



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 18, 2020 – 05:13 am BST

PDB ID : 2JE5  
Title : STRUCTURAL AND MECHANISTIC BASIS OF PENICILLIN BINDING  
PROTEIN INHIBITION BY LACTIVICINS  
Authors : Macheboeuf, P.; Fisher, D.S.; Brown, T.J.; Zervosen, A.; Luxen, A.; Joris, B.;  
Dessen, A.; Schofield, C.J.  
Deposited on : 2007-01-15  
Resolution : 2.60 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.

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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 : 2.11  
buster-report : 1.1.7 (2018)  
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

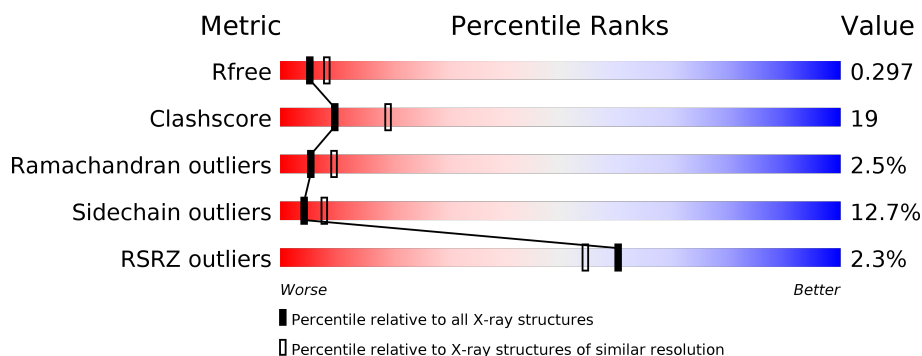
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	720	
1	B	720	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7239 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.

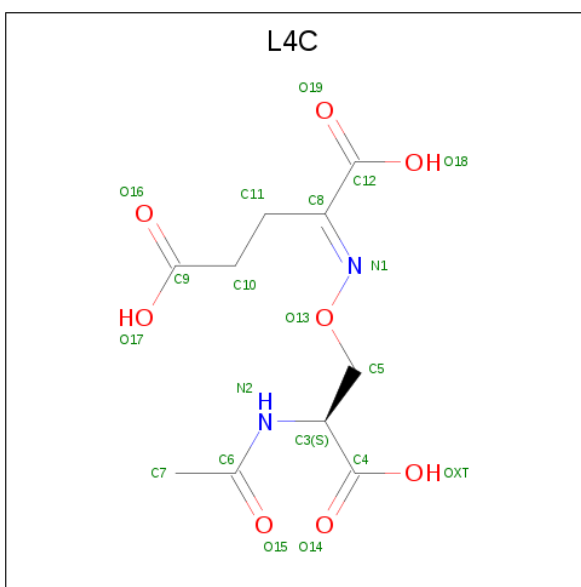
- Molecule 1 is a protein called PENICILLIN-BINDING PROTEIN 1B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	461	Total	C	N	O	S	0	1	0
			3555	2222	602	716	15			
1	B	462	Total	C	N	O	S	0	0	0
			3553	2222	602	714	15			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	73	SER	ALA	engineered mutation	UNP O70038
A	123	MET	LEU	engineered mutation	UNP O70038
A	158	ASN	LYS	engineered mutation	UNP O70038
A	162	PRO	ARG	engineered mutation	UNP O70038
A	336	GLN	ARG	engineered mutation	UNP O70038
A	686	GLN	ARG	engineered mutation	UNP O70038
A	687	GLN	ARG	engineered mutation	UNP O70038
B	73	SER	ALA	engineered mutation	UNP O70038
B	123	MET	LEU	engineered mutation	UNP O70038
B	158	ASN	LYS	engineered mutation	UNP O70038
B	162	PRO	ARG	engineered mutation	UNP O70038
B	336	GLN	ARG	engineered mutation	UNP O70038
B	686	GLN	ARG	engineered mutation	UNP O70038
B	687	GLN	ARG	engineered mutation	UNP O70038

- Molecule 2 is (2E)-2-([(2S)-2-(ACETYLAMINO)-2-CARBOXYETHOXY]IMINO)PENTANEDIOIC ACID (three-letter code: L4C) (formula: C<sub>10</sub>H<sub>14</sub>N<sub>2</sub>O<sub>8</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			19	10	2	7		
2	B	1	Total	C	N	O	0	0
			19	10	2	7		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

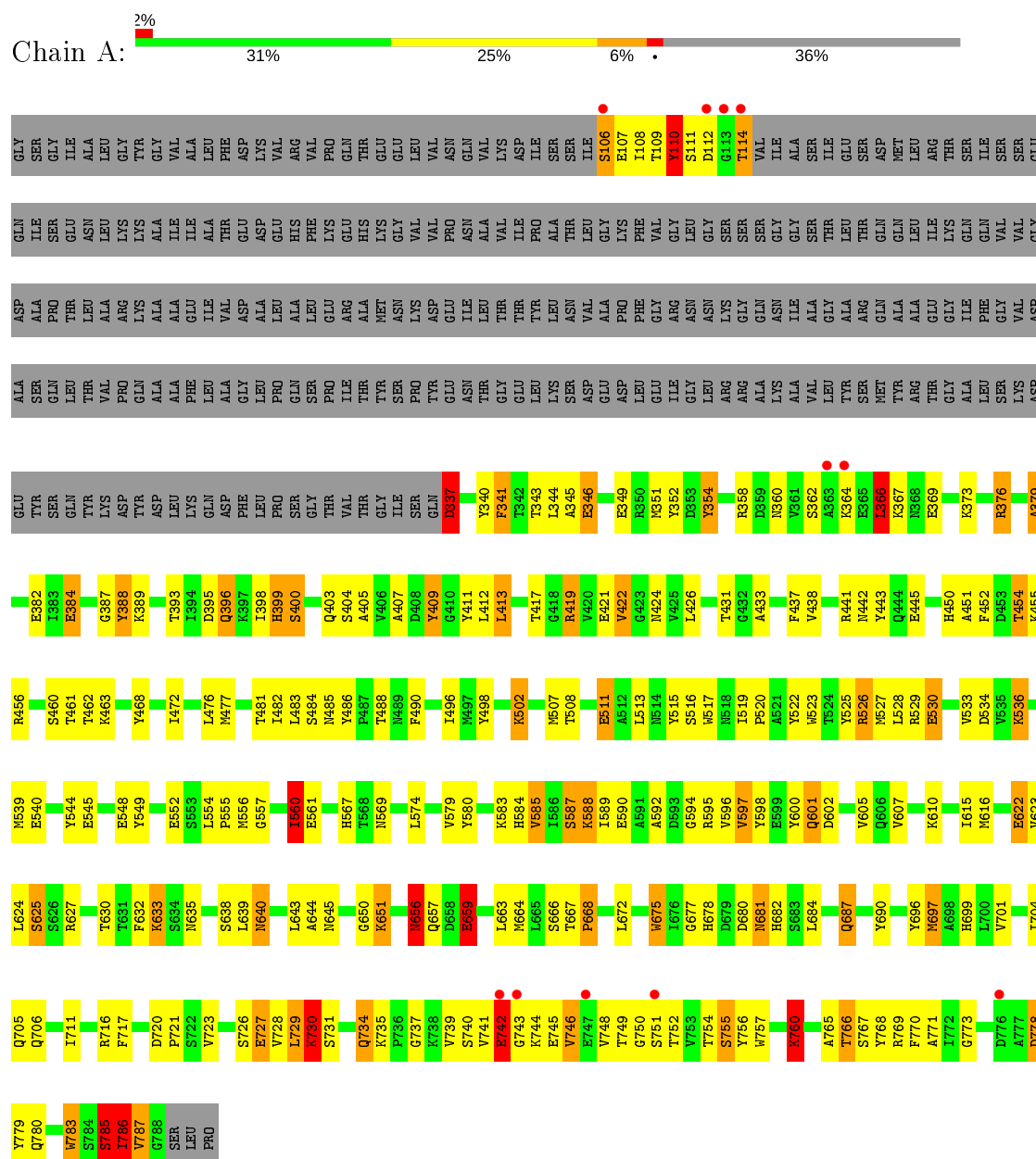
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	36	Total 36	O 36	0	0
5	B	43	Total 43	O 43	0	0

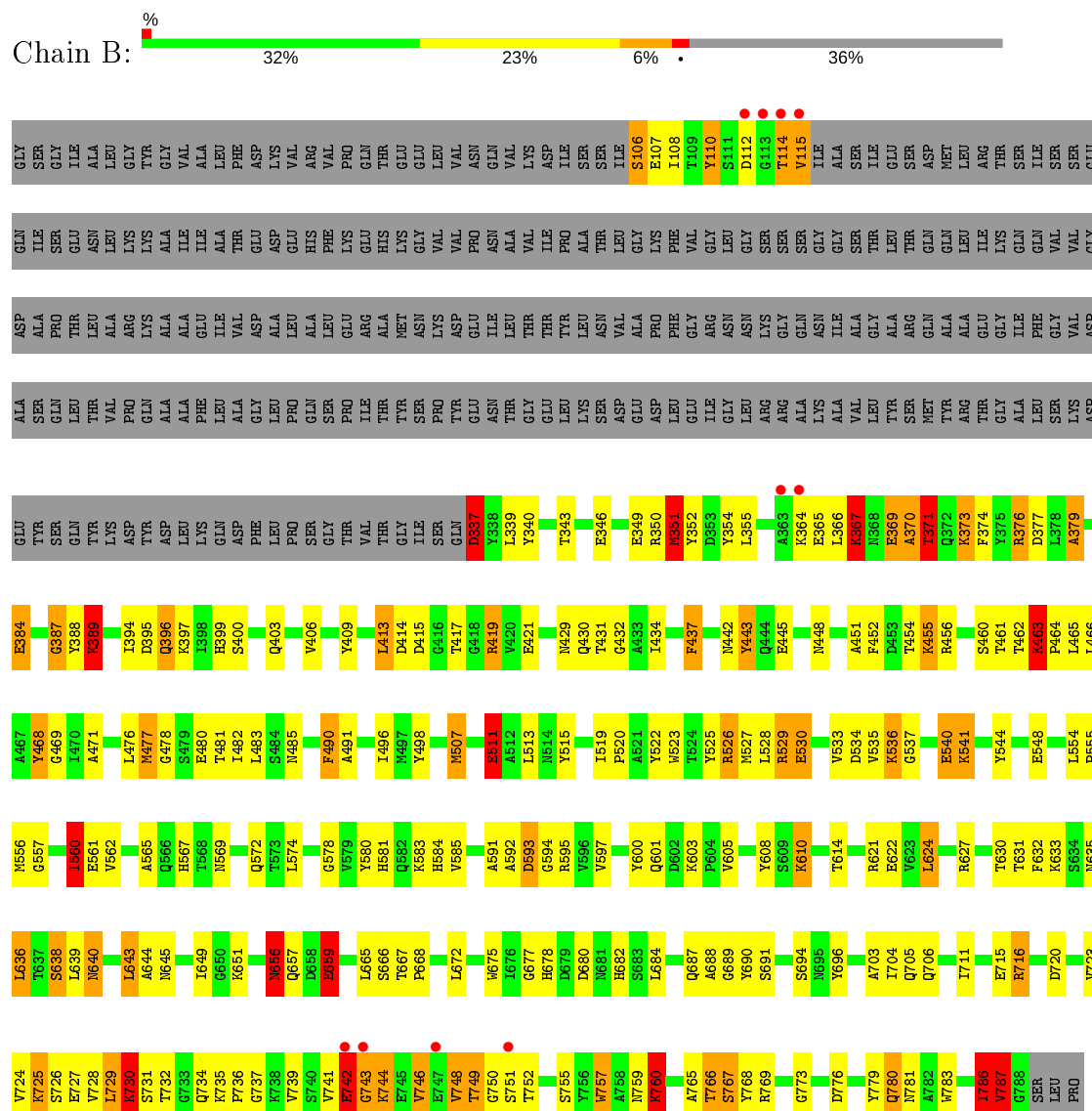
### 3 Residue-property plots

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: PENICILLIN-BINDING PROTEIN 1B



#### • Molecule 1: PENICILLIN-BINDING PROTEIN 1B



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.54Å 99.83Å 152.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	84.52 – 2.60 19.92 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.3 (84.52-2.60) 99.5 (19.92-2.60)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.04 (at 2.59Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.260 , 0.298 0.262 , 0.297	Depositor DCC
$R_{free}$ test set	2315 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.4	Xtriage
Anisotropy	0.309	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 36.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.000 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7239	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 96.99 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.9016e-10. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: L4C, SO4, 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	2.06	105/3628 (2.9%)	1.62	41/4929 (0.8%)
1	B	2.02	99/3626 (2.7%)	1.63	57/4927 (1.2%)
All	All	2.04	204/7254 (2.8%)	1.63	98/9856 (1.0%)

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	4
1	B	0	3
All	All	0	7

The worst 5 of 204 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	346[A]	GLU	CB-CG	15.94	1.82	1.52
1	A	346[B]	GLU	CB-CG	15.94	1.82	1.52
1	A	346[A]	GLU	CG-CD	14.33	1.73	1.51
1	A	346[B]	GLU	CG-CD	14.33	1.73	1.51
1	B	115	VAL	CA-CB	12.38	1.80	1.54

The worst 5 of 98 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	346[A]	GLU	OE1-CD-OE2	-17.73	102.02	123.30
1	A	346[B]	GLU	OE1-CD-OE2	-17.73	102.02	123.30
1	B	337	ASP	CB-CG-OD2	-15.36	104.48	118.30
1	B	337	ASP	CB-CG-OD1	13.81	130.73	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	377	ASP	CB-CG-OD1	11.91	129.02	118.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	109	THR	Peptide
1	A	112	ASP	Peptide
1	A	337	ASP	Peptide
1	A	760	LYS	Peptide
1	B	666	SER	Peptide

## 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	3555	0	3386	147	0
1	B	3553	0	3390	125	0
2	A	19	0	11	0	0
2	B	19	0	11	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	2	0	0	1	0
4	B	2	0	0	0	0
5	A	36	0	0	3	0
5	B	43	0	0	4	0
All	All	7239	0	6798	270	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 19.

The worst 5 of 270 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:366:LEU:CD2	1:A:366:LEU:CG	1.75	1.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:115:VAL:CA	1:B:115:VAL:CB	1.80	1.59
1:A:601:GLN:CA	1:A:601:GLN:CB	1.74	1.58
1:A:346[A]:GLU:CB	1:A:346[A]:GLU:CG	1.82	1.57
1:A:454:THR:CG2	1:A:454:THR:CB	1.75	1.56

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	458/720 (64%)	404 (88%)	41 (9%)	13 (3%)	5	7
1	B	458/720 (64%)	417 (91%)	31 (7%)	10 (2%)	6	12
All	All	916/1440 (64%)	821 (90%)	72 (8%)	23 (2%)	5	9

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	110	TYR
1	A	111	SER
1	A	740	SER
1	A	744	LYS
1	B	110	TYR

### 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	375/590 (64%)	323 (86%)	52 (14%)	3	6
1	B	375/590 (64%)	332 (88%)	43 (12%)	5	10
All	All	750/1180 (64%)	655 (87%)	95 (13%)	4	8

5 of 95 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	742	GLU
1	B	114	THR
1	B	742	GLU
1	A	746	VAL
1	A	778	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	734	GLN
1	B	424	ASN
1	B	686	GLN
1	B	348	GLN
1	B	429	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	L4C	B	1789	1	12,18,19	1.48	2 (16%)	12,22,24	2.78	6 (50%)
2	L4C	A	1789	1	12,18,19	1.39	1 (8%)	12,22,24	4.53	6 (50%)
3	SO4	A	1790	-	4,4,4	0.60	0	6,6,6	0.96	0
3	SO4	B	1790	-	4,4,4	0.66	0	6,6,6	0.48	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
2	L4C	B	1789	1	-	4/13/21/23	-
2	L4C	A	1789	1	-	6/13/21/23	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1789	L4C	C8-N1	3.14	1.31	1.28
2	A	1789	L4C	C12-C8	-2.81	1.47	1.52
2	B	1789	L4C	C12-C8	-2.21	1.48	1.52

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1789	L4C	C5-O13-N1	13.66	123.22	108.37
2	B	1789	L4C	C11-C10-C9	-4.90	104.46	112.67
2	B	1789	L4C	C5-O13-N1	4.65	113.43	108.37
2	A	1789	L4C	C4-C3-N2	4.14	117.19	109.73
2	B	1789	L4C	C4-C3-N2	3.99	116.93	109.73

There are no chirality outliers.

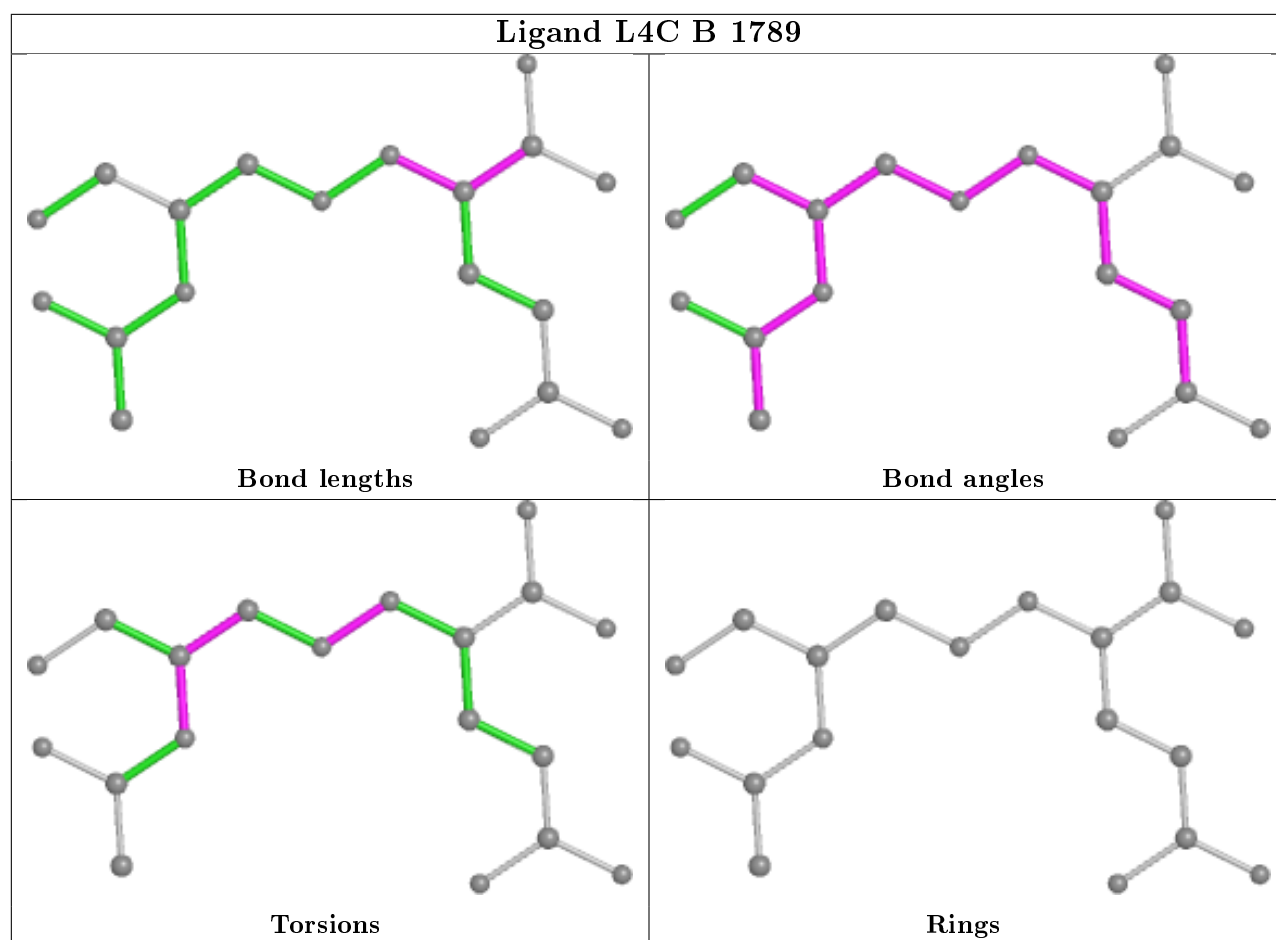
5 of 10 torsion outliers are listed below:

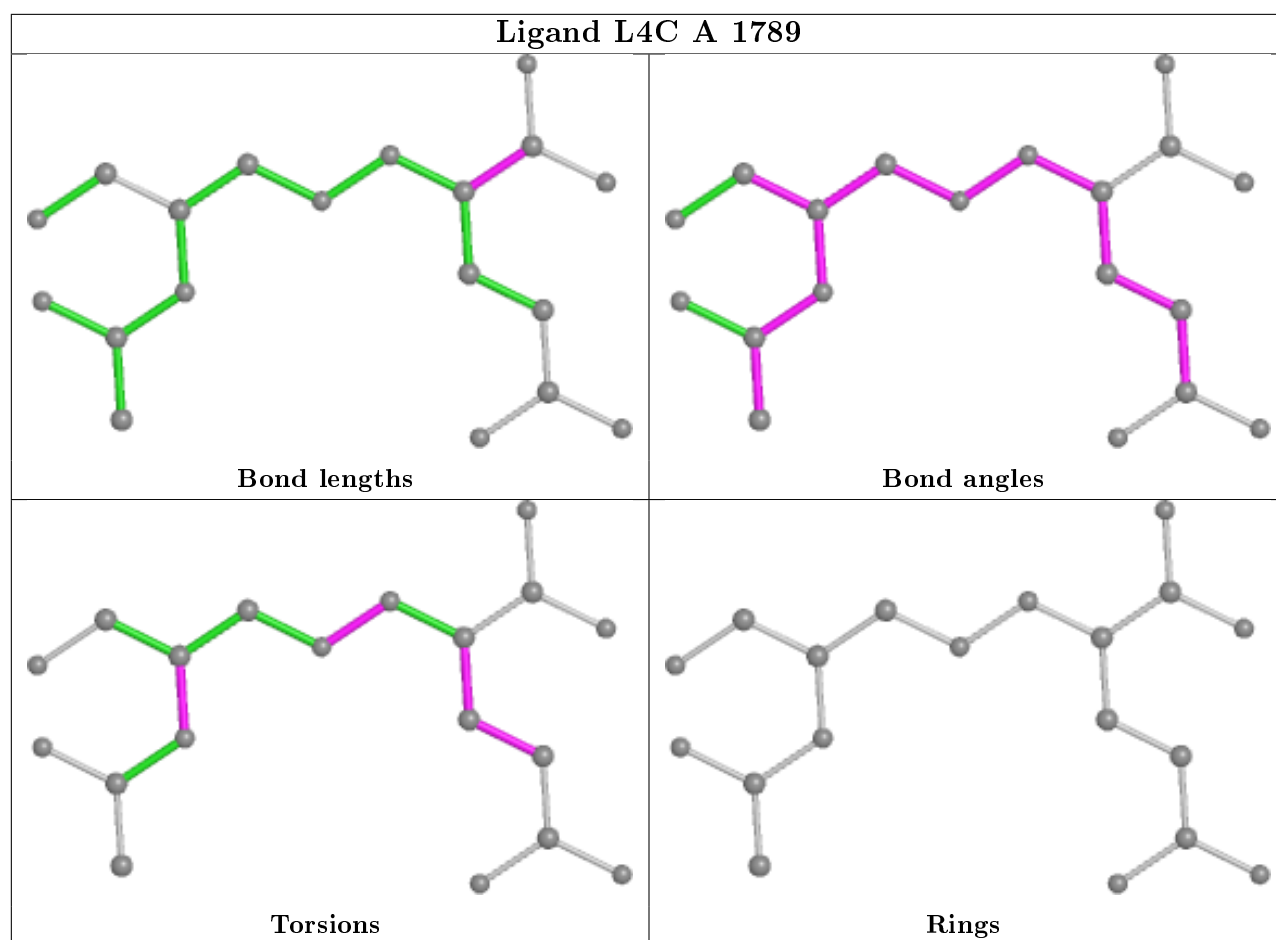
Mol	Chain	Res	Type	Atoms
2	B	1789	L4C	C4-C3-C5-O13
2	B	1789	L4C	C5-C3-N2-C6
2	B	1789	L4C	C4-C3-N2-C6
2	A	1789	L4C	C10-C11-C8-C12
2	A	1789	L4C	C10-C11-C8-N1

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 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	461/720 (64%)	-0.42	11 (2%) 59 53	14, 34, 78, 99	0
1	B	462/720 (64%)	-0.39	10 (2%) 62 56	13, 34, 77, 99	0
All	All	923/1440 (64%)	-0.40	21 (2%) 60 54	13, 34, 78, 99	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	115	VAL	8.4
1	B	114	THR	4.0
1	A	114	THR	4.0
1	B	364	LYS	3.5
1	A	112	ASP	3.4

### 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](#)

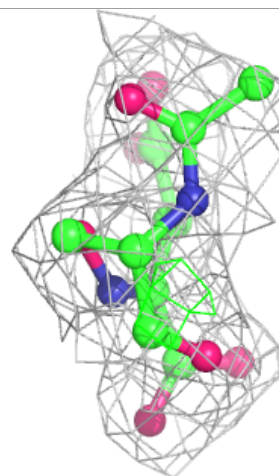
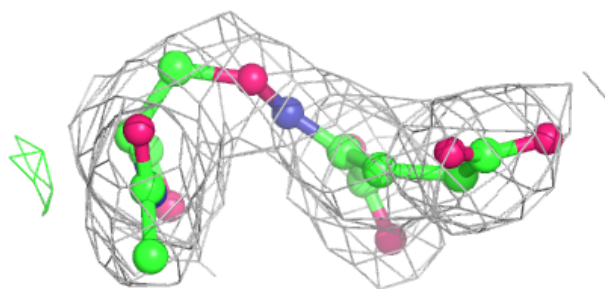
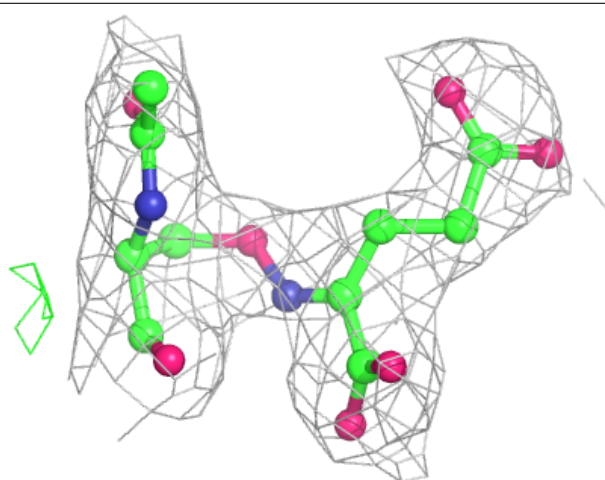
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

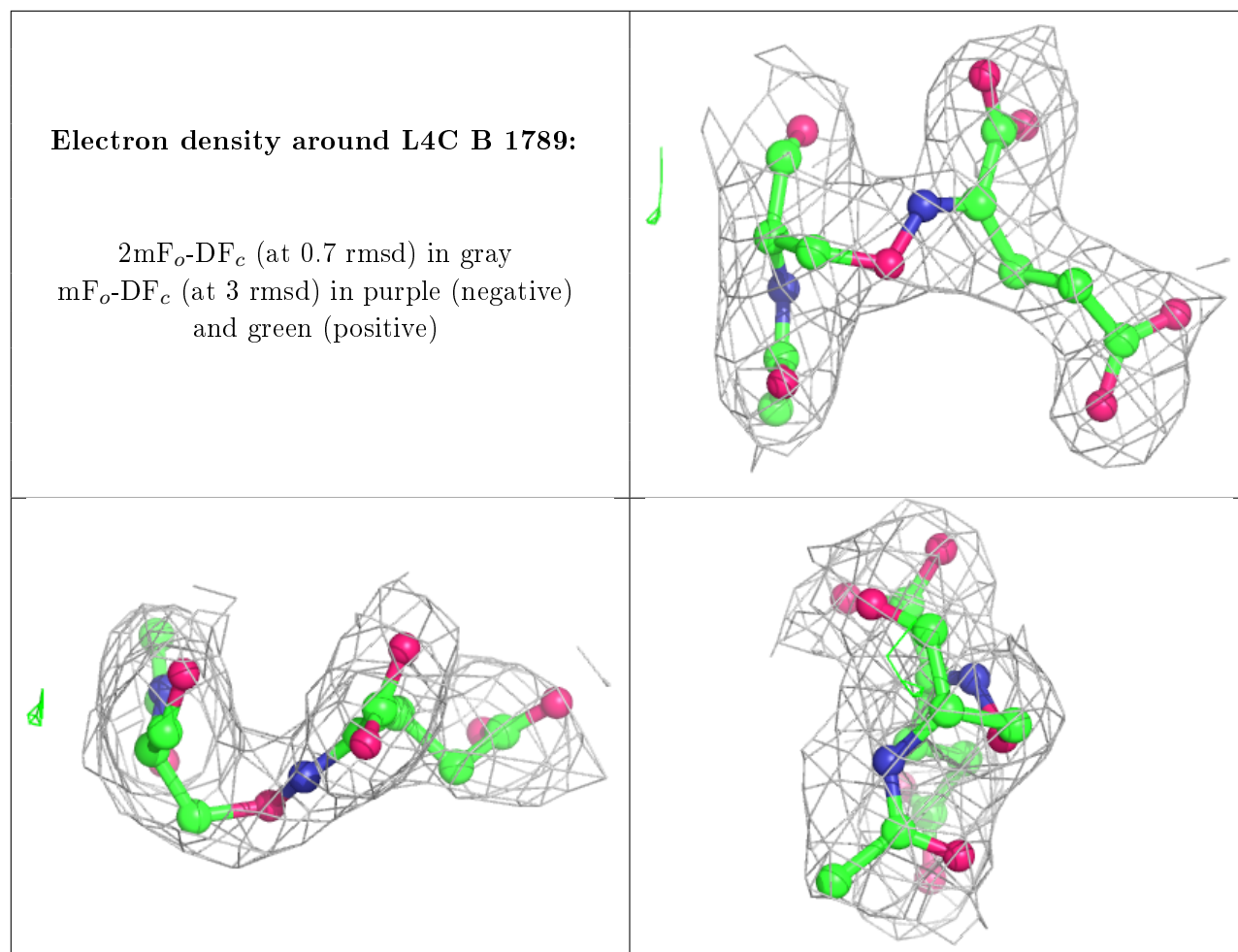
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	CL	B	1791	1/1	0.93	0.10	56,56,56,56	0
2	L4C	A	1789	19/20	0.95	0.13	25,47,60,66	0
2	L4C	B	1789	19/20	0.96	0.13	21,45,62,63	0
3	SO4	B	1790	5/5	0.96	0.19	53,57,59,59	0
3	SO4	A	1790	5/5	0.97	0.16	50,50,55,57	0
4	CL	A	1792	1/1	0.97	0.08	48,48,48,48	0
4	CL	A	1791	1/1	0.99	0.04	26,26,26,26	0
4	CL	B	1792	1/1	0.99	0.16	39,39,39,39	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around L4C A 1789:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.