



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:01 AM UTC

PDB ID : 7B6G / pdb_00007b6g
Title : Crystal structure of MurE from E.coli in complex with Z1675346324
Authors : Koekemoer, L.; Steindel, M.; Fairhead, M.; Talon, R.; Douangamath, A.; Arrowsmith, C.H.; Edwards, A.M.; Bountra, C.; von Delft, F.; Krojer, T.; Structural Genomics Consortium (SGC)
Deposited on : 2020-12-07
Resolution : 1.94 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

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>.

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

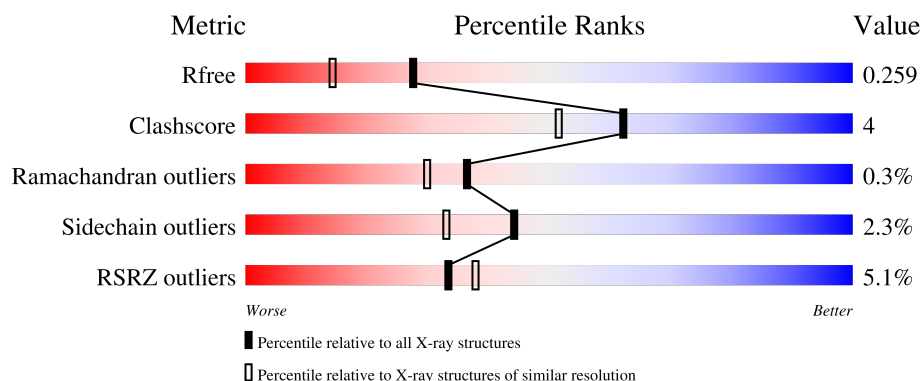
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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 ≥ 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	AAA	496	
1	BBB	496	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	DMS	AAA	501	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7649 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.

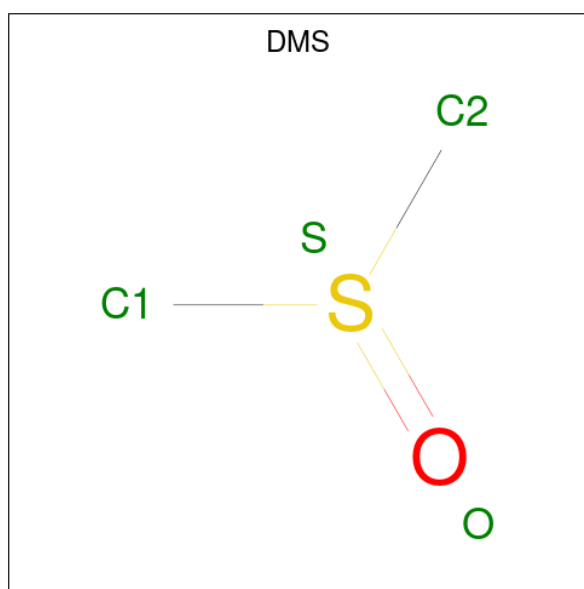
- Molecule 1 is a protein called UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	483	Total	C	N	O	S	0	7	0
			3716	2324	674	698	20			
1	BBB	477	Total	C	N	O	S	0	7	0
			3644	2279	651	692	22			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	0	SER	-	expression tag	UNP A0A5Q2GBT0
BBB	0	SER	-	expression tag	UNP A0A5Q2GBT0

- Molecule 2 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C₂H₆OS).



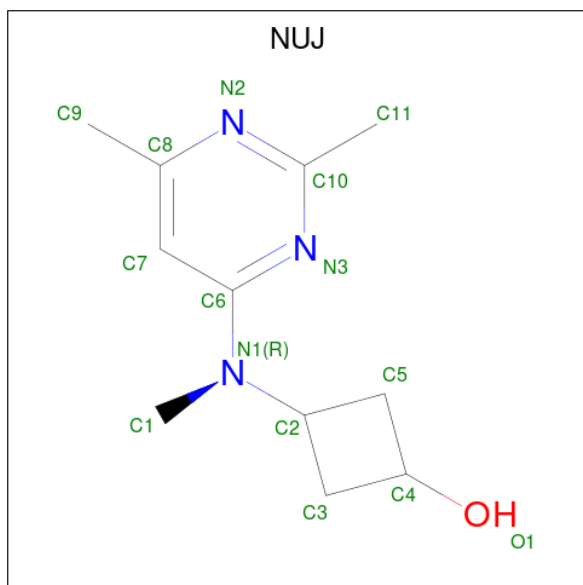
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	AAA	1	Total	C	O	S	0	0
			4	2	1	1		

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

- Molecule 3 is trans-3-[(2,6-dimethylpyrimidin-4-yl)(methyl)amino]cyclobutan-1-ol (CCD ID: NUJ) (formula: C₁₁H₁₇N₃O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	BBB	1	Total	C	N	O	0	0
			15	11	3	1		

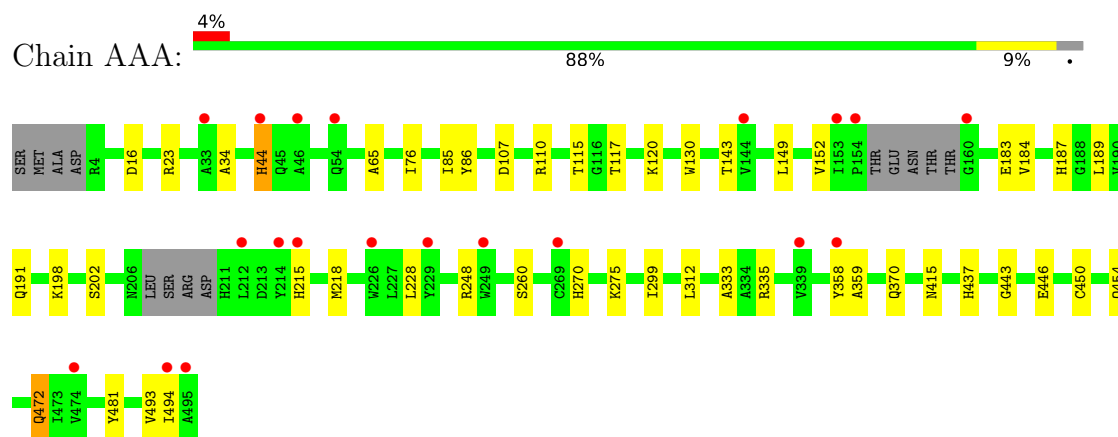
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	129	Total	O	0	0
			129	129		
4	BBB	137	Total	O	0	0
			137	137		

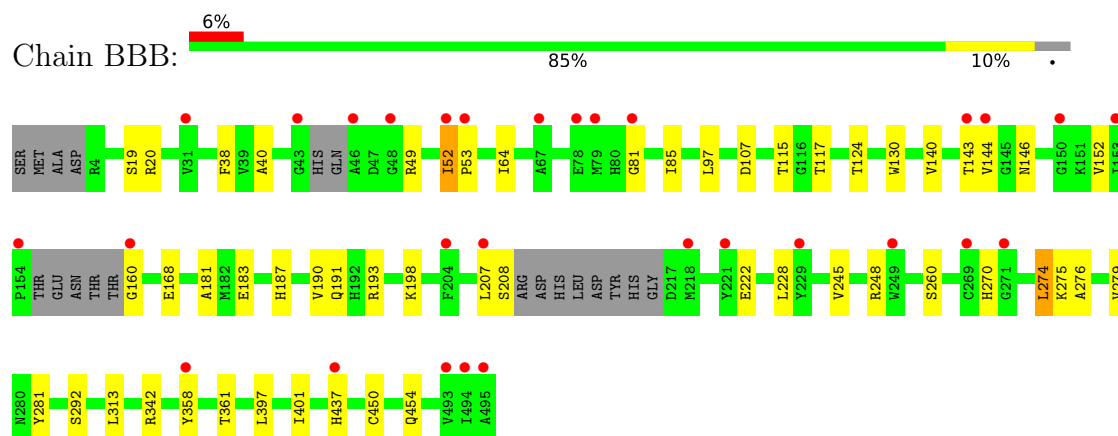
3 Residue-property plots [i](#)

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: UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase



- Molecule 1: UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	58.28Å 58.29Å 74.11Å 97.23° 91.45° 105.31°	Depositor
Resolution (Å)	73.39 – 1.94 73.39 – 1.94	Depositor EDS
% Data completeness (in resolution range)	95.6 (73.39-1.94) 95.6 (73.39-1.94)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.205 , 0.256 0.211 , 0.259	Depositor DCC
R_{free} test set	3393 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	33.4	Xtriage
Anisotropy	0.323	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 25.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7649	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.92% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: NUJ, DMS

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	AAA	1.07	0/3784	1.35	4/5133 (0.1%)
1	BBB	1.08	1/3710 (0.0%)	1.35	4/5034 (0.1%)
All	All	1.08	1/7494 (0.0%)	1.35	8/10167 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BBB	361	THR	N-CA	5.36	1.50	1.45

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	152	VAL	CA-C-N	5.33	126.43	122.59
1	AAA	152	VAL	C-N-CA	5.33	126.43	122.59
1	BBB	152	VAL	CA-C-N	5.24	126.36	122.59
1	BBB	152	VAL	C-N-CA	5.24	126.36	122.59
1	BBB	81	GLY	CA-C-N	5.19	126.33	122.59
1	BBB	81	GLY	C-N-CA	5.19	126.33	122.59
1	AAA	370	GLN	CA-C-N	5.12	127.09	120.44
1	AAA	370	GLN	C-N-CA	5.12	127.09	120.44

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	AAA	3716	0	3675	28	0
1	BBB	3644	0	3606	32	0
2	AAA	4	0	6	6	0
2	BBB	4	0	6	1	0
3	BBB	15	0	0	0	0
4	AAA	129	0	0	1	0
4	BBB	137	0	0	1	0
All	All	7649	0	7293	60	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 4.

All (60) 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:AAA:115:THR:HG22	1:AAA:184:VAL:HB	1.69	0.72
1:BBB:342:ARG:NH1	4:BBB:601:HOH:O	2.23	0.71
1:AAA:107:ASP:OD1	1:AAA:198:LYS:HD2	1.91	0.71
1:BBB:160:GLY:O	1:BBB:193:ARG:HD3	1.91	0.70
1:AAA:115:THR:CG2	2:AAA:501:DMS:H11	2.23	0.69
1:BBB:187:HIS:NE2	1:BBB:191:GLN:OE1	2.28	0.67
1:BBB:190:VAL:HA	1:BBB:228:LEU:HD11	1.77	0.65
1:AAA:450:CYS:SG	1:AAA:454:GLN:NE2	2.70	0.63
1:BBB:19:SER:O	1:BBB:20:ARG:HD3	1.99	0.63
1:AAA:189:LEU:HD13	2:AAA:501:DMS:H12	1.81	0.62
1:BBB:260:SER:O	1:BBB:275:LYS:HA	1.99	0.62
1:AAA:143:THR:HG23	1:AAA:183:GLU:OE1	2.02	0.59
1:BBB:49:ARG:HA	1:BBB:52:ILE:HD13	1.87	0.57
1:AAA:218:MET:HE2	1:AAA:248:ARG:HH21	1.71	0.56
1:BBB:52:ILE:N	1:BBB:53:PRO:HD2	2.20	0.56
1:BBB:274:LEU:HD12	1:BBB:292:SER:HB3	1.88	0.56
1:AAA:44:HIS:CG	1:AAA:44:HIS:O	2.59	0.56
1:AAA:184:VAL:HG11	2:AAA:501:DMS:C1	2.36	0.55
1:AAA:260:SER:O	1:AAA:275:LYS:HA	2.06	0.55
1:AAA:415:ASN:H	1:AAA:472:GLN:NE2	2.06	0.53
1:AAA:184:VAL:HG11	2:AAA:501:DMS:H13	1.90	0.53
1:AAA:115:THR:HG21	2:AAA:501:DMS:H11	1.90	0.53
1:AAA:189:LEU:HG	1:AAA:228:LEU:HD13	1.90	0.52
1:BBB:49:ARG:HA	1:BBB:52:ILE:CD1	2.39	0.52
1:BBB:117:THR:HG21	1:BBB:208:SER:H	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BBB:397:LEU:O	1:BBB:401:ILE:HG12	2.10	0.52
1:BBB:115[B]:THR:OG1	2:BBB:502:DMS:H11	2.10	0.51
1:BBB:40:ALA:HB2	1:BBB:52:ILE:HD11	1.92	0.51
1:BBB:207:LEU:HD23	1:BBB:245:VAL:HG21	1.91	0.51
1:BBB:146:ASN:ND2	1:BBB:168:GLU:HG2	2.26	0.51
1:AAA:44:HIS:O	1:AAA:44:HIS:ND1	2.45	0.50
1:BBB:107:ASP:OD1	1:BBB:198:LYS:HD2	2.12	0.49
1:AAA:493:VAL:C	1:AAA:494:ILE:HD12	2.38	0.48
1:BBB:143:THR:HG23	1:BBB:183:GLU:OE1	2.13	0.48
1:AAA:120[A]:LYS:NZ	4:AAA:607:HOH:O	2.47	0.47
1:BBB:40:ALA:CB	1:BBB:52:ILE:HD11	2.45	0.47
1:BBB:38:PHE:HE2	1:BBB:52:ILE:HD12	1.79	0.47
1:BBB:140:VAL:HA	1:BBB:181:ALA:O	2.15	0.47
1:BBB:279:VAL:HG11	1:BBB:281:TYR:CZ	2.51	0.46
1:AAA:493:VAL:O	1:AAA:494:ILE:HD12	2.16	0.46
1:BBB:222:GLU:OE2	1:BBB:248:ARG:NH1	2.46	0.46
1:BBB:146:ASN:HD22	1:BBB:168:GLU:HG2	1.80	0.45
1:BBB:64:ILE:HD13	1:BBB:97:LEU:HD21	1.97	0.45
1:BBB:64:ILE:HA	1:BBB:85:ILE:O	2.18	0.43
1:BBB:117:THR:HG23	1:BBB:207:LEU:HA	2.00	0.43
1:AAA:443:GLY:HA3	1:AAA:446:GLU:OE1	2.18	0.43
1:AAA:202:SER:OG	2:AAA:501:DMS:H23	2.19	0.43
1:AAA:312[A]:LEU:C	1:AAA:312[A]:LEU:HD23	2.44	0.43
1:BBB:187:HIS:CD2	1:BBB:191:GLN:OE1	2.71	0.43
1:BBB:276:ALA:HB2	1:BBB:313:LEU:HD11	1.99	0.43
1:AAA:23:ARG:HD2	1:AAA:34:ALA:O	2.19	0.42
1:AAA:187:HIS:NE2	1:AAA:191:GLN:OE1	2.53	0.42
1:BBB:450:CYS:SG	1:BBB:454:GLN:NE2	2.93	0.41
1:BBB:144:VAL:HG12	1:BBB:144:VAL:O	2.20	0.41
1:AAA:481:TYR:CD1	1:AAA:481:TYR:C	2.99	0.41
1:AAA:299:ILE:HG23	1:AAA:333:ALA:HB1	2.02	0.41
1:AAA:218:MET:HE2	1:AAA:248:ARG:NH2	2.33	0.40
1:BBB:222:GLU:CD	1:BBB:248:ARG:HH12	2.29	0.40
1:AAA:65:ALA:O	1:AAA:86:TYR:HA	2.21	0.40
1:AAA:76:ILE:HG12	1:AAA:85:ILE:HD12	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	AAA	484/496 (98%)	471 (97%)	11 (2%)	2 (0%)	30	22
1	BBB	476/496 (96%)	462 (97%)	13 (3%)	1 (0%)	43	37
All	All	960/992 (97%)	933 (97%)	24 (2%)	3 (0%)	36	30

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	BBB	270	HIS
1	AAA	270	HIS
1	AAA	359	ALA

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	AAA	382/387 (99%)	369 (97%)	13 (3%)	32	19
1	BBB	377/387 (97%)	370 (98%)	7 (2%)	50	40
All	All	759/774 (98%)	739 (97%)	20 (3%)	44	28

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

Mol	Chain	Res	Type
1	AAA	16	ASP
1	AAA	44	HIS
1	AAA	110[A]	ARG

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Mol	Chain	Res	Type
1	AAA	110[B]	ARG
1	AAA	117	THR
1	AAA	130	TRP
1	AAA	149	LEU
1	AAA	215	HIS
1	AAA	335[A]	ARG
1	AAA	335[B]	ARG
1	AAA	358	TYR
1	AAA	437	HIS
1	AAA	472	GLN
1	BBB	52	ILE
1	BBB	124[A]	THR
1	BBB	124[B]	THR
1	BBB	130	TRP
1	BBB	274	LEU
1	BBB	358	TYR
1	BBB	437	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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
2	DMS	AAA	501	-	3,3,3	0.23	0	3,3,3	0.17	0
2	DMS	BBB	502	-	3,3,3	0.24	0	3,3,3	0.05	0
3	NUJ	BBB	501	-	15,16,16	2.82	6 (40%)	12,23,23	1.23	2 (16%)

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	NUJ	BBB	501	-	-	0/4/16/16	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	BBB	501	NUJ	C6-N1	6.90	1.48	1.37
3	BBB	501	NUJ	C10-N2	3.81	1.40	1.34
3	BBB	501	NUJ	C6-N3	3.70	1.39	1.34
3	BBB	501	NUJ	C7-C6	3.59	1.45	1.39
3	BBB	501	NUJ	C10-N3	3.44	1.40	1.34
3	BBB	501	NUJ	C3-C4	2.07	1.57	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	BBB	501	NUJ	C3-C4-C5	-2.52	87.22	89.27
3	BBB	501	NUJ	N3-C6-N1	2.18	118.24	116.87

There are no chirality outliers.

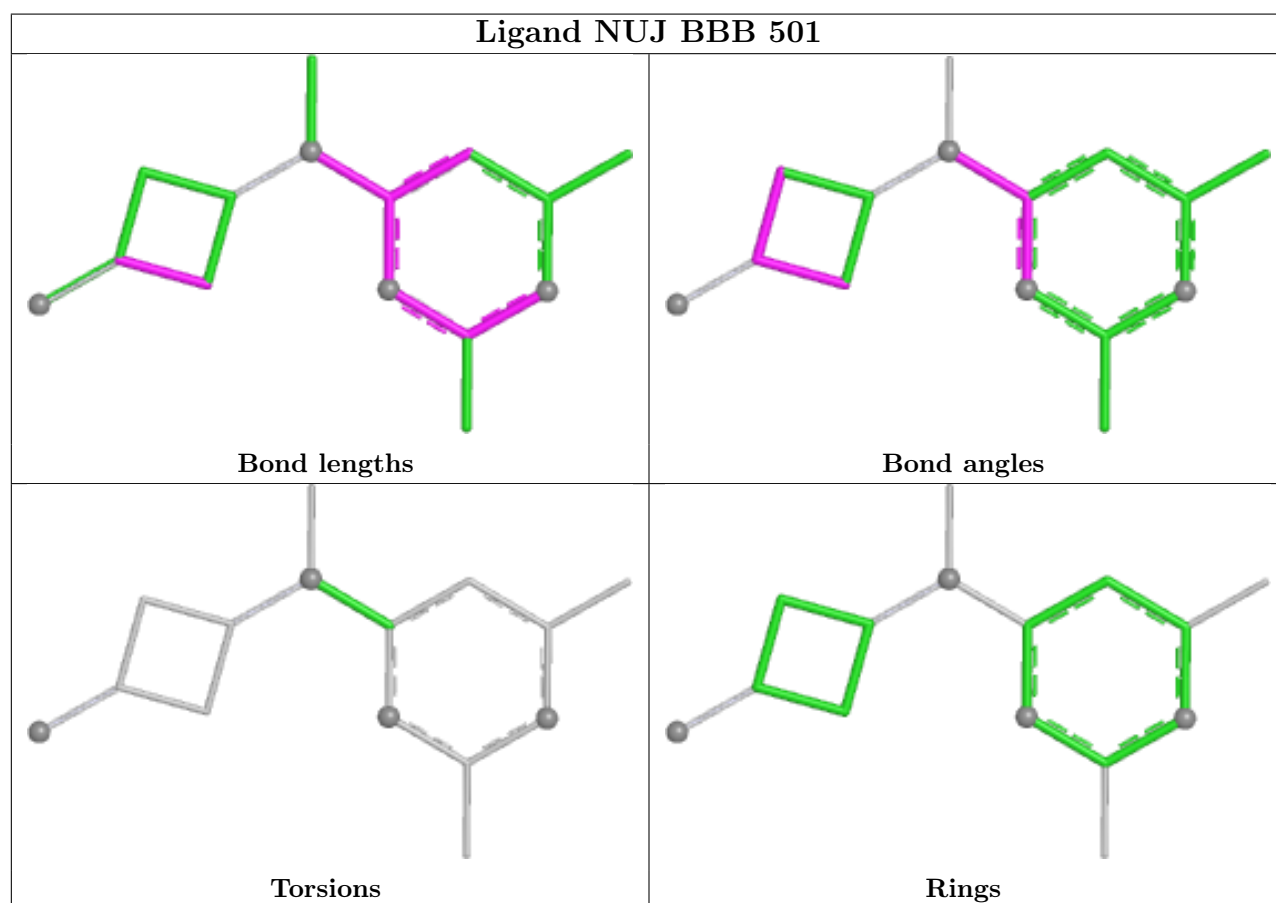
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AAA	501	DMS	6	0
2	BBB	502	DMS	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

6.1 Protein, DNA and RNA chains

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, 95th 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 ²)	Q<0.9
1	AAA	483/496 (97%)	0.46	20 (4%) 41 46	14, 39, 65, 102	7 (1%)
1	BBB	477/496 (96%)	0.45	29 (6%) 27 30	16, 38, 65, 88	7 (1%)
All	All	960/992 (96%)	0.46	49 (5%) 33 38	14, 38, 65, 102	14 (1%)

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	494	ILE	5.5
1	BBB	494	ILE	4.8
1	AAA	495	ALA	4.7
1	BBB	269	CYS	4.5
1	BBB	249	TRP	4.1
1	BBB	495	ALA	3.7
1	AAA	226	TRP	3.6
1	AAA	215	HIS	3.6
1	AAA	214	TYR	3.5
1	AAA	249	TRP	3.5
1	BBB	43	GLY	3.5
1	BBB	79	MET	3.3
1	BBB	358	TYR	3.3
1	AAA	229	TYR	3.2
1	BBB	154	PRO	3.2
1	BBB	271	GLY	3.1
1	AAA	358	TYR	3.0
1	AAA	212	LEU	2.9
1	AAA	269	CYS	2.9
1	AAA	154	PRO	2.9
1	BBB	160	GLY	2.9
1	BBB	229	TYR	2.7
1	AAA	474	VAL	2.7
1	BBB	81	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	BBB	144	VAL	2.5
1	BBB	221	TYR	2.5
1	BBB	52	ILE	2.5
1	BBB	31	VAL	2.4
1	AAA	160	GLY	2.4
1	BBB	493	VAL	2.4
1	BBB	46	ALA	2.3
1	AAA	44	HIS	2.3
1	AAA	46	ALA	2.3
1	BBB	53	PRO	2.3
1	AAA	153	ILE	2.3
1	BBB	48	GLY	2.2
1	BBB	153	ILE	2.2
1	BBB	437	HIS	2.2
1	BBB	207	LEU	2.2
1	BBB	204	PHE	2.2
1	AAA	339	VAL	2.2
1	AAA	54	GLN	2.2
1	AAA	33	ALA	2.2
1	BBB	78	GLU	2.1
1	BBB	218	MET	2.1
1	BBB	67	ALA	2.1
1	BBB	143	THR	2.0
1	BBB	150	GLY	2.0
1	AAA	144	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

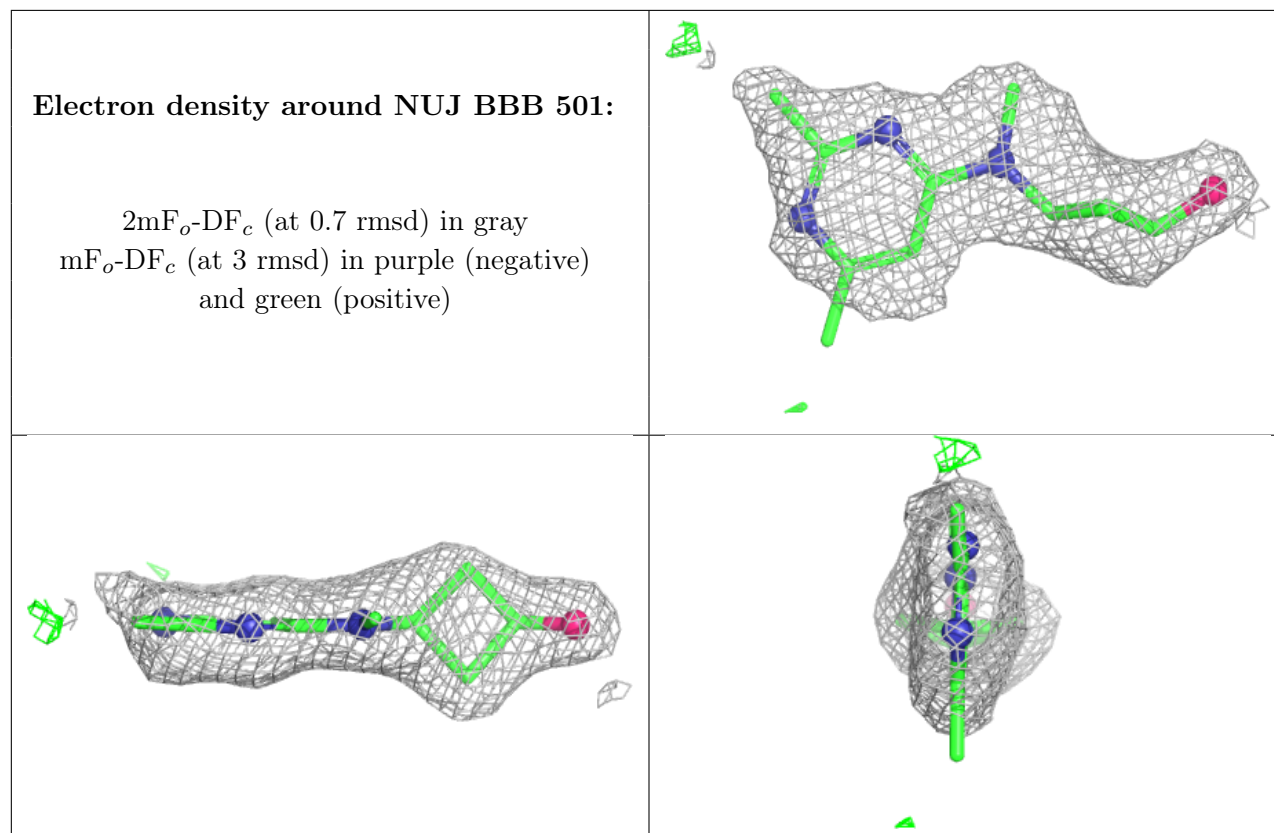
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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, 95th 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	NUJ	BBB	501	15/15	0.86	0.14	41,53,69,69	0
2	DMS	AAA	501	4/4	0.92	0.14	50,57,62,63	0
2	DMS	BBB	502	4/4	0.95	0.10	59,64,65,66	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.