



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 4, 2026 – 10:56 PM UTC

PDB ID : 9YCE / pdb\_00009yce  
Title : Active site of MtgB, a glycine betaine methyltransferase from the MttB superfamily  
Authors : Picking, J.; Li, Y.; Ticak, T.; Ferguson, D.J.; Hao, B.; Krzycki, J.A.  
Deposited on : 2025-09-18  
Resolution : 2.35 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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

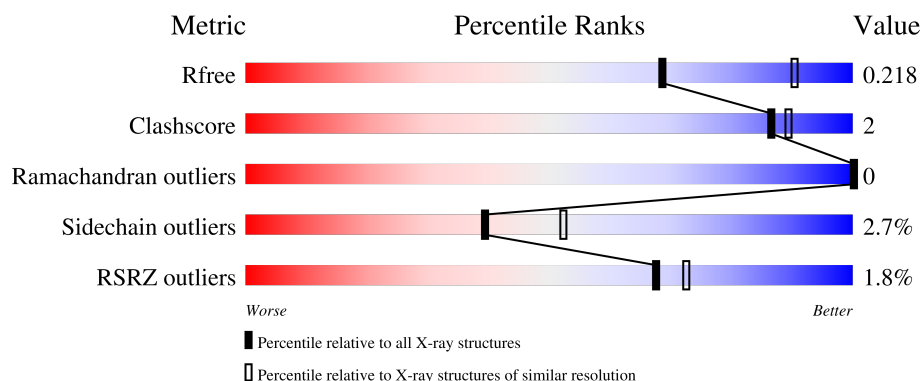
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 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))
$R_{free}$	180053	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	477	<div> <div>%</div> <div> <div></div> <div>92%</div> <div>7%</div> <div>.</div> </div> </div>
1	B	477	<div> <div>3%</div> <div> <div></div> <div>90%</div> <div>8%</div> <div>.</div> </div> </div>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7469 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.

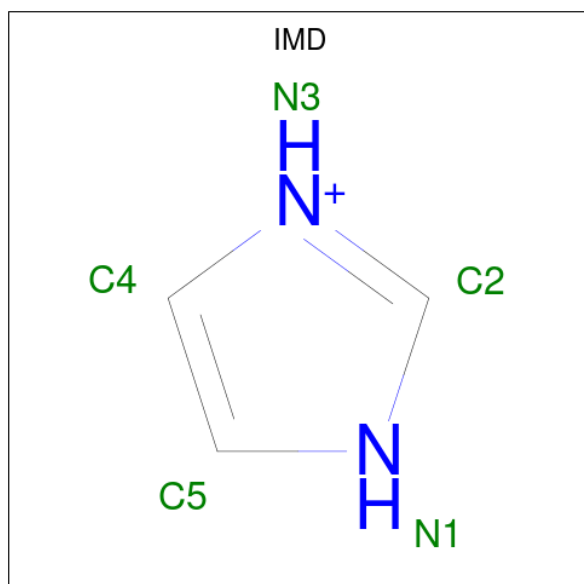
- Molecule 1 is a protein called Glycine betaine methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	0	1	0
			3623	2299	600	702	22			
1	B	475	Total	C	N	O	S	0	2	0
			3588	2273	597	696	22			

There are 4 discrepancies between the modelled and reference sequences:

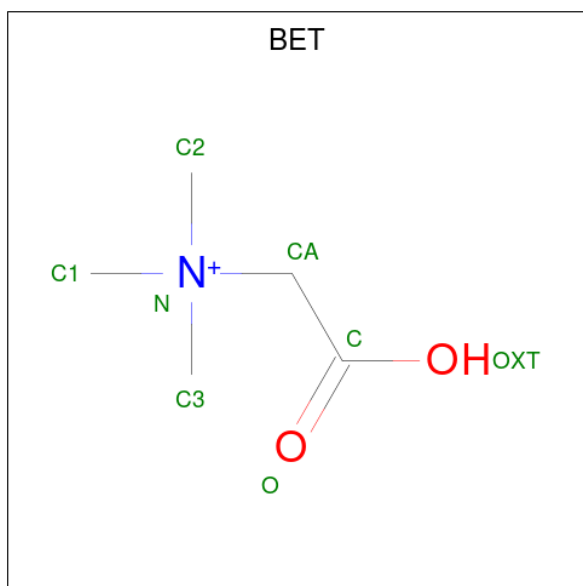
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q24SP7
A	1	MET	-	expression tag	UNP Q24SP7
B	0	GLY	-	expression tag	UNP Q24SP7
B	1	MET	-	expression tag	UNP Q24SP7

- Molecule 2 is IMIDAZOLE (CCD ID: IMD) (formula: C<sub>3</sub>H<sub>5</sub>N<sub>2</sub>).



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

- Molecule 3 is TRIMETHYL GLYCINE (CCD ID: BET) (formula:  $C_5H_{12}NO_2$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	8	0
			8	5	1	2		
3	B	1	Total	C	N	O	8	0
			8	5	1	2		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula:  $C_2H_6O_2$ ).



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

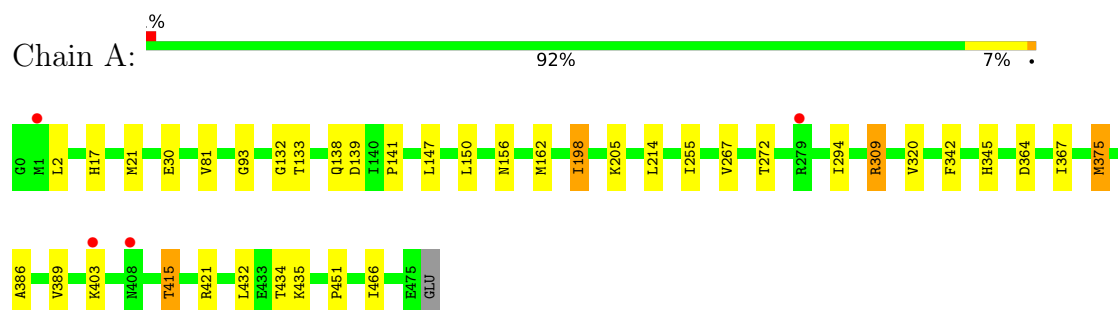
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	171	Total	O	0	0
			171	171		
5	B	62	Total	O	0	0
			62	62		

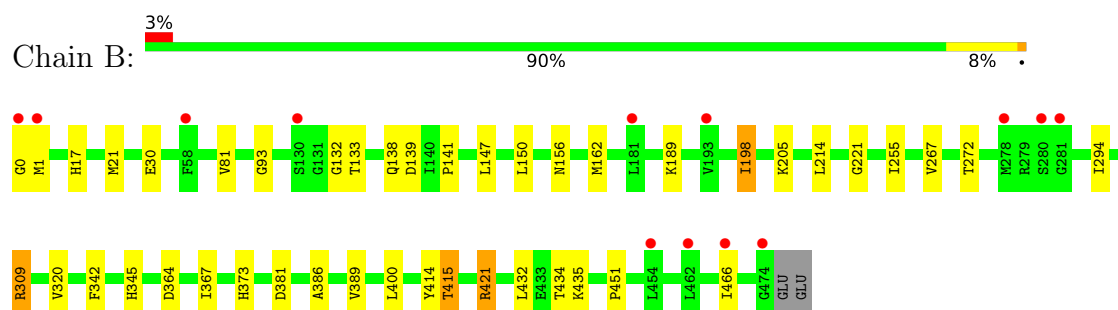
### 3 Residue-property plots [i](#)

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: Glycine betaine methyltransferase



- Molecule 1: Glycine betaine methyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	123.47Å 123.47Å 123.53Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.26 – 2.35 34.26 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.5 (34.26-2.35) 99.4 (34.26-2.35)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.55 (at 2.34Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, $R_{free}$	0.191 , 0.216 0.198 , 0.218	Depositor DCC
$R_{free}$ test set	2157 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	55.9	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 53.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.022 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7469	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.41% 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: IMD, BET, EDO

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	0.75	1/3693 (0.0%)	1.30	10/4992 (0.2%)
1	B	0.73	0/3659	1.32	11/4954 (0.2%)
All	All	0.74	1/7352 (0.0%)	1.31	21/9946 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	375	MET	SD-CE	-7.68	1.60	1.79

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	138	GLN	CA-C-N	8.76	132.02	120.28
1	A	138	GLN	C-N-CA	8.76	132.02	120.28
1	B	138	GLN	CA-C-N	8.64	131.86	120.28
1	B	138	GLN	C-N-CA	8.64	131.86	120.28
1	A	434	THR	CA-C-N	6.29	129.03	120.54
1	A	434	THR	C-N-CA	6.29	129.03	120.54
1	B	434	THR	CA-C-N	6.18	128.88	120.54
1	B	434	THR	C-N-CA	6.18	128.88	120.54
1	A	415	THR	CB-CA-C	5.65	116.29	109.85
1	B	415	THR	CB-CA-C	5.46	116.08	109.85
1	B	139	ASP	CA-CB-CG	5.33	117.93	112.60
1	A	139	ASP	CA-CB-CG	5.22	117.82	112.60
1	A	294	ILE	CA-C-N	5.16	127.15	120.44
1	A	294	ILE	C-N-CA	5.16	127.15	120.44
1	B	141	PRO	CA-C-N	5.13	127.87	120.38
1	B	141	PRO	C-N-CA	5.13	127.87	120.38
1	B	294	ILE	CA-C-N	5.08	127.04	120.44
1	B	294	ILE	C-N-CA	5.08	127.04	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	381	ASP	CA-CB-CG	5.08	117.68	112.60
1	A	141	PRO	CA-C-N	5.03	127.72	120.38
1	A	141	PRO	C-N-CA	5.03	127.72	120.38

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	3623	0	3545	14	0
1	B	3588	0	3456	16	0
2	A	5	0	5	0	0
3	A	8	0	11	0	0
3	B	8	0	11	0	0
4	B	4	0	6	0	0
5	A	171	0	0	1	0
5	B	62	0	0	0	0
All	All	7469	0	7034	30	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 (30) 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:93:GLY:HA2	1:B:345:HIS:HA	1.84	0.60
1:A:93:GLY:HA2	1:A:345:HIS:HA	1.85	0.59
1:B:189:LYS:HA	1:B:221:GLY:HA3	1.85	0.58
1:A:17:HIS:NE2	1:A:21:MET:HE2	2.19	0.57
1:B:17:HIS:NE2	1:B:21:MET:HE2	2.21	0.56
1:A:198:ILE:HG21	1:A:214:LEU:HD12	1.90	0.54
5:A:602:HOH:O	1:B:421:ARG:HD2	2.08	0.54
1:B:0:GLY:HA2	1:B:1:MET:SD	2.47	0.53
1:B:198:ILE:HG21	1:B:214:LEU:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:GLY:HA3	1:A:162:MET:HB2	1.93	0.50
1:B:132:GLY:HA3	1:B:162:MET:HB2	1.94	0.49
1:B:364:ASP:HA	1:B:367:ILE:HG12	1.95	0.48
1:A:364:ASP:HA	1:A:367:ILE:HG12	1.95	0.48
1:A:30:GLU:HB2	1:A:205:LYS:HG2	1.96	0.48
1:A:2:LEU:HD23	1:A:375:MET:HE2	1.97	0.47
1:A:386:ALA:HB1	1:A:389:VAL:HG12	1.97	0.47
1:B:30:GLU:HB2	1:B:205:LYS:HG2	1.96	0.46
1:B:147:LEU:HB3	1:B:466:ILE:HG12	1.98	0.46
1:B:386:ALA:HB1	1:B:389:VAL:HG12	1.99	0.45
1:B:373:HIS:CG	1:B:414:TYR:HB2	2.52	0.44
1:B:156:ASN:HA	1:B:451:PRO:HB3	2.00	0.44
1:B:320:VAL:HB	1:B:435:LYS:HG3	1.98	0.44
1:A:320:VAL:HB	1:A:435:LYS:HG3	1.99	0.43
1:A:147:LEU:HB3	1:A:466:ILE:HG12	2.00	0.43
1:A:156:ASN:HA	1:A:451:PRO:HB3	2.01	0.42
1:B:309:ARG:HA	1:B:342:PHE:O	2.19	0.42
1:B:255:ILE:HG23	1:B:267:VAL:HG21	2.02	0.41
1:A:255:ILE:HG23	1:A:267:VAL:HG21	2.03	0.41
1:A:309:ARG:HA	1:A:342:PHE:O	2.20	0.41
1:A:386:ALA:HB1	1:A:389:VAL:CG1	2.51	0.41

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	475/477 (100%)	462 (97%)	13 (3%)	0	100	100
1	B	475/477 (100%)	456 (96%)	19 (4%)	0	100	100
All	All	950/954 (100%)	918 (97%)	32 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	373/388 (96%)	363 (97%)	10 (3%)	39	52
1	B	363/388 (94%)	353 (97%)	10 (3%)	38	51
All	All	736/776 (95%)	716 (97%)	20 (3%)	39	52

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

Mol	Chain	Res	Type
1	A	81	VAL
1	A	133	THR
1	A	150	LEU
1	A	198	ILE
1	A	272	THR
1	A	309	ARG
1	A	403	LYS
1	A	415	THR
1	A	421	ARG
1	A	432	LEU
1	B	81	VAL
1	B	133	THR
1	B	150	LEU
1	B	198	ILE
1	B	272	THR
1	B	309	ARG
1	B	400	LEU
1	B	415	THR
1	B	421	ARG
1	B	432	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	HIS
1	A	87	ASN
1	A	138	GLN
1	A	148	GLN
1	A	156	ASN
1	A	247	GLN
1	A	402	GLN
1	B	17	HIS
1	B	87	ASN
1	B	138	GLN
1	B	148	GLN
1	B	156	ASN
1	B	247	GLN
1	B	402	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](#)

4 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	BET	B	502	-	7,7,7	0.93	0	10,10,10	1.19	1 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	IMD	A	501	-	5,5,5	0.33	0	5,5,5	0.55	0
4	EDO	B	501	-	3,3,3	0.45	0	2,2,2	0.20	0
3	BET	A	502	-	7,7,7	0.99	0	10,10,10	1.19	1 (10%)

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	BET	B	502	-	-	5/5/5/5	-
2	IMD	A	501	-	-	-	0/1/1/1
4	EDO	B	501	-	-	0/1/1/1	-
3	BET	A	502	-	-	5/5/5/5	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	BET	C-CA-N	2.42	119.58	116.31
3	B	502	BET	C-CA-N	2.15	119.22	116.31

There are no chirality outliers.

All (10) torsion outliers are listed below:

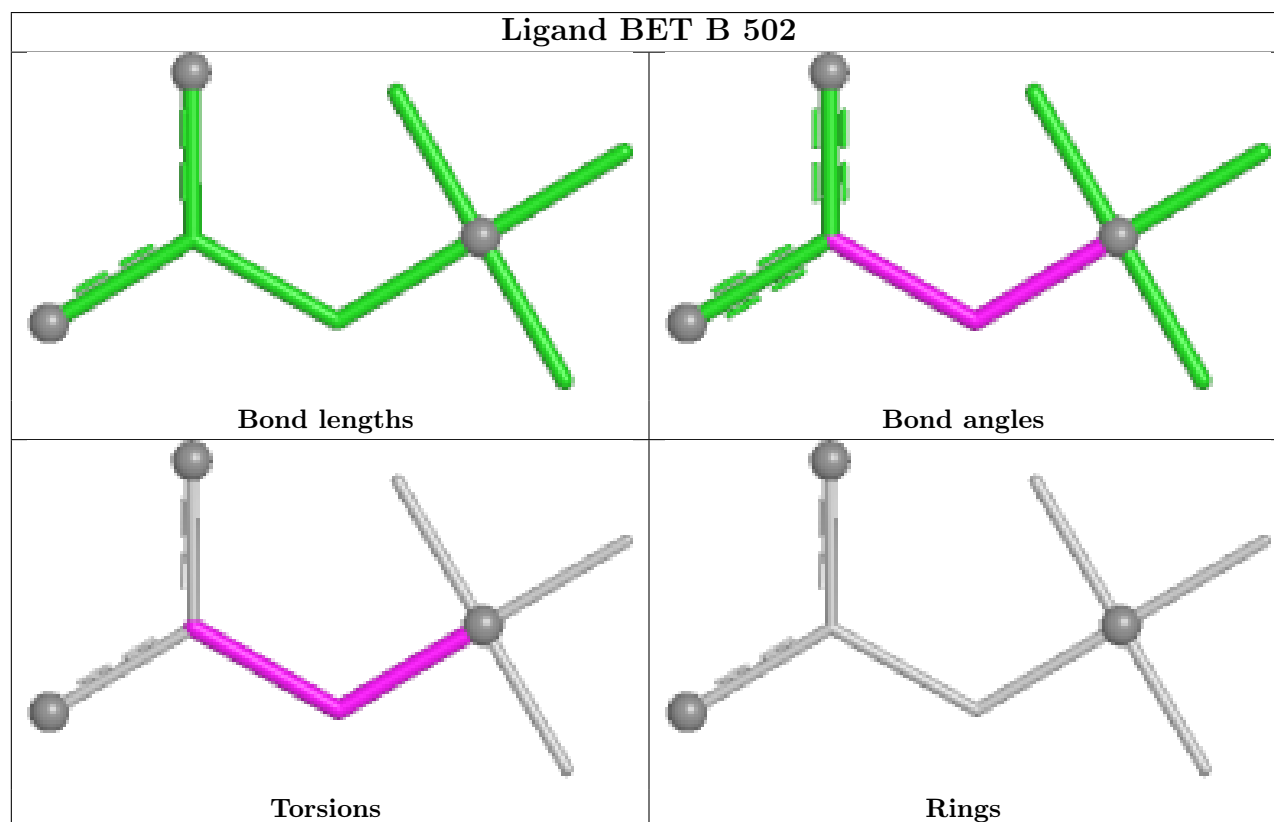
Mol	Chain	Res	Type	Atoms
3	A	502	BET	O-C-CA-N
3	A	502	BET	OXT-C-CA-N
3	B	502	BET	O-C-CA-N
3	B	502	BET	OXT-C-CA-N
3	A	502	BET	C-CA-N-C3
3	B	502	BET	C-CA-N-C3
3	A	502	BET	C-CA-N-C2
3	B	502	BET	C-CA-N-C2
3	A	502	BET	C-CA-N-C1
3	B	502	BET	C-CA-N-C1

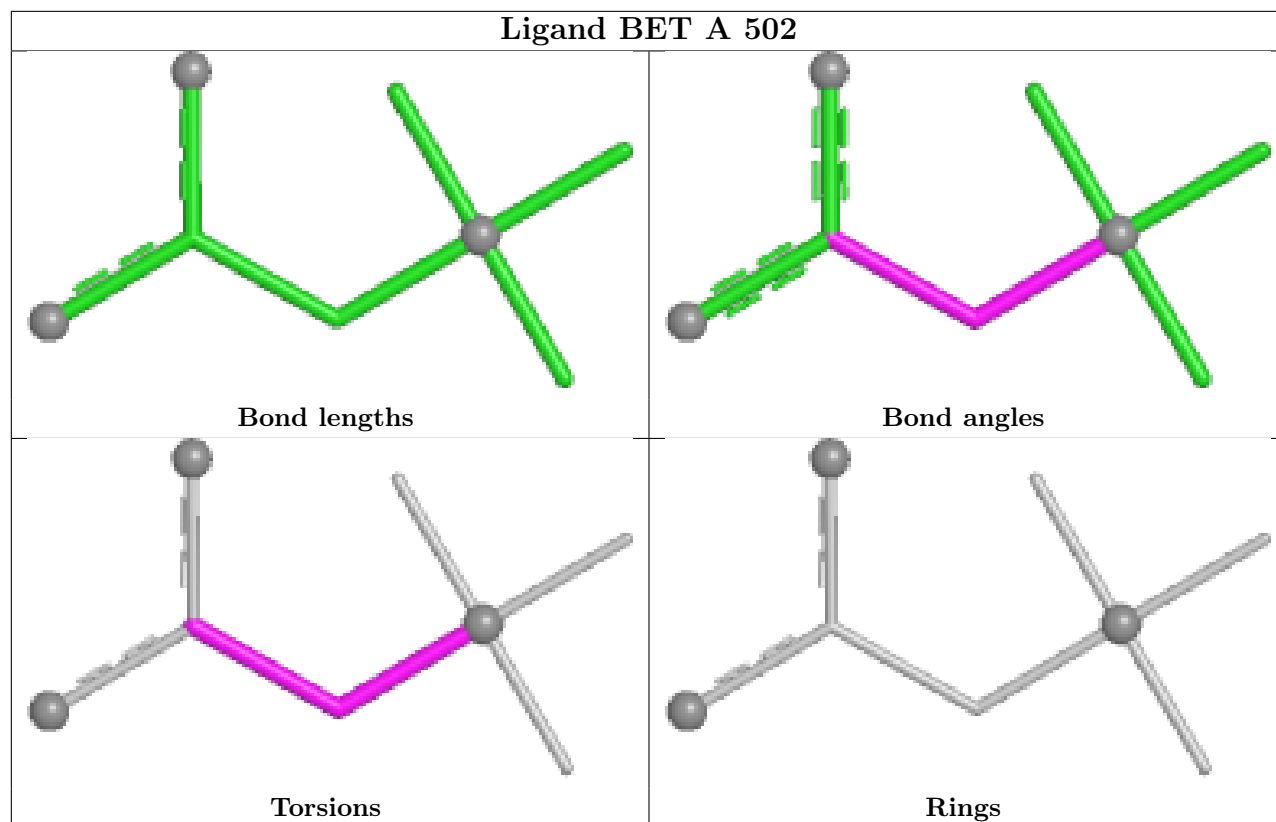
There are no ring outliers.

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	476/477 (99%)	-0.12	4 (0%) 82 86	33, 56, 96, 143	1 (0%)
1	B	475/477 (99%)	0.40	13 (2%) 56 63	36, 91, 158, 193	2 (0%)
All	All	951/954 (99%)	0.14	17 (1%) 67 72	33, 69, 149, 193	3 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	MET	4.2
1	A	1	MET	4.1
1	B	466	ILE	3.3
1	B	278	MET	3.2
1	B	280	SER	3.0
1	B	474	GLY	2.7
1	B	193	VAL	2.6
1	B	58	PHE	2.5
1	A	403	LYS	2.4
1	B	181	LEU	2.4
1	A	279	ARG	2.3
1	B	130	SER	2.2
1	B	0	GLY	2.2
1	B	454	LEU	2.1
1	A	408	ASN	2.1
1	B	281	GLY	2.1
1	B	462	LEU	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 oligosaccharides in this entry.

### 6.4 Ligands [i](#)

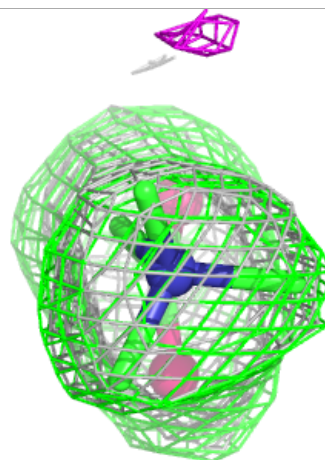
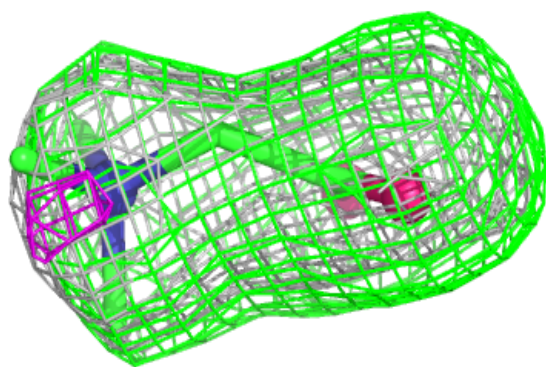
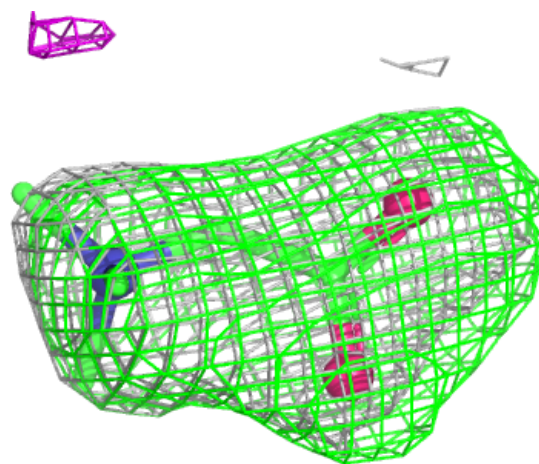
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

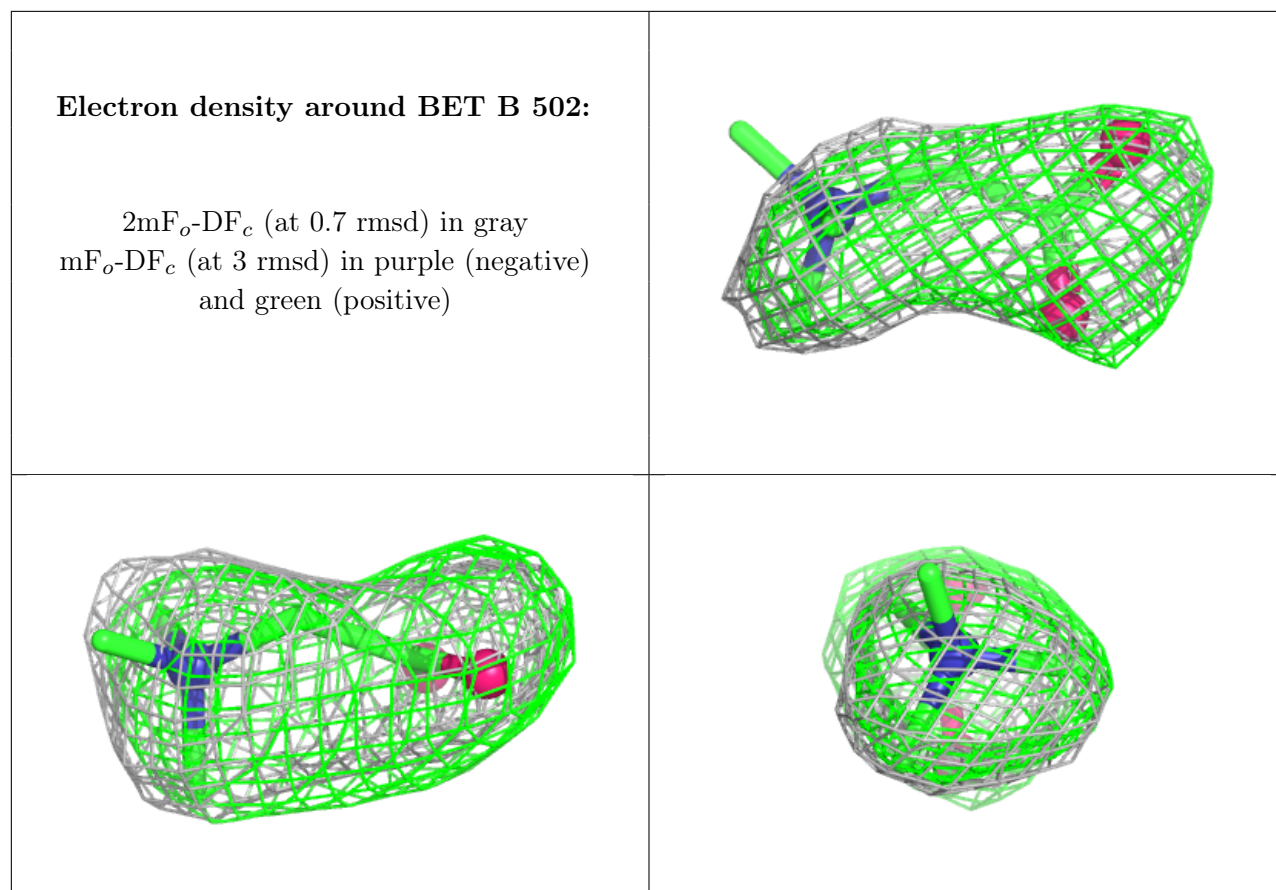
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	IMD	A	501	5/5	-	-	95,95,96,97	5
3	BET	A	502	8/8	-	-	72,73,74,74	8
3	BET	B	502	8/8	-	-	104,107,109,109	8
4	EDO	B	501	4/4	-	-	89,90,91,91	4

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 BET A 502:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.