



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 09:01 pm BST

PDB ID : 4K17  
Title : Crystal Structure of mouse CARMIL residues 1-668  
Authors : Zwolak, A.; Dominguez, R.  
Deposited on : 2013-04-04  
Resolution : 2.90 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 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 : 2.11  
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) : 2.11

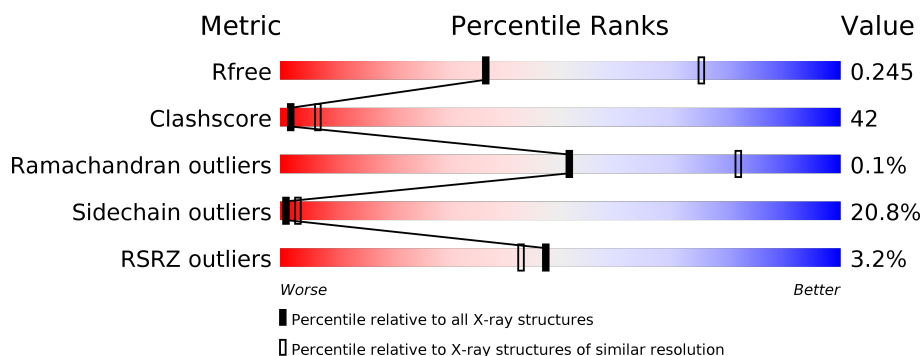
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 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	669	<div> <div>2%</div> <div> <div></div> <div>47%</div> <div>41%</div> <div>10%</div> <div>..</div> </div> </div>
1	B	669	<div> <div>3%</div> <div> <div></div> <div>48%</div> <div>39%</div> <div>11%</div> <div>..</div> </div> </div>
1	C	669	<div> <div>%</div> <div> <div></div> <div>42%</div> <div>46%</div> <div>10%</div> <div>..</div> </div> </div>
1	D	669	<div> <div>7%</div> <div> <div></div> <div>42%</div> <div>42%</div> <div>14%</div> <div>..</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
3	CL	B	702	-	-	X	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 20371 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.

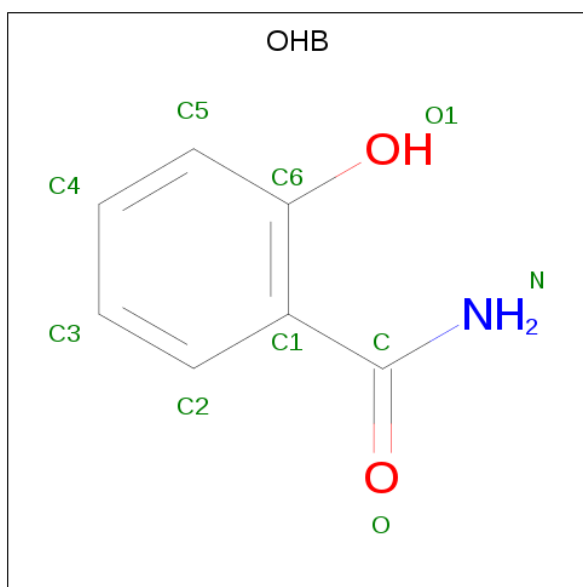
- Molecule 1 is a protein called Leucine-rich repeat-containing protein 16A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	660	Total	C	N	O	S	Se	0	2	0
			5112	3220	888	969	17	18			
1	B	660	Total	C	N	O	S	Se	0	0	0
			5102	3211	884	973	16	18			
1	C	656	Total	C	N	O	S	Se	0	0	0
			5073	3196	880	963	16	18			
1	D	655	Total	C	N	O	S	Se	0	0	0
			5066	3191	879	962	16	18			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP Q6EDY6
B	0	SER	-	EXPRESSION TAG	UNP Q6EDY6
C	0	SER	-	EXPRESSION TAG	UNP Q6EDY6
D	0	SER	-	EXPRESSION TAG	UNP Q6EDY6

- Molecule 2 is salicylamide (three-letter code: OHB) (formula: C<sub>7</sub>H<sub>7</sub>NO<sub>2</sub>).

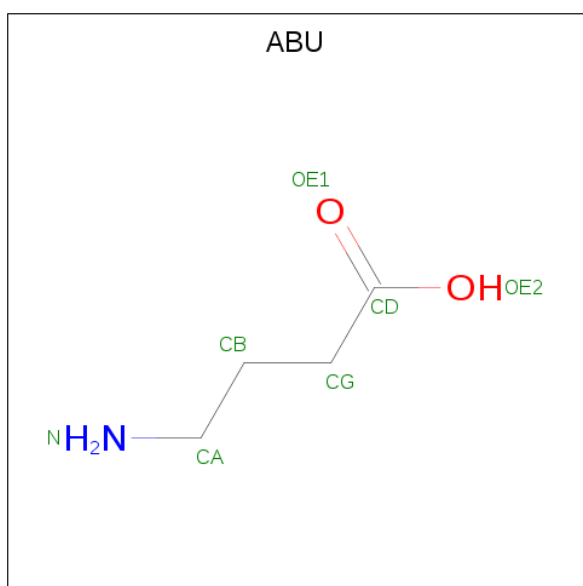


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			10	7	1	2		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		

- Molecule 4 is GAMMA-AMINO-BUTANOIC ACID (three-letter code: ABU) (formula: C<sub>4</sub>H<sub>9</sub>NO<sub>2</sub>).

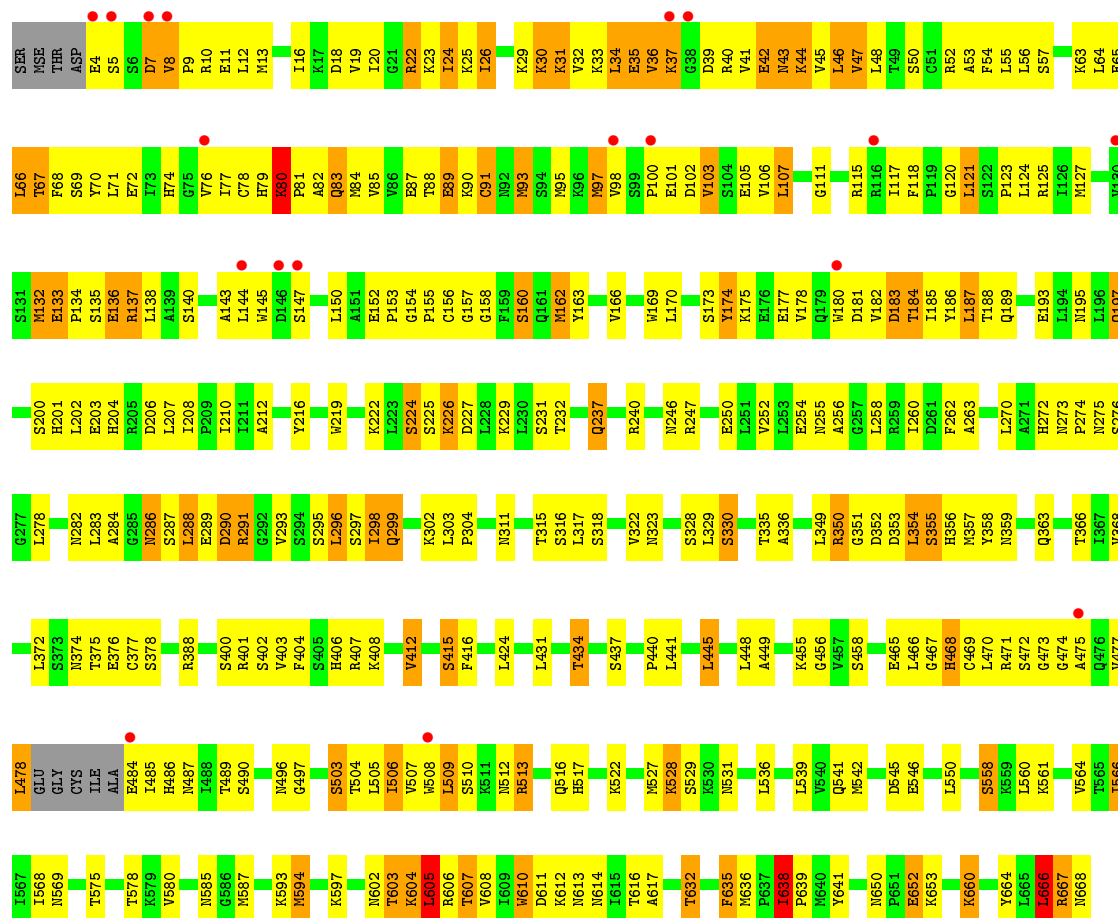


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	1	Total	C	N	O	0	0
			7	4	1	2		

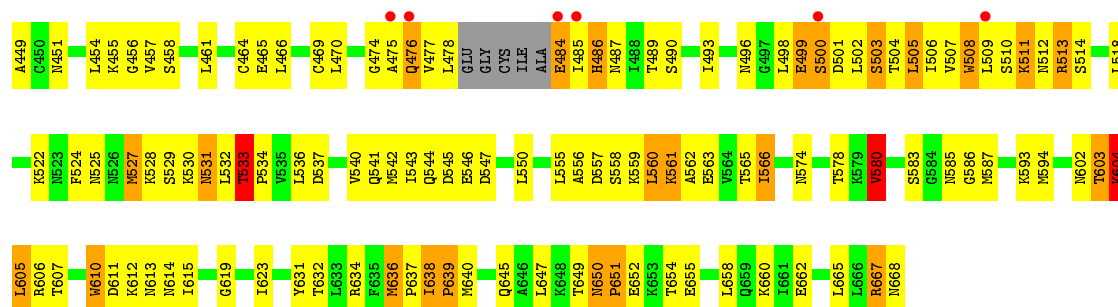
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

- Chain A: 

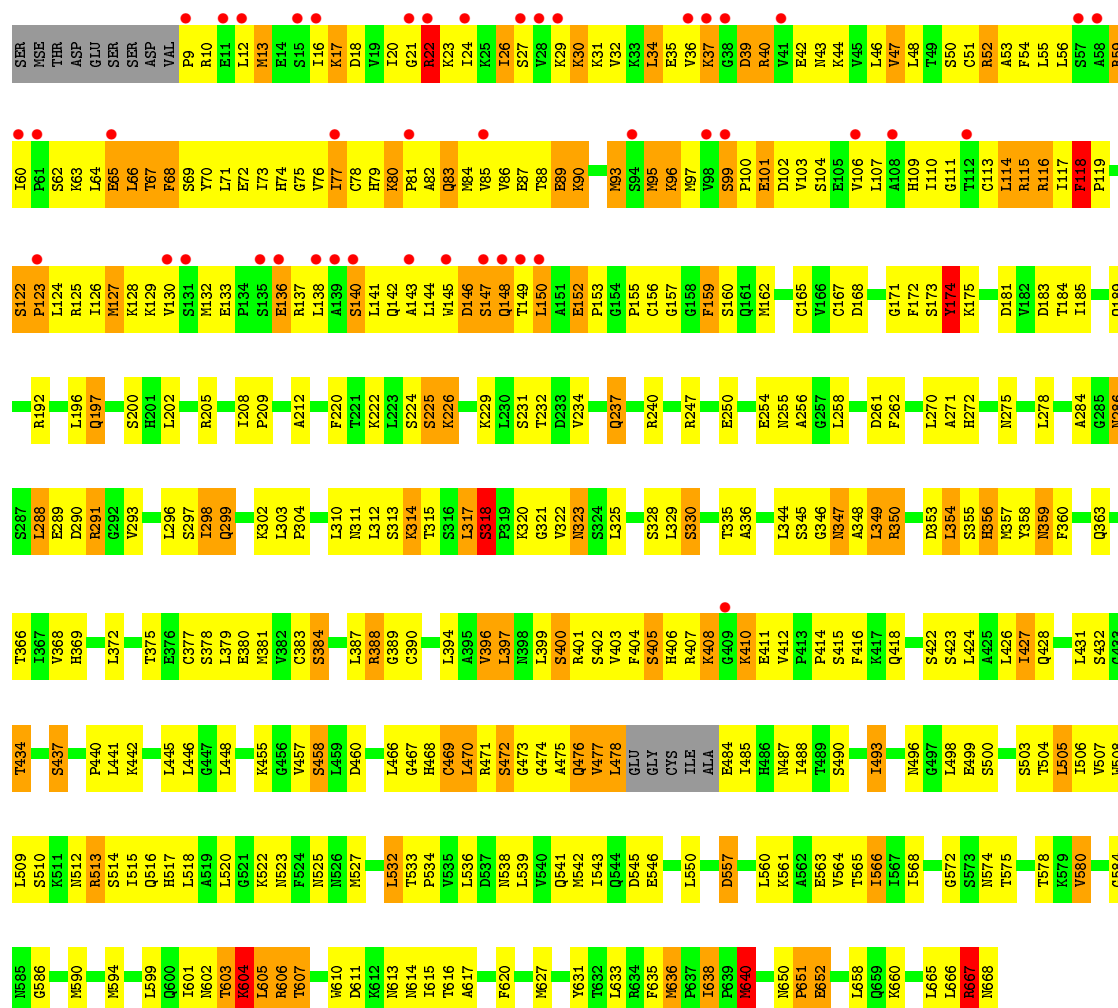
- Chain B: 







• Molecule 1: Leucine-rich repeat-containing protein 16A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.17Å 67.99Å 212.15Å 92.73° 96.95° 110.15°	Depositor
Resolution (Å)	49.76 – 2.90 49.76 – 2.90	Depositor EDS
% Data completeness (in resolution range)	83.4 (49.76-2.90) 67.1 (49.76-2.90)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.30 (at 2.91Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.215 , 0.259 0.196 , 0.245	Depositor DCC
$R_{free}$ test set	1583 reflections (3.49%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.5	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 53.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	20371	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% 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: ABU, OHB, 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	1.09	5/5179 (0.1%)	0.99	15/6967 (0.2%)
1	B	1.03	5/5160 (0.1%)	0.98	15/6941 (0.2%)
1	C	0.99	5/5131 (0.1%)	0.96	12/6902 (0.2%)
1	D	0.87	5/5124 (0.1%)	1.08	26/6891 (0.4%)
All	All	1.00	20/20594 (0.1%)	1.01	68/27701 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	C	0	3
All	All	0	6

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	666	LEU	CG-CD1	-6.07	1.29	1.51
1	D	174	TYR	CE2-CZ	-5.92	1.30	1.38
1	A	519	ALA	CA-CB	-5.77	1.40	1.52
1	B	605	LEU	CG-CD1	-5.72	1.30	1.51
1	A	237	GLN	CD-NE2	-5.55	1.19	1.32

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	22	ARG	NE-CZ-NH2	-23.32	108.64	120.30
1	D	192	ARG	NE-CZ-NH1	-18.59	111.01	120.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	192	ARG	NE-CZ-NH2	18.24	129.42	120.30
1	D	22	ARG	NE-CZ-NH1	16.50	128.55	120.30
1	D	17	LYS	CD-CE-NZ	8.39	131.00	111.70

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	23	LYS	Peptide
1	A	481	CYS	Peptide
1	A	525	ASN	Peptide
1	C	410	LYS	Peptide
1	C	604	LYS	Mainchain

## 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	5112	0	5253	411	1
1	B	5102	0	5239	368	1
1	C	5073	0	5217	458	3
1	D	5066	0	5213	515	3
2	B	10	0	7	2	0
3	B	1	0	0	3	1
4	C	7	0	5	0	0
All	All	20371	0	20934	1733	5

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 42.

The worst 5 of 1733 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:C:478:LEU:HG	1:C:508:TRP:CZ2	1.28	1.59
1:B:350:ARG:HG3	1:B:406:HIS:CE1	1.35	1.57

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:258:LEU:HD23	1:D:262:PHE:CE2	1.44	1.53
1:B:54:PHE:CD1	1:B:67:THR:HG21	1.46	1.49
1:A:474:GLY:HA2	1:A:477:VAL:CG1	1.43	1.46

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:392:GLN:O	1:C:649:THR:OG1[1_655]	1.32	0.88
1:C:289:GLU:OE1	1:D:513:ARG:CG[1_545]	1.55	0.65
1:C:289:GLU:OE2	1:D:513:ARG:NH2[1_545]	1.64	0.56
1:A:415:SER:OG	3:B:702:CL:CL[1_465]	1.74	0.46
1:B:35:GLU:OE2	1:D:476:GLN:NE2[1_545]	1.90	0.30

## 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	660/669 (99%)	628 (95%)	31 (5%)	1 (0%)	47	78
1	B	656/669 (98%)	635 (97%)	21 (3%)	0	100	100
1	C	652/669 (98%)	631 (97%)	20 (3%)	1 (0%)	47	78
1	D	651/669 (97%)	628 (96%)	23 (4%)	0	100	100
All	All	2619/2676 (98%)	2522 (96%)	95 (4%)	2 (0%)	51	82

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	15	SER
1	C	11	GLU

### 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	585/573 (102%)	472 (81%)	113 (19%)	1	4
1	B	585/573 (102%)	464 (79%)	121 (21%)	1	3
1	C	581/573 (101%)	460 (79%)	121 (21%)	1	3
1	D	580/573 (101%)	450 (78%)	130 (22%)	1	2
All	All	2331/2292 (102%)	1846 (79%)	485 (21%)	1	3

5 of 485 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	575	THR
1	C	152	GLU
1	D	427	ILE
1	B	607	THR
1	C	50	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	486	HIS
1	C	189	GLN
1	D	512	ASN
1	B	525	ASN
1	B	645	GLN

### 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

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	OHB	B	701	-	10,10,10	1.85	1 (10%)	13,13,13	2.32	2 (15%)
4	ABU	C	701	-	3,6,6	0.34	0	2,6,6	2.00	1 (50%)

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	OHB	B	701	-	-	1/4/4/4	0/1/1/1
4	ABU	C	701	-	-	1/2/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	701	OHB	C-N	5.39	1.43	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	701	OHB	C6-C1-C	7.00	123.62	119.18
2	B	701	OHB	O-C-C1	2.73	123.46	120.24
4	C	701	ABU	CA-CB-CG	2.51	120.29	112.84

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	701	ABU	CA-CB-CG-CD
2	B	701	OHB	N-C-C1-C2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	701	OHB	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	642/669 (95%)	-0.29	14 (2%) 62 59	8, 38, 107, 159	0
1	B	642/669 (95%)	-0.22	18 (2%) 53 49	8, 41, 113, 176	0
1	C	638/669 (95%)	-0.36	6 (0%) 84 84	13, 43, 89, 142	0
1	D	637/669 (95%)	0.14	44 (6%) 16 13	20, 52, 120, 175	0
All	All	2559/2676 (95%)	-0.18	82 (3%) 47 43	8, 45, 109, 176	0

The worst 5 of 82 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	8	VAL	5.8
1	D	140	SER	5.7
1	D	131	SER	5.2
1	D	143	ALA	5.0
1	D	61	PRO	4.9

### 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. 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( $\text{\AA}^2$ )	Q<0.9
4	ABU	C	701	7/7	0.89	0.27	31,54,83,85	0
2	OHB	B	701	10/10	0.95	0.20	10,42,92,98	0
3	CL	B	702	1/1	0.98	0.14	2,2,2,2	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.