



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 9, 2017 – 09:08 PM EDT

PDB ID : 2FW3  
Title : Crystal structure of rat carnitine palmitoyltransferase 2 in complex with anti-diabetic drug ST1326  
Authors : Rufer, A.C.; Thoma, R.; Benz, J.; Stihle, M.; Gsell, B.; De Roo, E.; Banner, D.W.; Mueller, F.; Chomienne, O.; Hennig, M.  
Deposited on : unknown  
Resolution : 2.50 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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-20030345

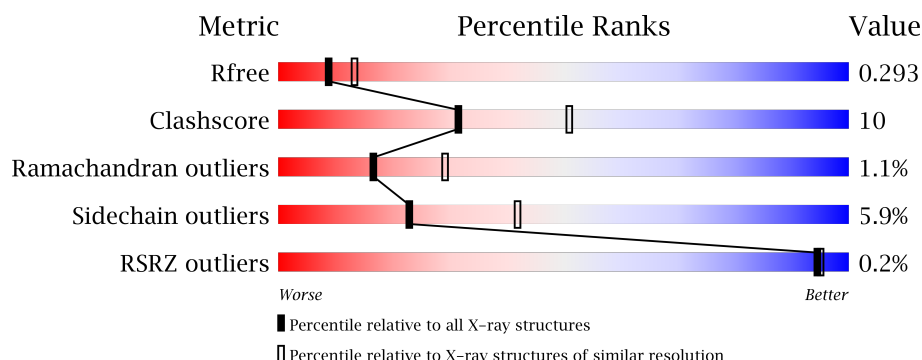
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


The reported resolution of this entry is 2.50 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))
$R_{free}$	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

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	653	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5143 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.

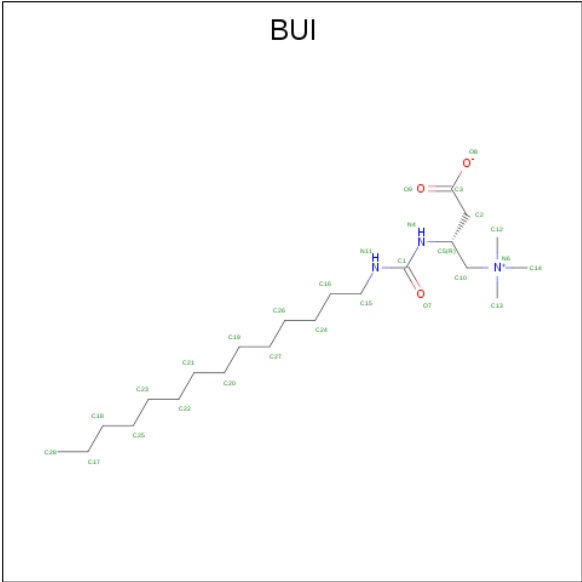
- Molecule 1 is a protein called Carnitine O-palmitoyltransferase II, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	623	4963	3159	855	928	21	0	0	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	MET	-	EXPRESSION TAG	UNP P18886
A	7	GLY	-	EXPRESSION TAG	UNP P18886
A	8	SER	-	EXPRESSION TAG	UNP P18886
A	9	SER	-	EXPRESSION TAG	UNP P18886
A	10	HIS	-	EXPRESSION TAG	UNP P18886
A	11	HIS	-	EXPRESSION TAG	UNP P18886
A	12	HIS	-	EXPRESSION TAG	UNP P18886
A	13	HIS	-	EXPRESSION TAG	UNP P18886
A	14	HIS	-	EXPRESSION TAG	UNP P18886
A	15	HIS	-	EXPRESSION TAG	UNP P18886
A	16	SER	-	EXPRESSION TAG	UNP P18886
A	17	SER	-	EXPRESSION TAG	UNP P18886
A	18	GLY	-	EXPRESSION TAG	UNP P18886
A	19	LEU	-	EXPRESSION TAG	UNP P18886
A	20	VAL	-	EXPRESSION TAG	UNP P18886
A	21	PRO	-	EXPRESSION TAG	UNP P18886
A	22	ARG	-	EXPRESSION TAG	UNP P18886
A	23	GLY	-	EXPRESSION TAG	UNP P18886
A	24	SER	-	EXPRESSION TAG	UNP P18886
A	25	HIS	-	EXPRESSION TAG	UNP P18886
A	26	MET	-	EXPRESSION TAG	UNP P18886

- Molecule 2 is (3R)-3-[[[(TETRADECYLAMINO)CARBONYL]AMINO}-4-(TRIMETHYL AMMONIO)BUTANOATE (three-letter code: BUI) (formula: C<sub>22</sub>H<sub>45</sub>N<sub>3</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			28	22	3	3		

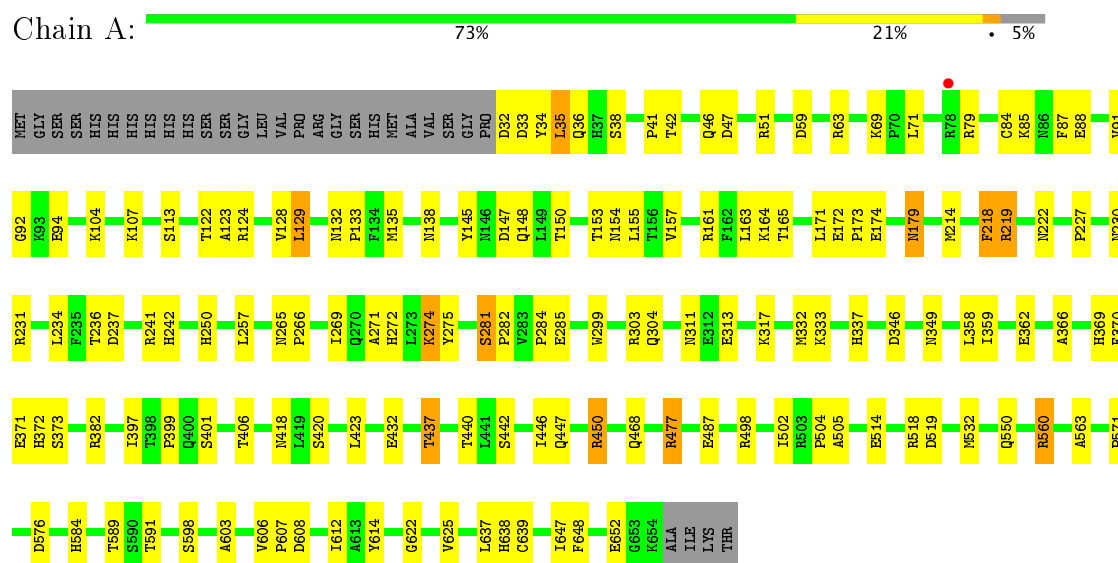
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	152	Total	O	0	0
			152	152		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: Carnitine O-palmitoyltransferase II, mitochondrial



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.80 Å 96.20 Å 124.30 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.50 44.86 – 2.27	Depositor EDS
% Data completeness (in resolution range)	95.8 (15.00-2.50) 93.9 (44.86-2.27)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.72 (at 2.27 Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.241 , 0.296 0.240 , 0.293	Depositor DCC
$R_{free}$ test set	1765 reflections (5.37%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.4	Xtriage
Anisotropy	0.770	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 44.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	5143	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: BUI

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	0.67	0/5089	0.74	2/6903 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	219	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	A	219	ARG	NE-CZ-NH2	-5.83	117.38	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	4963	0	4847	101	0
2	A	28	0	45	2	0
3	A	152	0	0	14	0
All	All	5143	0	4892	101	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 10.

All (101) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:THR:O	1:A:124:ARG:HD2	1.55	1.03
1:A:36:GLN:NE2	1:A:172:GLU:H	1.71	0.88
1:A:157:VAL:O	1:A:161:ARG:HG3	1.80	0.81
1:A:242:HIS:HD2	3:A:932:HOH:O	1.63	0.80
1:A:35:LEU:H	1:A:165:THR:HG21	1.45	0.79
1:A:132:ASN:HD22	1:A:369:HIS:HE1	1.28	0.78
1:A:34:TYR:HA	1:A:165:THR:HG22	1.64	0.77
1:A:46:GLN:HE22	1:A:214:MET:H	1.34	0.74
1:A:154:ASN:HD21	1:A:397:ILE:H	1.33	0.74
1:A:477:ARG:HG2	1:A:639:CYS:SG	2.29	0.72
1:A:34:TYR:HA	1:A:165:THR:CG2	2.21	0.69
1:A:36:GLN:HE21	1:A:172:GLU:H	1.40	0.69
1:A:33:ASP:HA	1:A:161:ARG:HH21	1.61	0.66
1:A:487:GLU:HB3	1:A:502:ILE:HB	1.77	0.66
1:A:332:MET:HA	1:A:337:HIS:HD2	1.62	0.65
1:A:219:ARG:HD3	3:A:964:HOH:O	1.97	0.64
1:A:34:TYR:CA	1:A:165:THR:HG22	2.30	0.62
1:A:153:THR:O	1:A:157:VAL:HG23	1.99	0.61
1:A:514:GLU:HG2	1:A:518:ARG:HE	1.66	0.60
1:A:59:ASP:HB3	1:A:63:ARG:HH11	1.65	0.60
1:A:311:ASN:HD21	1:A:418:ASN:H	1.47	0.60
1:A:128:VAL:HG12	1:A:129:LEU:HD13	1.83	0.60
1:A:132:ASN:HB3	1:A:369:HIS:CE1	2.38	0.59
1:A:94:GLU:OE1	1:A:94:GLU:HA	2.03	0.59
1:A:34:TYR:CB	1:A:165:THR:HG22	2.33	0.58
1:A:550:GLN:HG3	3:A:1023:HOH:O	2.03	0.57
1:A:122:THR:O	1:A:124:ARG:CD	2.44	0.57
1:A:46:GLN:NE2	1:A:214:MET:H	2.03	0.57
1:A:589:THR:HG22	1:A:612:ILE:HD13	1.87	0.56
1:A:35:LEU:N	1:A:165:THR:HG21	2.19	0.55
1:A:138:ASN:ND2	1:A:598:SER:HB3	2.22	0.54
1:A:32:ASP:HB2	3:A:929:HOH:O	2.05	0.54
1:A:154:ASN:ND2	1:A:397:ILE:H	2.03	0.54
1:A:242:HIS:CD2	3:A:932:HOH:O	2.46	0.54
1:A:128:VAL:O	1:A:129:LEU:HB2	2.08	0.54
1:A:502:ILE:O	1:A:504:PRO:HD3	2.08	0.54
1:A:132:ASN:HD22	1:A:369:HIS:CE1	2.18	0.54
1:A:132:ASN:ND2	1:A:369:HIS:HE1	2.04	0.53
1:A:227:PRO:HG3	1:A:299:TRP:CD1	2.43	0.53
1:A:129:LEU:O	1:A:603:ALA:HB3	2.09	0.53
1:A:532:MET:CE	1:A:647:ILE:HG12	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:332:MET:HA	1:A:337:HIS:CD2	2.44	0.52
1:A:227:PRO:HG3	1:A:299:TRP:NE1	2.25	0.52
1:A:32:ASP:N	3:A:1017:HOH:O	2.43	0.51
1:A:272:HIS:CE1	3:A:930:HOH:O	2.63	0.51
1:A:532:MET:HE2	1:A:647:ILE:HG12	1.93	0.51
1:A:446:ILE:HG12	1:A:637:LEU:HD22	1.92	0.51
1:A:359:ILE:O	1:A:366:ALA:HA	2.11	0.50
1:A:63:ARG:HA	3:A:903:HOH:O	2.11	0.50
1:A:34:TYR:HB3	1:A:165:THR:HG22	1.93	0.50
1:A:265:ASN:O	1:A:266:PRO:C	2.50	0.49
1:A:612:ILE:HG23	1:A:625:VAL:HG22	1.93	0.49
1:A:59:ASP:HB3	1:A:63:ARG:NH1	2.28	0.49
1:A:450:ARG:NH2	1:A:648:PHE:HB3	2.27	0.49
1:A:227:PRO:HG3	1:A:299:TRP:CE2	2.48	0.49
1:A:437:THR:O	1:A:440:THR:OG1	2.24	0.49
1:A:576:ASP:OD1	1:A:576:ASP:C	2.51	0.49
1:A:371:GLU:OE1	1:A:373:SER:OG	2.25	0.49
1:A:148:GLN:OE1	1:A:362:GLU:HA	2.13	0.48
1:A:51:ARG:NH1	1:A:107:LYS:HG2	2.29	0.47
1:A:161:ARG:O	1:A:165:THR:HG23	2.14	0.47
1:A:41:PRO:HG2	3:A:1009:HOH:O	2.14	0.47
1:A:591:THR:OG1	1:A:614:TYR:O	2.25	0.47
1:A:638:HIS:HB3	3:A:1029:HOH:O	2.13	0.47
1:A:477:ARG:HG3	1:A:477:ARG:O	2.14	0.47
1:A:47:ASP:HB3	3:A:1020:HOH:O	2.15	0.47
1:A:150:THR:HA	1:A:397:ILE:HD11	1.97	0.46
1:A:153:THR:HG23	1:A:269:ILE:HG22	1.97	0.46
1:A:133:PRO:HG2	1:A:370:PHE:CZ	2.51	0.46
1:A:333:LYS:H	1:A:337:HIS:CD2	2.33	0.46
1:A:164:LYS:HE3	1:A:164:LYS:HB3	1.62	0.45
1:A:560:ARG:HD3	3:A:1051:HOH:O	2.15	0.45
1:A:179:ASN:HD22	1:A:179:ASN:C	2.19	0.45
1:A:265:ASN:HA	1:A:266:PRO:HD2	1.89	0.45
1:A:145:TYR:CZ	1:A:399:PRO:HD3	2.51	0.45
1:A:36:GLN:HE21	1:A:171:LEU:HA	1.81	0.45
1:A:622:GLY:HA3	2:A:900:BUI:H171	1.99	0.45
1:A:447:GLN:HE21	2:A:900:BUI:H281	1.81	0.45
1:A:241:ARG:HD2	1:A:257:LEU:O	2.17	0.45
1:A:38:SER:HB2	1:A:172:GLU:HG2	2.00	0.44
1:A:498:ARG:HA	3:A:939:HOH:O	2.18	0.44
1:A:84:CYS:O	1:A:88:GLU:HB2	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:LEU:HB3	1:A:358:LEU:HD21	2.00	0.43
1:A:468:GLN:NE2	1:A:487:GLU:HG3	2.34	0.43
1:A:606:VAL:HB	1:A:607:PRO:HD2	2.00	0.43
1:A:87:PHE:O	1:A:92:GLY:HA3	2.19	0.43
1:A:281:SER:HA	1:A:282:PRO:HD3	1.75	0.42
1:A:36:GLN:HE22	1:A:382:ARG:NH2	2.16	0.42
1:A:584:HIS:HE1	1:A:608:ASP:OD1	2.02	0.42
1:A:346:ASP:C	1:A:346:ASP:OD1	2.58	0.42
1:A:34:TYR:HD1	1:A:165:THR:HG22	1.85	0.42
1:A:91:VAL:HG11	1:A:571:PRO:HB3	2.00	0.42
1:A:222:ASN:HB3	1:A:237:ASP:O	2.21	0.41
1:A:242:HIS:HE1	1:A:317:LYS:O	2.03	0.41
1:A:271:ALA:O	1:A:274:LYS:HG2	2.20	0.41
1:A:234:LEU:HB3	3:A:964:HOH:O	2.21	0.41
1:A:42:THR:HA	1:A:173:PRO:HD3	2.03	0.41
1:A:299:TRP:CH2	1:A:303:ARG:HG3	2.55	0.41
1:A:250:HIS:CE1	1:A:284:PRO:HG3	2.56	0.40
1:A:218:PHE:CE1	1:A:236:THR:HG21	2.56	0.40
1:A:34:TYR:CD1	1:A:165:THR:HG22	2.55	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	621/653 (95%)	564 (91%)	50 (8%)	7 (1%)	17	29

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	230	ASN
1	A	563	ALA

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Mol	Chain	Res	Type
1	A	401	SER
1	A	505	ALA
1	A	123	ALA
1	A	420	SER
1	A	450	ARG

### 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	541/565 (96%)	509 (94%)	32 (6%)	23	42

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	LEU
1	A	69	LYS
1	A	71	LEU
1	A	79	ARG
1	A	85	LYS
1	A	104	LYS
1	A	113	SER
1	A	129	LEU
1	A	135	MET
1	A	147	ASP
1	A	163	LEU
1	A	174	GLU
1	A	179	ASN
1	A	218	PHE
1	A	231	ARG
1	A	274	LYS
1	A	275	TYR
1	A	281	SER
1	A	285	GLU
1	A	304	GLN
1	A	313	GLU

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Mol	Chain	Res	Type
1	A	349	ASN
1	A	372	HIS
1	A	406	THR
1	A	423	LEU
1	A	432	GLU
1	A	437	THR
1	A	442	SER
1	A	477	ARG
1	A	519	ASP
1	A	560	ARG
1	A	652	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	GLN
1	A	46	GLN
1	A	138	ASN
1	A	154	ASN
1	A	177	HIS
1	A	179	ASN
1	A	242	HIS
1	A	262	ASN
1	A	272	HIS
1	A	311	ASN
1	A	337	HIS
1	A	349	ASN
1	A	369	HIS
1	A	447	GLN
1	A	460	GLN
1	A	539	HIS
1	A	584	HIS

### 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

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	BUI	A	900	-	23,27,27	0.45	0	28,32,32	1.56	7 (25%)

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	BUI	A	900	-	-	0/26/28/28	0/0/0/0

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	900	BUI	C2-C5-N4	-2.37	105.83	110.47
2	A	900	BUI	C5-N4-C1	-2.32	118.86	123.08
2	A	900	BUI	C16-C15-N11	-2.30	105.56	112.18
2	A	900	BUI	O7-C1-N4	-2.19	118.42	122.61
2	A	900	BUI	N11-C1-N4	2.23	121.58	115.83
2	A	900	BUI	C15-N11-C1	3.22	127.90	121.72
2	A	900	BUI	C10-C5-C2	4.23	114.34	109.50

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	900	BUI	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	623/653 (95%)	-0.30	1 (0%) 94 95	11, 41, 59, 71	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	78	ARG	2.1

### 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
2	BUI	A	900	28/28	0.92	0.16	0.32	18,27,35,37	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.