



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 11, 2023 – 12:59 AM EDT

PDB ID : 4KWT  
Title : Crystal structure of unliganded anabolic ornithine carbamoyltransferase from *Vibrio vulnificus* at 1.86 Å resolution  
Authors : Shabalin, I.G.; Bacal, P.; Bajor, J.; Winsor, J.; Grimshaw, S.; Anderson, W.F.; Minor, W.; Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : 2013-05-24  
Resolution : 1.86 Å (reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

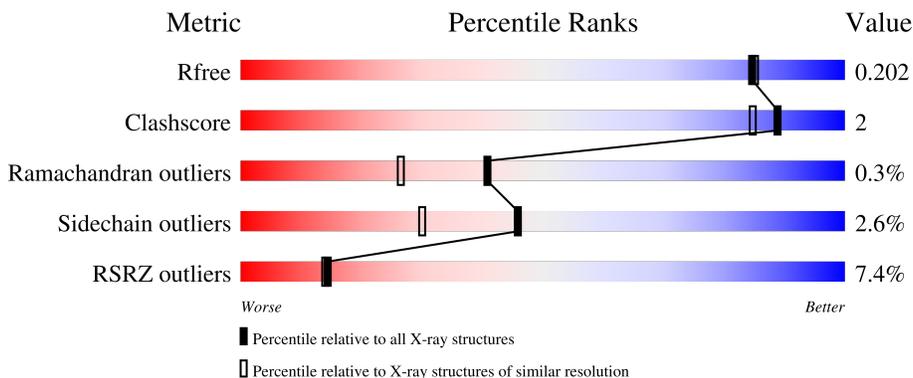
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.86 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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	358	
1	B	358	
1	C	358	

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 8036 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 Ornithine carbamoyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	323	2481	1574	419	471	17	0	1	0
1	B	327	2511	1596	423	475	17	0	0	0
1	C	328	2543	1616	425	485	17	0	3	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	expression tag	UNP Q8DCF5
A	-22	HIS	-	expression tag	UNP Q8DCF5
A	-21	HIS	-	expression tag	UNP Q8DCF5
A	-20	HIS	-	expression tag	UNP Q8DCF5
A	-19	HIS	-	expression tag	UNP Q8DCF5
A	-18	HIS	-	expression tag	UNP Q8DCF5
A	-17	HIS	-	expression tag	UNP Q8DCF5
A	-16	SER	-	expression tag	UNP Q8DCF5
A	-15	SER	-	expression tag	UNP Q8DCF5
A	-14	GLY	-	expression tag	UNP Q8DCF5
A	-13	VAL	-	expression tag	UNP Q8DCF5
A	-12	ASP	-	expression tag	UNP Q8DCF5
A	-11	LEU	-	expression tag	UNP Q8DCF5
A	-10	GLY	-	expression tag	UNP Q8DCF5
A	-9	THR	-	expression tag	UNP Q8DCF5
A	-8	GLU	-	expression tag	UNP Q8DCF5
A	-7	ASN	-	expression tag	UNP Q8DCF5
A	-6	LEU	-	expression tag	UNP Q8DCF5
A	-5	TYR	-	expression tag	UNP Q8DCF5
A	-4	PHE	-	expression tag	UNP Q8DCF5
A	-3	GLN	-	expression tag	UNP Q8DCF5
A	-2	SER	-	expression tag	UNP Q8DCF5
A	-1	ASN	-	expression tag	UNP Q8DCF5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	-	expression tag	UNP Q8DCF5
B	-23	MET	-	expression tag	UNP Q8DCF5
B	-22	HIS	-	expression tag	UNP Q8DCF5
B	-21	HIS	-	expression tag	UNP Q8DCF5
B	-20	HIS	-	expression tag	UNP Q8DCF5
B	-19	HIS	-	expression tag	UNP Q8DCF5
B	-18	HIS	-	expression tag	UNP Q8DCF5
B	-17	HIS	-	expression tag	UNP Q8DCF5
B	-16	SER	-	expression tag	UNP Q8DCF5
B	-15	SER	-	expression tag	UNP Q8DCF5
B	-14	GLY	-	expression tag	UNP Q8DCF5
B	-13	VAL	-	expression tag	UNP Q8DCF5
B	-12	ASP	-	expression tag	UNP Q8DCF5
B	-11	LEU	-	expression tag	UNP Q8DCF5
B	-10	GLY	-	expression tag	UNP Q8DCF5
B	-9	THR	-	expression tag	UNP Q8DCF5
B	-8	GLU	-	expression tag	UNP Q8DCF5
B	-7	ASN	-	expression tag	UNP Q8DCF5
B	-6	LEU	-	expression tag	UNP Q8DCF5
B	-5	TYR	-	expression tag	UNP Q8DCF5
B	-4	PHE	-	expression tag	UNP Q8DCF5
B	-3	GLN	-	expression tag	UNP Q8DCF5
B	-2	SER	-	expression tag	UNP Q8DCF5
B	-1	ASN	-	expression tag	UNP Q8DCF5
B	0	ALA	-	expression tag	UNP Q8DCF5
C	-23	MET	-	expression tag	UNP Q8DCF5
C	-22	HIS	-	expression tag	UNP Q8DCF5
C	-21	HIS	-	expression tag	UNP Q8DCF5
C	-20	HIS	-	expression tag	UNP Q8DCF5
C	-19	HIS	-	expression tag	UNP Q8DCF5
C	-18	HIS	-	expression tag	UNP Q8DCF5
C	-17	HIS	-	expression tag	UNP Q8DCF5
C	-16	SER	-	expression tag	UNP Q8DCF5
C	-15	SER	-	expression tag	UNP Q8DCF5
C	-14	GLY	-	expression tag	UNP Q8DCF5
C	-13	VAL	-	expression tag	UNP Q8DCF5
C	-12	ASP	-	expression tag	UNP Q8DCF5
C	-11	LEU	-	expression tag	UNP Q8DCF5
C	-10	GLY	-	expression tag	UNP Q8DCF5
C	-9	THR	-	expression tag	UNP Q8DCF5
C	-8	GLU	-	expression tag	UNP Q8DCF5
C	-7	ASN	-	expression tag	UNP Q8DCF5

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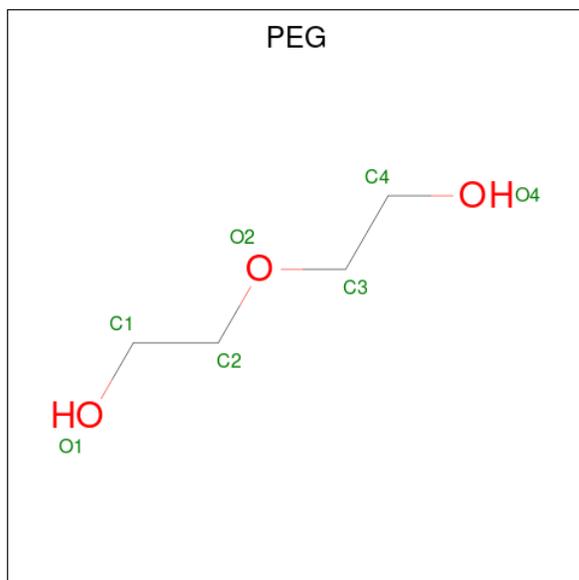
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Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	LEU	-	expression tag	UNP Q8DCF5
C	-5	TYR	-	expression tag	UNP Q8DCF5
C	-4	PHE	-	expression tag	UNP Q8DCF5
C	-3	GLN	-	expression tag	UNP Q8DCF5
C	-2	SER	-	expression tag	UNP Q8DCF5
C	-1	ASN	-	expression tag	UNP Q8DCF5
C	0	ALA	-	expression tag	UNP Q8DCF5

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

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

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C O 6 4 2	0	0

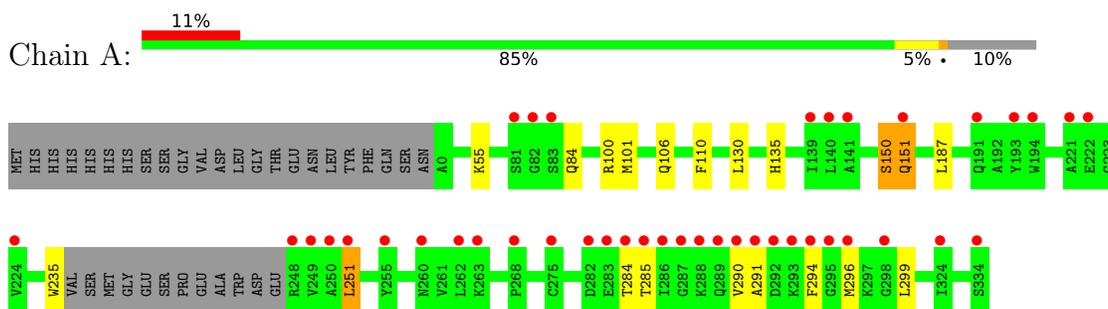
- Molecule 4 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	A	138	Total 139	O 139	0	1
4	B	166	Total 167	O 167	0	1
4	C	183	Total 184	O 184	0	1

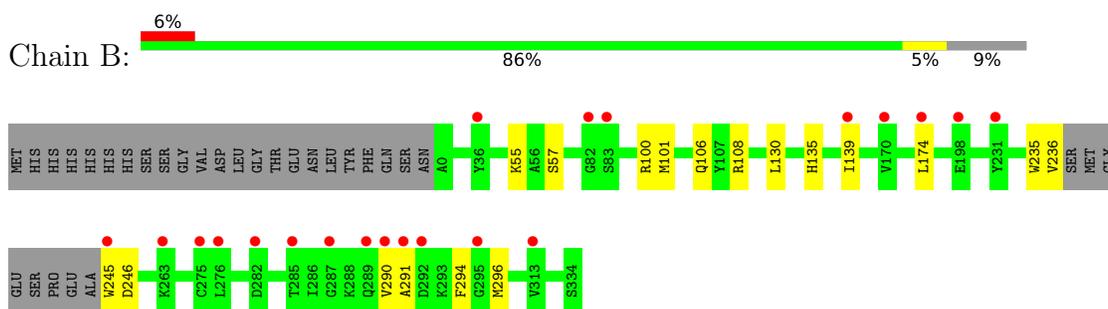
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

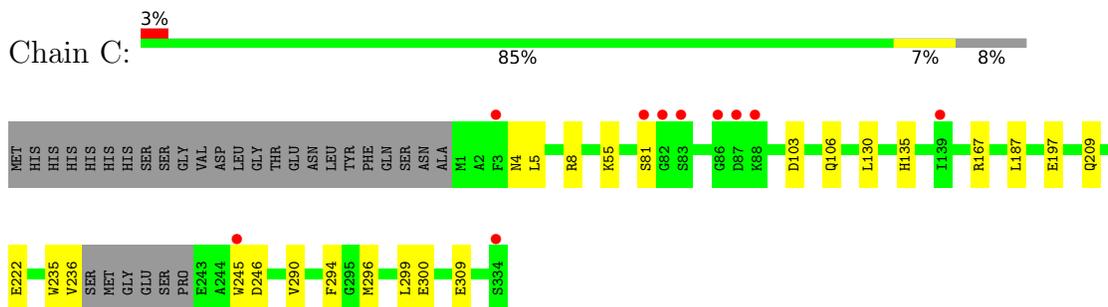
- Molecule 1: Ornithine carbamoyltransferase



- Molecule 1: Ornithine carbamoyltransferase



- Molecule 1: Ornithine carbamoyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.81Å 82.65Å 150.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.50 – 1.86 35.47 – 1.86	Depositor EDS
% Data completeness (in resolution range)	98.3 (35.50-1.86) 97.9 (35.47-1.86)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.34 (at 1.85Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.160 , 0.195 0.170 , 0.202	Depositor DCC
$R_{free}$ test set	4056 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.6	Xtrriage
Anisotropy	0.464	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 49.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8036	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% 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: PEG, 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	0.95	1/2530 (0.0%)	0.89	3/3415 (0.1%)
1	B	0.90	0/2557	0.90	2/3453 (0.1%)
1	C	0.94	0/2598	0.89	3/3506 (0.1%)
All	All	0.93	1/7685 (0.0%)	0.89	8/10374 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	150	SER	CB-OG	-5.27	1.35	1.42

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	100	ARG	NE-CZ-NH1	-5.82	117.39	120.30
1	A	251	LEU	CB-CG-CD2	-5.48	101.69	111.00
1	B	100	ARG	NE-CZ-NH2	5.43	123.02	120.30
1	C	103	ASP	CB-CG-OD2	5.41	123.17	118.30
1	C	187	LEU	CA-CB-CG	-5.41	102.87	115.30
1	A	187	LEU	CA-CB-CG	-5.38	102.92	115.30
1	A	100	ARG	NE-CZ-NH1	-5.22	117.69	120.30
1	C	167	ARG	NE-CZ-NH1	5.04	122.82	120.30

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	2481	0	2437	8	0
1	B	2511	0	2463	7	0
1	C	2543	0	2505	13	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
2	C	2	0	0	0	0
3	C	6	0	7	0	0
4	A	139	0	0	0	0
4	B	167	0	0	0	0
4	C	184	0	0	2	0
All	All	8036	0	7412	28	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (28) 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:291:ALA:HB1	1:B:296:MET:O	1.71	0.90
1:A:291:ALA:HA	1:A:296:MET:O	1.81	0.81
1:B:246:ASP:HA	1:B:294:PHE:CZ	2.26	0.70
1:B:290:VAL:O	1:B:294:PHE:HD1	1.75	0.68
1:B:246:ASP:HA	1:B:294:PHE:HZ	1.61	0.66
1:A:55:LYS:HE3	1:A:110:PHE:CD1	2.37	0.60
1:A:150:SER:C	1:A:151:GLN:HG2	2.26	0.56
1:C:209:GLN:NE2	4:C:634:HOH:O	2.40	0.54
1:C:236:VAL:HB	1:C:245:TRP:CE3	2.42	0.53
1:C:236:VAL:HB	1:C:245:TRP:CD2	2.44	0.53
1:C:309[B]:GLU:CD	1:C:309[B]:GLU:H	2.13	0.51
1:C:294:PHE:HB2	1:C:296:MET:HE2	1.94	0.49
1:A:290:VAL:HG11	1:A:299:LEU:HD21	1.93	0.49
1:B:57:SER:HB2	1:B:108:ARG:CZ	2.43	0.48
1:C:197:GLU:H	1:C:197:GLU:CD	2.17	0.48
1:C:5:LEU:HA	1:C:8:ARG:HG3	1.96	0.47
1:C:235:TRP:CZ2	1:C:300:GLU:HA	2.50	0.47
1:C:81:SER:HB3	4:C:667:HOH:O	2.16	0.46
1:A:251:LEU:C	1:A:251:LEU:HD23	2.37	0.45
1:C:294:PHE:CB	1:C:296:MET:HE2	2.48	0.44
1:A:294:PHE:CB	1:A:296:MET:HE2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:TRP:N	1:B:245:TRP:CD1	2.87	0.41
1:A:251:LEU:HD23	1:A:251:LEU:O	2.21	0.41
1:A:296:MET:HE1	1:A:299:LEU:CD2	2.51	0.41
1:C:245:TRP:CE3	1:C:290:VAL:HG21	2.55	0.41
1:B:139:ILE:HG13	1:B:174:LEU:HD23	2.03	0.40
1:C:296:MET:HE1	1:C:299:LEU:CD2	2.52	0.40
1:C:296:MET:HB2	1:C:296:MET:HE3	1.96	0.40

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	320/358 (89%)	311 (97%)	8 (2%)	1 (0%)	41	26
1	B	323/358 (90%)	313 (97%)	9 (3%)	1 (0%)	41	26
1	C	327/358 (91%)	318 (97%)	8 (2%)	1 (0%)	41	26
All	All	970/1074 (90%)	942 (97%)	25 (3%)	3 (0%)	41	26

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	130	LEU
1	B	130	LEU
1	C	130	LEU

### 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	256/292 (88%)	248 (97%)	8 (3%)	40	23
1	B	258/292 (88%)	252 (98%)	6 (2%)	50	34
1	C	265/292 (91%)	259 (98%)	6 (2%)	50	34
All	All	779/876 (89%)	759 (97%)	20 (3%)	46	30

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	84	GLN
1	A	101	MET
1	A	106	GLN
1	A	135	HIS
1	A	151	GLN
1	A	235	TRP
1	A	284	THR
1	A	285	THR
1	B	55	LYS
1	B	101	MET
1	B	106	GLN
1	B	135	HIS
1	B	235	TRP
1	B	236	VAL
1	C	4	ASN
1	C	55	LYS
1	C	106	GLN
1	C	135	HIS
1	C	222	GLU
1	C	246	ASP

Sometimes 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 [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 [i](#)

Of 6 ligands modelled in this entry, 5 are monoatomic - leaving 1 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	$\# Z  > 2$
3	PEG	C	403	-	5,5,6	0.47	0	4,4,5	0.55	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
3	PEG	C	403	-	-	1/3/3/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	403	PEG	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

## 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	323/358 (90%)	0.52	41 (12%) <b>3</b> <b>3</b>	23, 38, 84, 113	0
1	B	327/358 (91%)	0.20	21 (6%) <b>19</b> <b>18</b>	22, 36, 65, 101	0
1	C	328/358 (91%)	-0.03	10 (3%) 50 48	23, 33, 59, 88	0
All	All	978/1074 (91%)	0.23	72 (7%) <b>14</b> <b>14</b>	22, 36, 67, 113	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	294	PHE	7.6
1	A	292	ASP	7.2
1	A	250	ALA	7.0
1	A	289	GLN	6.2
1	A	291	ALA	6.1
1	A	287	GLY	5.7
1	A	82	GLY	5.4
1	A	285	THR	5.3
1	C	82	GLY	5.1
1	A	249	VAL	5.1
1	B	245	TRP	5.0
1	B	290	VAL	4.8
1	A	296	MET	4.6
1	A	293	LYS	4.3
1	A	288	LYS	4.3
1	B	292	ASP	4.2
1	C	81	SER	4.1
1	C	83	SER	4.1
1	A	268	PRO	4.1
1	A	251	LEU	3.8
1	B	170	VAL	3.8
1	A	255	TYR	3.7
1	B	82	GLY	3.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	282	ASP	3.6
1	C	86	GLY	3.5
1	A	83	SER	3.4
1	B	285	THR	3.3
1	A	262	LEU	3.3
1	C	3	PHE	3.2
1	A	295	GLY	3.2
1	A	284	THR	3.1
1	B	289	GLN	3.1
1	A	81	SER	3.0
1	A	283	GLU	3.0
1	A	151	GLN	3.0
1	B	313	VAL	3.0
1	A	324	ILE	3.0
1	B	287	GLY	3.0
1	B	295	GLY	3.0
1	B	275	CYS	2.9
1	B	276	LEU	2.9
1	A	263	LYS	2.9
1	B	139	ILE	2.8
1	B	36	TYR	2.8
1	B	263	LYS	2.7
1	A	139	ILE	2.7
1	B	291	ALA	2.7
1	B	231	TYR	2.5
1	A	282	ASP	2.5
1	C	245	TRP	2.5
1	A	298	GLY	2.5
1	A	248	ARG	2.5
1	A	334	SER	2.4
1	A	193	TYR	2.4
1	A	224	VAL	2.4
1	B	174	LEU	2.4
1	A	275	CYS	2.3
1	B	83	SER	2.3
1	A	222	GLU	2.2
1	A	260	ASN	2.2
1	A	141	ALA	2.2
1	B	198	GLU	2.2
1	A	286	ILE	2.2
1	A	221	ALA	2.2
1	C	139	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	191[A]	GLN	2.2
1	A	194	TRP	2.1
1	A	290	VAL	2.1
1	C	87	ASP	2.1
1	A	140	LEU	2.0
1	C	88	LYS	2.0
1	C	334	SER	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 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
3	PEG	C	403	6/7	0.79	0.19	50,60,63,69	0
2	CL	C	401	1/1	0.93	0.19	54,54,54,54	0
2	CL	A	401	1/1	0.96	0.07	53,53,53,53	0
2	CL	C	402	1/1	0.99	0.14	28,28,28,28	0
2	CL	A	402	1/1	0.99	0.12	31,31,31,31	0
2	CL	B	401	1/1	1.00	0.07	31,31,31,31	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.