.21	44,49,52,54	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	ACT	B	503	4/4	0.87	0.13	59,63,65,66	0
5	GOL	A	504	6/6	0.90	0.16	45,51,53,53	0
3	MG	C	502	1/1	0.94	0.07	52,52,52,52	1
4	ACT	A	503	4/4	0.94	0.16	54,58,59,64	0
3	MG	B	502	1/1	0.94	0.11	53,53,53,53	1
5	GOL	B	504	6/6	0.95	0.15	50,51,56,57	0
3	MG	A	502	1/1	0.96	0.07	47,47,47,47	1
5	GOL	C	504	6/6	0.97	0.17	44,51,57,62	0
2	CL	A	501	1/1	0.97	0.09	50,50,50,50	0
2	CL	C	501	1/1	0.98	0.09	49,49,49,49	0
2	CL	B	501	1/1	0.99	0.08	49,49,49,49	0

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.