



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 24, 2025 – 06:06 PM EST

PDB ID : 9MUM  
Title : Crystal structure of GluN1/GluN2A ligand-binding domain in complex with Compound 11, Glycine and Glutamate  
Authors : Shaffer, P.L.; Duda, D.M.  
Deposited on : 2025-01-14  
Resolution : 1.97 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>.

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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 : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.21  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.004 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.41.4

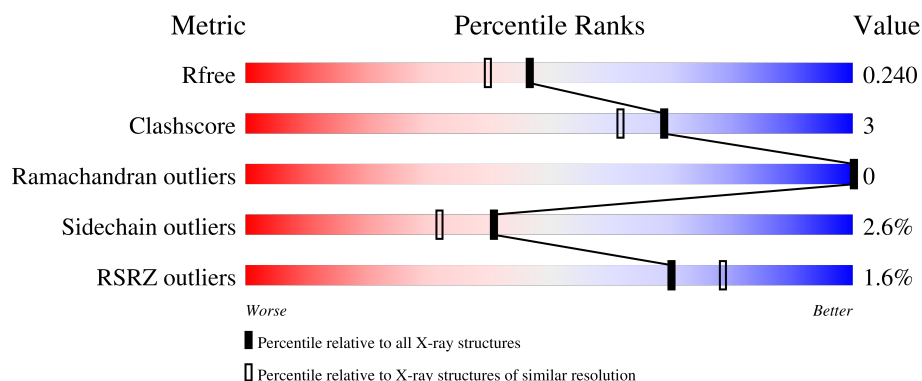
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.97 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))
$R_{free}$	164625	1356 (1.98-1.98)
Clashscore	180529	1437 (1.98-1.98)
Ramachandran outliers	177936	1426 (1.98-1.98)
Sidechain outliers	177891	1426 (1.98-1.98)
RSRZ outliers	164620	1356 (1.98-1.98)

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	306	
2	B	297	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4583 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 Glutamate receptor ionotropic, NMDA 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	273	Total	C	N	O	S	0	0	0
			2155	1376	367	398	14			

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	379	MET	-	initiating methionine	UNP Q05586
A	380	HIS	-	expression tag	UNP Q05586
A	381	HIS	-	expression tag	UNP Q05586
A	382	HIS	-	expression tag	UNP Q05586
A	383	HIS	-	expression tag	UNP Q05586
A	384	HIS	-	expression tag	UNP Q05586
A	385	HIS	-	expression tag	UNP Q05586
A	386	GLU	-	expression tag	UNP Q05586
A	387	ASN	-	expression tag	UNP Q05586
A	388	LEU	-	expression tag	UNP Q05586
A	389	TYR	-	expression tag	UNP Q05586
A	390	PHE	-	expression tag	UNP Q05586
A	391	GLN	-	expression tag	UNP Q05586
A	392	GLY	-	expression tag	UNP Q05586
A	393	SER	-	expression tag	UNP Q05586
A	545	GLY	-	linker	UNP Q05586
A	546	THR	-	linker	UNP Q05586

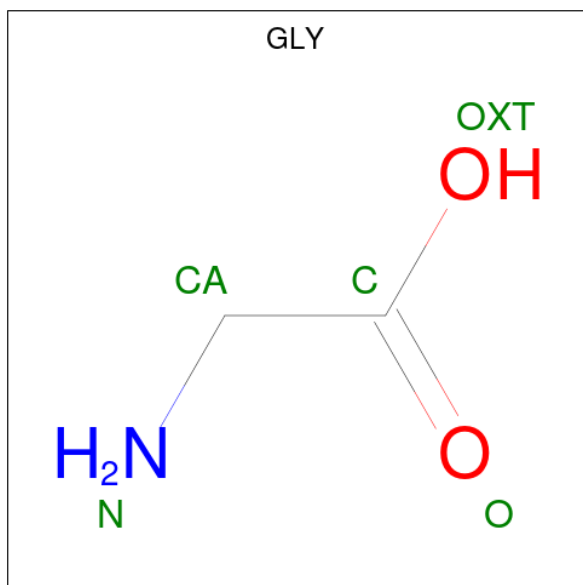
- Molecule 2 is a protein called Glutamate receptor ionotropic, NMDA 2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	275	Total	C	N	O	S	0	0	0
			2139	1362	365	398	14			

There are 16 discrepancies between the modelled and reference sequences:

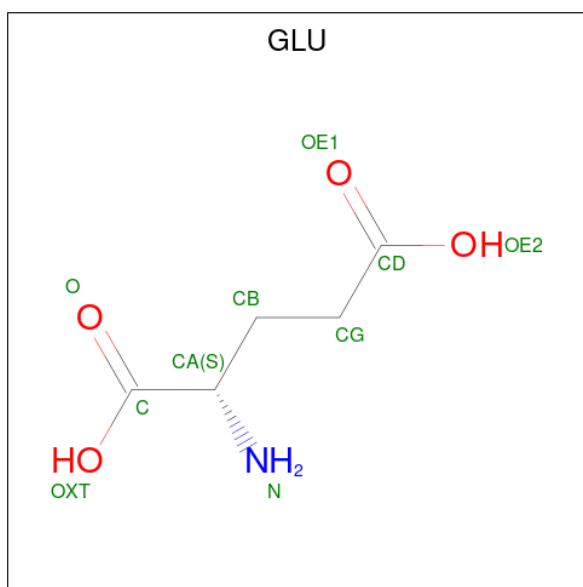
Chain	Residue	Modelled	Actual	Comment	Reference
B	387	MET	-	initiating methionine	UNP Q12879
B	388	HIS	-	expression tag	UNP Q12879
B	389	HIS	-	expression tag	UNP Q12879
B	390	HIS	-	expression tag	UNP Q12879
B	391	HIS	-	expression tag	UNP Q12879
B	392	HIS	-	expression tag	UNP Q12879
B	393	HIS	-	expression tag	UNP Q12879
B	394	GLU	-	expression tag	UNP Q12879
B	395	ASN	-	expression tag	UNP Q12879
B	396	LEU	-	expression tag	UNP Q12879
B	397	TYR	-	expression tag	UNP Q12879
B	398	PHE	-	expression tag	UNP Q12879
B	399	GLN	-	expression tag	UNP Q12879
B	400	GLY	-	expression tag	UNP Q12879
B	540	GLY	-	linker	UNP Q12879
B	541	THR	-	linker	UNP Q12879

- Molecule 3 is GLYCINE (three-letter code: GLY) (formula:  $C_2H_5NO_2$ ).



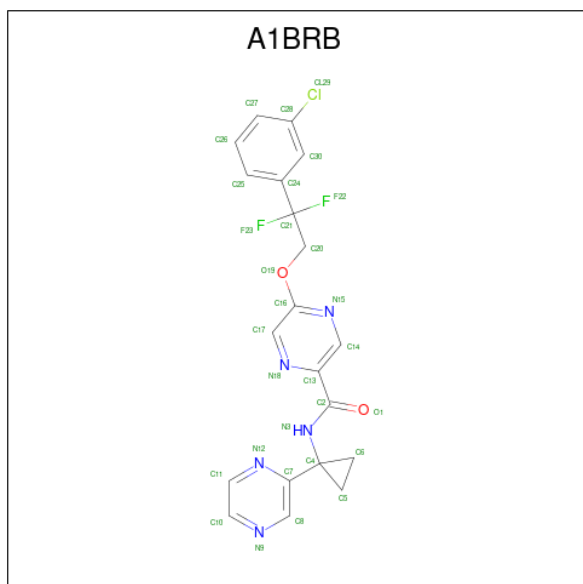
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			5	2	1	2		

- Molecule 4 is GLUTAMIC ACID (three-letter code: GLU) (formula:  $C_5H_9NO_4$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O		0	0
			10	5	1	4			

- Molecule 5 is 5-[2-(3-chlorophenyl)-2,2-difluoroethoxy]-N-[1-(pyrazin-2-yl)cyclopropyl]pyrazine-2-carboxamide (three-letter code: A1BRB) (formula: C<sub>20</sub>H<sub>16</sub>ClF<sub>2</sub>N<sub>5</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	Cl	F	N	O	
			30	20	1	2	5	2	0

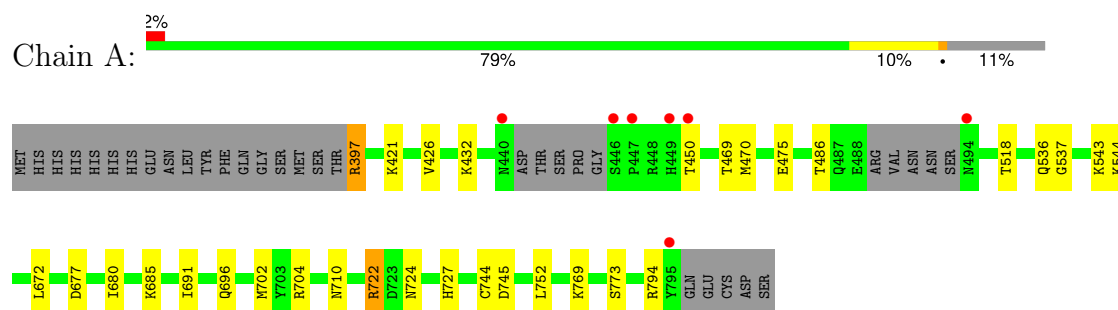
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	116	Total 116	O 116	0	0
6	B	128	Total 128	O 128	0	0

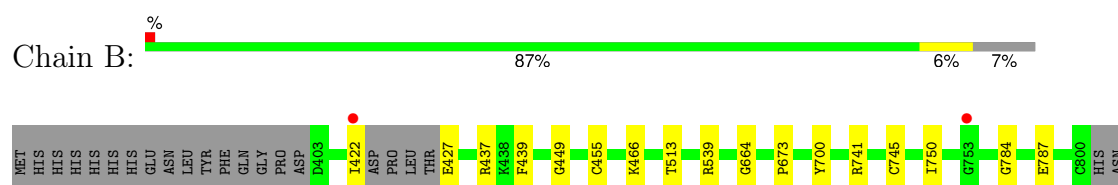
### 3 Residue-property plots [i](#)

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: Glutamate receptor ionotropic, NMDA 1



- Molecule 2: Glutamate receptor ionotropic, NMDA 2A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.50Å 90.00Å 124.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.80 – 1.97 37.80 – 1.97	Depositor EDS
% Data completeness (in resolution range)	90.9 (37.80-1.97) 90.9 (37.80-1.97)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.22 (at 1.97Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.192 , 0.241 0.192 , 0.240	Depositor DCC
$R_{free}$ test set	2298 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.0	Xtriage
Anisotropy	0.232	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 31.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4583	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.47% 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: A1BRB

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	0.39	0/2202	0.58	0/2978
2	B	0.40	0/2180	0.59	0/2949
All	All	0.39	0/4382	0.59	0/5927

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	2155	0	2098	17	0
2	B	2139	0	2121	12	0
3	A	5	0	2	1	0
4	B	10	0	5	1	0
5	B	30	0	0	1	0
6	A	116	0	0	5	0
6	B	128	0	0	3	0
All	All	4583	0	4226	29	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 3.

The worst 5 of 29 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:744:CYS:SG	6:A:1201:HOH:O	2.30	0.89
1:A:680:ILE:H	1:A:727:HIS:HD2	1.21	0.88
1:A:680:ILE:H	1:A:727:HIS:CD2	2.10	0.68
2:B:427:GLU:N	6:B:1103:HOH:O	2.28	0.67
1:A:518:THR:HG1	3:A:1001:GLY:N	1.94	0.64

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	267/306 (87%)	259 (97%)	8 (3%)	0	100	100
2	B	271/297 (91%)	262 (97%)	9 (3%)	0	100	100
All	All	538/603 (89%)	521 (97%)	17 (3%)	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	232/274 (85%)	221 (95%)	11 (5%)	22	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	234/261 (90%)	233 (100%)	1 (0%)	89	89
All	All	466/535 (87%)	454 (97%)	12 (3%)	41	32

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	724	ASN
1	A	769	LYS
2	B	741	ARG
1	A	773	SER
1	A	536	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	525	GLN
1	A	727	HIS
2	B	671	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 [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

3 ligands are 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
3	GLY	A	1001	-	4,4,4	1.24	1 (25%)	3,4,4	1.36	0
5	A1BRB	B	1002	-	29,33,33	0.93	1 (3%)	42,48,48	1.56	6 (14%)
4	GLU	B	1001	-	8,9,9	1.21	1 (12%)	8,11,11	0.92	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	GLY	A	1001	-	-	1/2/2/2	-
5	A1BRB	B	1002	-	-	3/25/31/31	0/4/4/4
4	GLU	B	1001	-	-	3/9/9/9	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1001	GLU	OXT-C	-2.38	1.23	1.30
3	A	1001	GLY	OXT-C	-2.32	1.23	1.30
5	B	1002	A1BRB	C2-N3	2.27	1.38	1.34

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1002	A1BRB	C6-C4-C7	-4.49	113.72	119.93
5	B	1002	A1BRB	C5-C4-N3	4.10	120.89	115.21
5	B	1002	A1BRB	O19-C20-C21	4.04	112.34	106.24
5	B	1002	A1BRB	C5-C4-C7	-3.87	114.58	119.93
5	B	1002	A1BRB	C6-C4-N3	2.64	118.86	115.21

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1002	A1BRB	O19-C20-C21-F23
4	B	1001	GLU	OE2-CD-CG-CB

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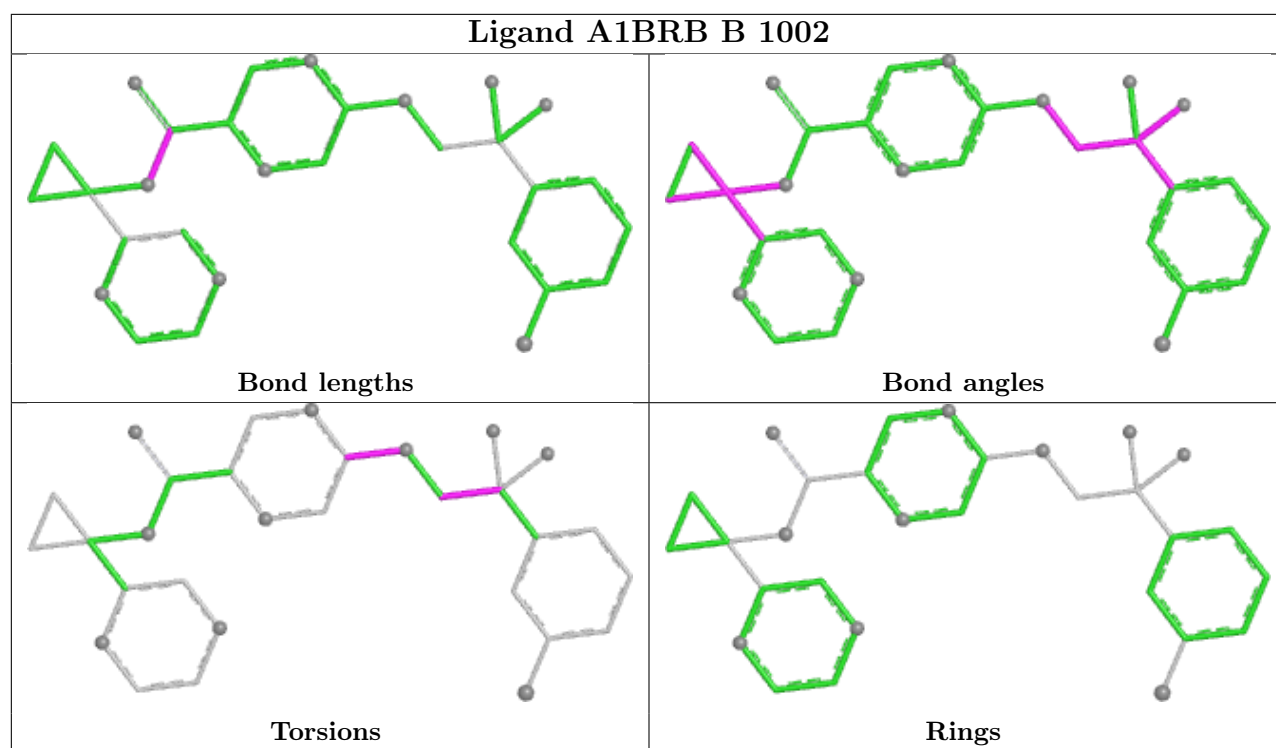
Mol	Chain	Res	Type	Atoms
5	B	1002	A1BRB	C17-C16-O19-C20
4	B	1001	GLU	OE1-CD-CG-CB
3	A	1001	GLY	OXT-C-CA-N

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1001	GLY	1	0
5	B	1002	A1BRB	1	0
4	B	1001	GLU	1	0

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	273/306 (89%)	0.12	7 (2%) 57 67	30, 43, 64, 82	0
2	B	275/297 (92%)	0.03	2 (0%) 84 88	29, 40, 59, 97	0
All	All	548/603 (90%)	0.07	9 (1%) 70 78	29, 41, 61, 97	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	795	TYR	3.2
1	A	449	HIS	2.9
2	B	422	ILE	2.9
1	A	447	PRO	2.4
1	A	494	ASN	2.3

### 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](#)

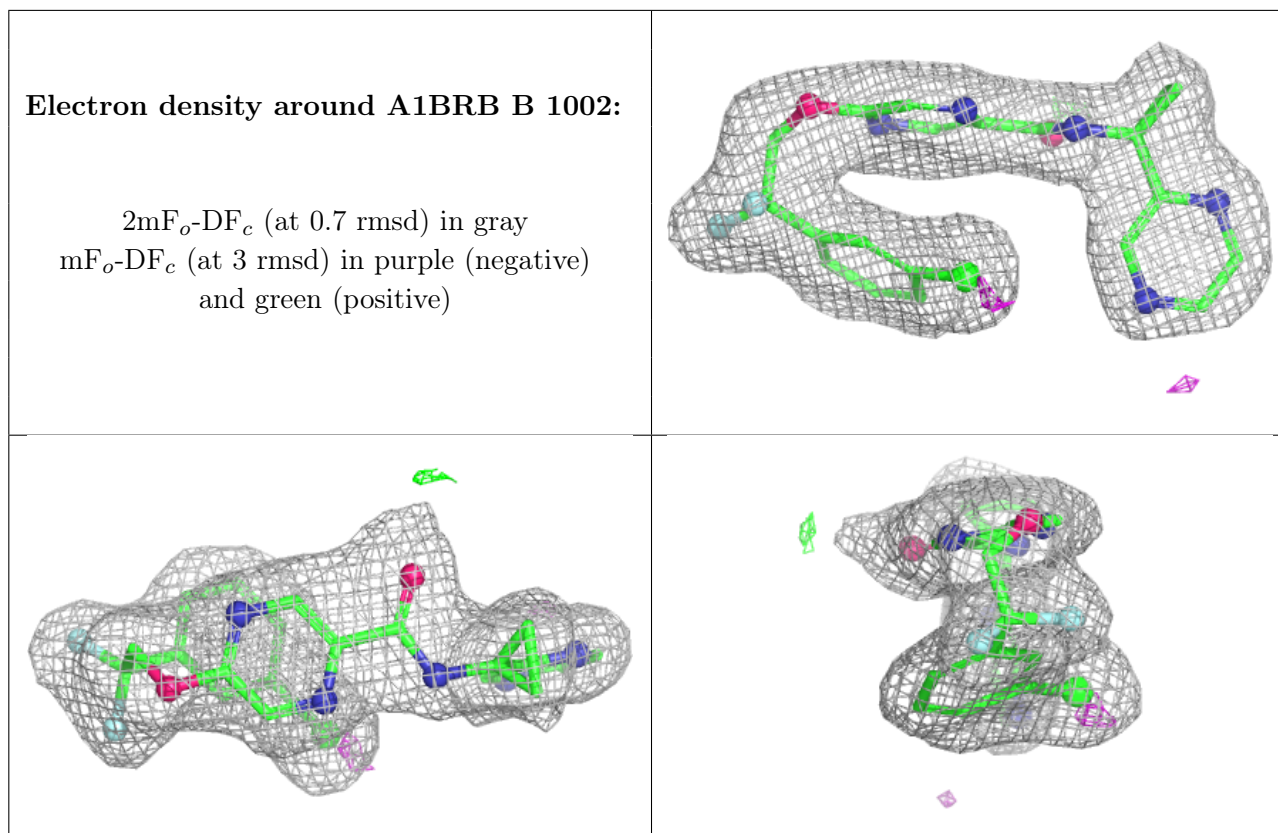
There are no monosaccharides in this entry.

### 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( $\text{\AA}^2$ )	Q<0.9
3	GLY	A	1001	5/5	0.95	0.07	29,29,32,33	0
4	GLU	B	1001	10/10	0.95	0.07	28,29,33,35	0
5	A1BRB	B	1002	30/30	0.96	0.06	30,35,37,41	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.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.