



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 26, 2023 – 10:09 PM JST

PDB ID : 8HWJ  
Title : Bacterial STING from *Epilithonimonas lactis* in complex with 3'3'-c-di-AMP  
Authors : Wang, Y.-C.; Yang, C.-S.; Hou, M.-H.; Chen, Y.  
Deposited on : 2022-12-30  
Resolution : 2.55 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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

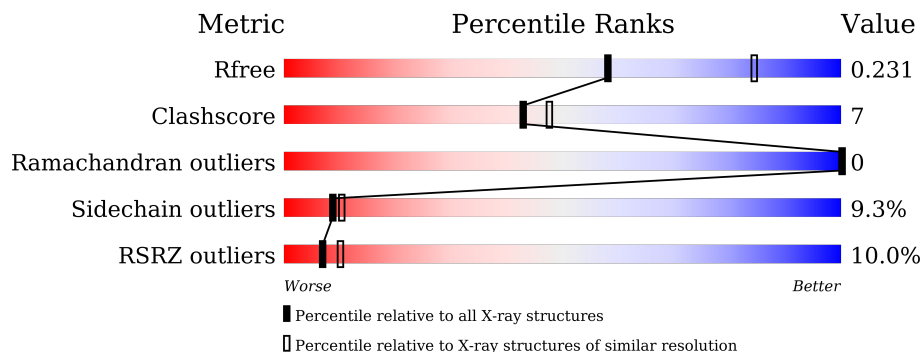
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*





The reported resolution of this entry is 2.55 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	1279 (2.58-2.54)
Clashscore	141614	1327 (2.58-2.54)
Ramachandran outliers	138981	1312 (2.58-2.54)
Sidechain outliers	138945	1312 (2.58-2.54)
RSRZ outliers	127900	1269 (2.58-2.54)

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	165	
1	B	165	
1	C	165	
1	D	165	

## 2 Entry composition i

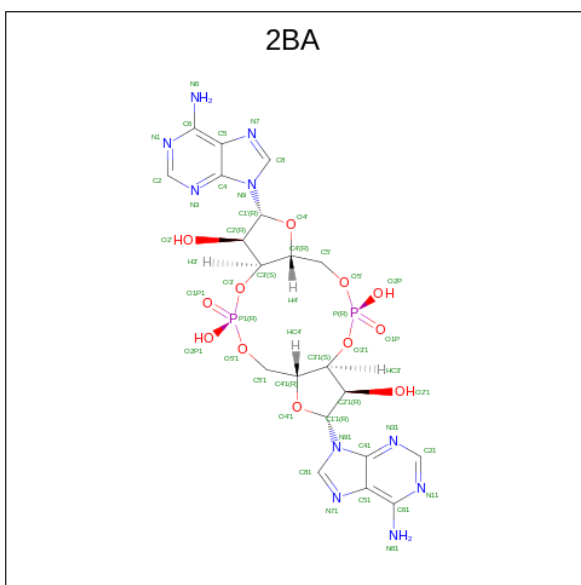
There are 3 unique types of molecules in this entry. The entry contains 5411 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 CD-NTase-associated protein 12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	162	Total	C	N	O	S	0	0	0
			1301	834	212	250	5			
1	B	155	Total	C	N	O	S	0	0	0
			1248	801	201	241	5			
1	C	162	Total	C	N	O	S	0	0	0
			1301	834	212	250	5			
1	D	162	Total	C	N	O	S	0	0	0
			1301	834	212	250	5			

- Molecule 2 is (2R,3R,3aS,5R,7aR,9R,10R,10aS,12R,14aR)-2,9-bis(6-amino-9H-purin-9-yl)octahydro-2H,7H-difuro[3,2-d:3',2'-j][1,3,7,9,2,8]tetraoxadiphosphacyclododecine-3,5,10,12-tetrol 5,12-dioxide (three-letter code: 2BA) (formula: C<sub>20</sub>H<sub>24</sub>N<sub>10</sub>O<sub>12</sub>P<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	B	1	Total	C	N	O	P	0	0
			44	20	10	12	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	C	1	44	20	10	12	2	0	0

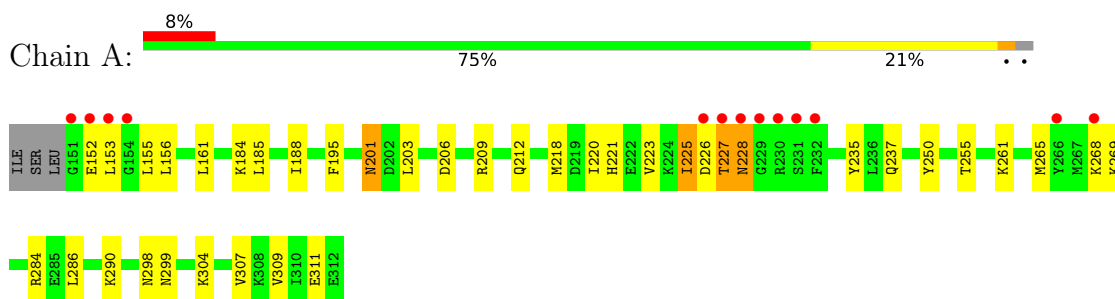
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	38	Total	O	0	0
			38	38		
3	B	43	Total	O	0	0
			43	43		
3	C	55	Total	O	0	0
			55	55		
3	D	36	Total	O	0	0
			36	36		

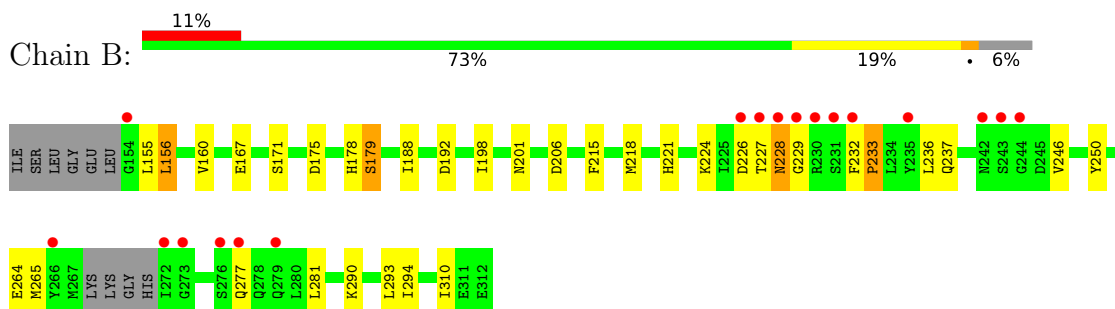
### 3 Residue-property plots

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.

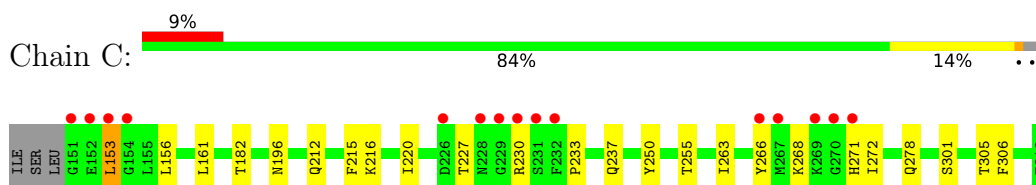
- Molecule 1: CD-NTase-associated protein 12



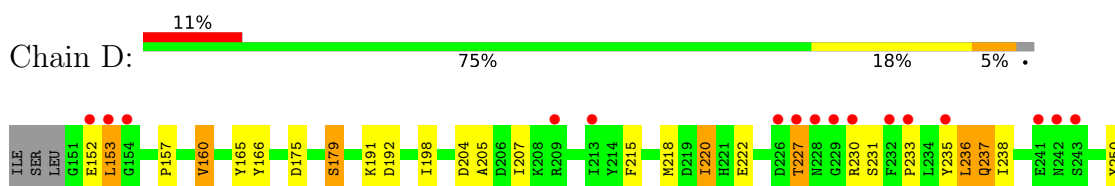
- Molecule 1: CD-NTase-associated protein 12

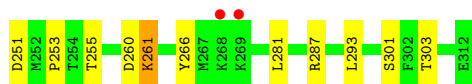


- Molecule 1: CD-NTase-associated protein 12



- Molecule 1: CD-NTase-associated protein 12





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	157.17Å 52.71Å 88.93Å 90.00° 114.88° 90.00°	Depositor
Resolution (Å)	25.77 – 2.55 25.76 – 2.55	Depositor EDS
% Data completeness (in resolution range)	89.8 (25.77-2.55) 89.9 (25.76-2.55)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.81 (at 2.57Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.195 , 0.228 0.199 , 0.231	Depositor DCC
$R_{free}$ test set	962 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.2	Xtrriage
Anisotropy	0.021	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 42.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5411	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.27% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 2BA

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	0.67	0/1323	0.80	0/1785
1	B	0.65	0/1268	0.80	1/1712 (0.1%)
1	C	0.66	0/1323	0.79	0/1785
1	D	0.67	0/1323	0.81	0/1785
All	All	0.66	0/5237	0.80	1/7067 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	228	ASN	CB-CA-C	5.31	121.03	110.40

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	1301	0	1314	21	0
1	B	1248	0	1257	15	0
1	C	1301	0	1314	18	0
1	D	1301	0	1314	24	0
2	B	44	0	23	0	0
2	C	44	0	23	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	38	0	0	1	0
3	B	43	0	0	1	0
3	C	55	0	0	2	0
3	D	36	0	0	1	0
All	All	5411	0	5245	71	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 7.

All (71) 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:178:HIS:HD2	3:B:433:HOH:O	1.68	0.74
1:B:179:SER:HB2	1:B:228:ASN:HD22	1.55	0.70
1:A:235:TYR:OH	1:B:233:PRO:HD2	1.92	0.70
1:D:220:ILE:HD11	1:D:237:GLN:HB2	1.75	0.69
1:D:227:THR:HA	3:D:417:HOH:O	1.93	0.67
1:B:192:ASP:HB3	1:B:246:VAL:HG22	1.78	0.64
1:C:153:LEU:HD22	1:D:281:LEU:HD22	1.81	0.61
1:A:290:LYS:HG3	1:A:309:VAL:HG11	1.83	0.61
1:D:218:MET:HB2	1:D:220:ILE:HG22	1.83	0.60
1:D:215:PHE:CD1	1:D:220:ILE:HD13	2.38	0.58
1:A:261:LYS:HD2	1:B:167:GLU:HG3	1.85	0.58
1:D:204:ASP:O	1:D:260:ASP:OD1	2.22	0.57
1:C:263:ILE:HG22	1:C:278:GLN:HG3	1.85	0.57
1:B:198:ILE:CD1	1:B:310:ILE:HD11	2.35	0.56
1:C:305:THR:HG22	1:C:306:PHE:CE2	2.40	0.56
1:A:218:MET:HB2	1:A:220:ILE:HG13	1.88	0.55
1:A:184:LYS:HA	1:A:188:ILE:O	2.07	0.54
1:D:220:ILE:HD12	1:D:250:TYR:CD2	2.44	0.53
1:A:220:ILE:HD13	1:A:250:TYR:CD2	2.44	0.52
1:C:212:GLN:NE2	3:C:401:HOH:O	2.41	0.52
1:B:175:ASP:O	1:B:179:SER:OG	2.26	0.52
1:A:201:ASN:HA	3:A:408:HOH:O	2.08	0.52
1:D:204:ASP:C	1:D:260:ASP:OD1	2.48	0.52
1:D:157:PRO:O	1:D:160:VAL:HG12	2.09	0.51
1:A:195:PHE:O	1:A:307:VAL:HA	2.11	0.51
1:C:271:HIS:CD2	1:C:272:ILE:O	2.63	0.50
1:C:212:GLN:HA	1:C:212:GLN:OE1	2.13	0.49
1:C:212:GLN:O	1:C:216:LYS:HG2	2.12	0.49
1:D:198:ILE:HD11	1:D:250:TYR:HD1	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:175:ASP:O	1:D:179:SER:HB3	2.13	0.48
1:B:198:ILE:HD11	1:B:250:TYR:HD1	1.79	0.48
1:D:236:LEU:C	1:D:237:GLN:HG2	2.34	0.47
1:B:227:THR:HG23	1:B:229:GLY:H	1.81	0.46
1:A:220:ILE:HG22	1:A:237:GLN:HB3	1.96	0.46
1:A:161:LEU:HD22	1:A:255:THR:OG1	2.15	0.46
1:A:269:LYS:HA	1:C:268:LYS:O	2.16	0.46
1:A:153:LEU:HG	1:A:155:LEU:HB2	1.98	0.46
1:D:165:TYR:CZ	1:D:253:PRO:HG3	2.52	0.44
1:B:215:PHE:CE2	1:B:237:GLN:HG3	2.52	0.44
1:B:277:GLN:O	1:B:281:LEU:HG	2.16	0.44
1:D:153:LEU:HD22	1:D:153:LEU:HA	1.72	0.44
1:A:203:LEU:HD21	1:A:286:LEU:HD21	2.00	0.44
2:C:501:2BA:O5'1	2:C:501:2BA:HC8	2.18	0.44
1:D:238:ILE:O	1:D:238:ILE:HG23	2.17	0.44
1:C:233:PRO:HD2	1:D:235:TYR:CE2	2.53	0.44
1:B:156:LEU:HD12	1:B:156:LEU:HA	1.88	0.44
1:C:272:ILE:HA	3:C:413:HOH:O	2.17	0.44
1:D:166:TYR:CE1	1:D:303:THR:HG21	2.53	0.43
1:C:305:THR:CG2	1:C:306:PHE:CE2	3.01	0.43
1:A:209:ARG:NE	1:D:175:ASP:OD2	2.52	0.43
1:C:196:ASN:O	1:C:250:TYR:HA	2.19	0.43
1:C:233:PRO:HD2	1:D:235:TYR:HE2	1.84	0.43
1:D:205:ALA:O	1:D:261:LYS:NZ	2.51	0.42
1:C:215:PHE:HD1	1:C:220:ILE:HD11	1.83	0.42
1:C:233:PRO:O	1:D:233:PRO:HB3	2.19	0.42
1:D:165:TYR:OH	1:D:251:ASP:OD2	2.25	0.42
1:C:227:THR:HB	1:C:230:ARG:HB2	2.01	0.42
2:C:501:2BA:O3'1	1:D:255:THR:HB	2.19	0.42
1:C:215:PHE:CZ	1:C:237:GLN:HG3	2.55	0.42
1:A:155:LEU:HD12	1:A:155:LEU:HA	1.78	0.42
1:A:227:THR:HB	1:A:228:ASN:H	1.62	0.41
1:A:218:MET:CB	1:A:220:ILE:HG13	2.49	0.41
1:A:225:ILE:HG22	1:A:226:ASP:H	1.86	0.41
1:A:221:HIS:O	1:A:237:GLN:HA	2.21	0.41
1:B:227:THR:HG22	1:B:232:PHE:H	1.84	0.41
1:A:185:LEU:HB3	1:A:223:VAL:HG21	2.03	0.41
1:B:198:ILE:HD11	1:B:250:TYR:CD1	2.56	0.40
1:C:161:LEU:HD22	1:C:255:THR:OG1	2.21	0.40
1:D:235:TYR:C	1:D:236:LEU:HD23	2.42	0.40
1:A:298:ASN:O	1:A:304:LYS:HD2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:290:LYS:O	1:B:294:ILE:HG13	2.21	0.40

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	160/165 (97%)	151 (94%)	9 (6%)	0	100	100
1	B	151/165 (92%)	143 (95%)	8 (5%)	0	100	100
1	C	160/165 (97%)	150 (94%)	10 (6%)	0	100	100
1	D	160/165 (97%)	154 (96%)	6 (4%)	0	100	100
All	All	631/660 (96%)	598 (95%)	33 (5%)	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	146/149 (98%)	133 (91%)	13 (9%)	9	12
1	B	141/149 (95%)	124 (88%)	17 (12%)	5	5
1	C	146/149 (98%)	141 (97%)	5 (3%)	37	49
1	D	146/149 (98%)	127 (87%)	19 (13%)	4	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	579/596 (97%)	525 (91%)	54 (9%)	9 10

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	152	GLU
1	A	156	LEU
1	A	201	ASN
1	A	206	ASP
1	A	212	GLN
1	A	225	ILE
1	A	227	THR
1	A	228	ASN
1	A	265	MET
1	A	268	LYS
1	A	284	ARG
1	A	299	ASN
1	A	311	GLU
1	B	155	LEU
1	B	156	LEU
1	B	160	VAL
1	B	171	SER
1	B	179	SER
1	B	188	ILE
1	B	201	ASN
1	B	206	ASP
1	B	218	MET
1	B	221	HIS
1	B	224	LYS
1	B	226	ASP
1	B	233	PRO
1	B	236	LEU
1	B	264	GLU
1	B	265	MET
1	B	293	LEU
1	C	153	LEU
1	C	156	LEU
1	C	182	THR
1	C	266	TYR
1	C	301	SER
1	D	152	GLU
1	D	153	LEU

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Mol	Chain	Res	Type
1	D	160	VAL
1	D	179	SER
1	D	191	LYS
1	D	192	ASP
1	D	207	ILE
1	D	220	ILE
1	D	222	GLU
1	D	227	THR
1	D	230	ARG
1	D	231	SER
1	D	236	LEU
1	D	237	GLN
1	D	261	LYS
1	D	266	TYR
1	D	287	ARG
1	D	293	LEU
1	D	301	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	186	ASN
1	A	279	GLN
1	B	178	HIS
1	B	201	ASN
1	B	228	ASN
1	B	242	ASN
1	B	277	GLN
1	B	279	GLN
1	B	299	ASN
1	C	186	ASN
1	C	271	HIS
1	C	278	GLN
1	C	299	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

2 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	2BA	B	501	-	44,50,50	0.66	1 (2%)	50,78,78	0.90	1 (2%)
2	2BA	C	501	-	44,50,50	0.63	0	50,78,78	0.93	1 (2%)

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	2BA	B	501	-	-	0/22/62/62	0/6/7/7
2	2BA	C	501	-	-	0/22/62/62	0/6/7/7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	2BA	C8-N7	-2.08	1.31	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	2BA	C51-C61-N61	2.14	123.61	120.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	2BA	C5-C6-N6	2.12	123.57	120.35

There are no chirality outliers.

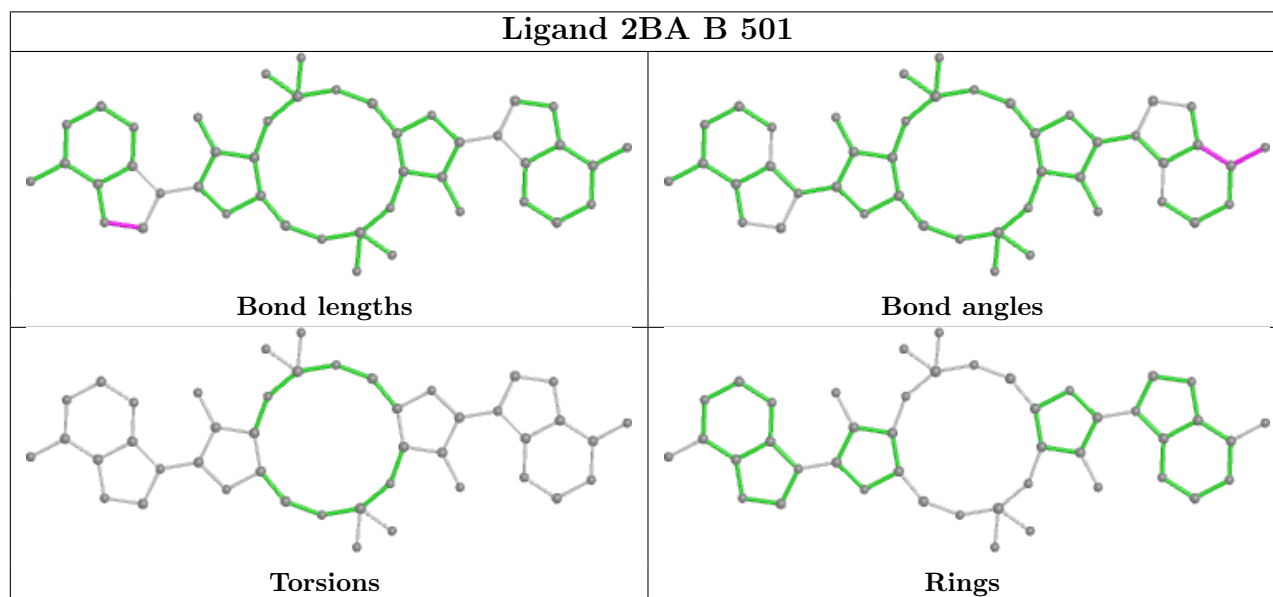
There are no torsion outliers.

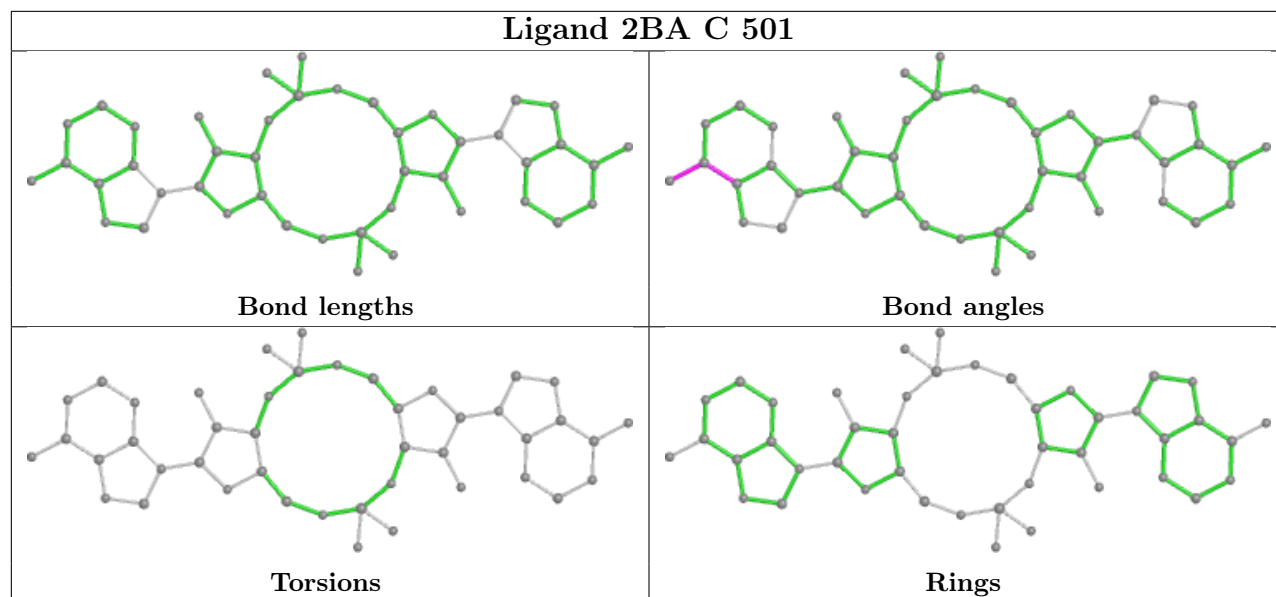
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	2BA	2	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, 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	162/165 (98%)	0.09	13 (8%) <b>12</b> <b>17</b>	22, 35, 107, 148	0
1	B	155/165 (93%)	0.43	18 (11%) <b>4</b> <b>7</b>	25, 44, 107, 137	0
1	C	162/165 (98%)	0.23	15 (9%) <b>8</b> <b>12</b>	20, 38, 109, 140	0
1	D	162/165 (98%)	0.32	18 (11%) <b>5</b> <b>7</b>	18, 42, 103, 126	0
All	All	641/660 (97%)	0.26	64 (9%) <b>7</b> <b>10</b>	18, 39, 109, 148	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	229	GLY	8.5
1	B	243	SER	8.4
1	D	229	GLY	8.2
1	B	228	ASN	6.8
1	C	270	GLY	6.8
1	B	244	GLY	6.5
1	B	230	ARG	6.5
1	A	151	GLY	5.8
1	A	228	ASN	5.8
1	B	229	GLY	5.4
1	C	232	PHE	4.9
1	C	229	GLY	4.9
1	D	228	ASN	4.9
1	D	230	ARG	4.7
1	C	230	ARG	4.7
1	D	268	LYS	4.7
1	D	241	GLU	4.5
1	B	276	SER	4.5
1	B	235	TYR	4.4
1	D	226	ASP	4.2
1	D	242	ASN	4.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	C	231	SER	4.1
1	A	232	PHE	4.1
1	A	230	ARG	4.1
1	A	227	THR	4.1
1	A	231	SER	4.0
1	C	266	TYR	3.9
1	A	266	TYR	3.9
1	B	272	ILE	3.8
1	D	152	GLU	3.7
1	A	152	GLU	3.6
1	B	232	PHE	3.6
1	B	227	THR	3.5
1	C	153	LEU	3.4
1	C	226	ASP	3.3
1	A	153	LEU	3.2
1	B	242	ASN	3.2
1	C	152	GLU	3.2
1	B	266	TYR	3.1
1	D	269	LYS	3.1
1	C	154	GLY	3.1
1	D	243	SER	3.0
1	C	271	HIS	3.0
1	B	154	GLY	3.0
1	B	277	GLN	3.0
1	D	235	TYR	3.0
1	B	273	GLY	2.9
1	A	154	GLY	2.9
1	A	268	LYS	2.9
1	D	154	GLY	2.9
1	D	233	PRO	2.8
1	B	231	SER	2.8
1	D	232	PHE	2.7
1	D	153	LEU	2.5
1	C	228	ASN	2.4
1	D	227	THR	2.3
1	C	151	GLY	2.3
1	D	209	ARG	2.2
1	B	226	ASP	2.2
1	C	267	MET	2.2
1	C	269	LYS	2.2
1	D	213	ILE	2.2
1	B	279	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	226	ASP	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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

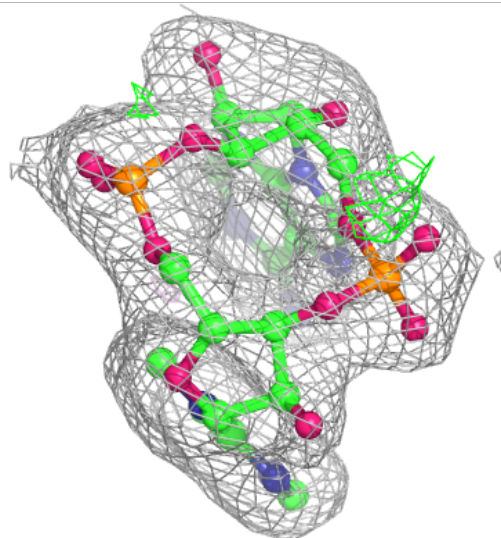
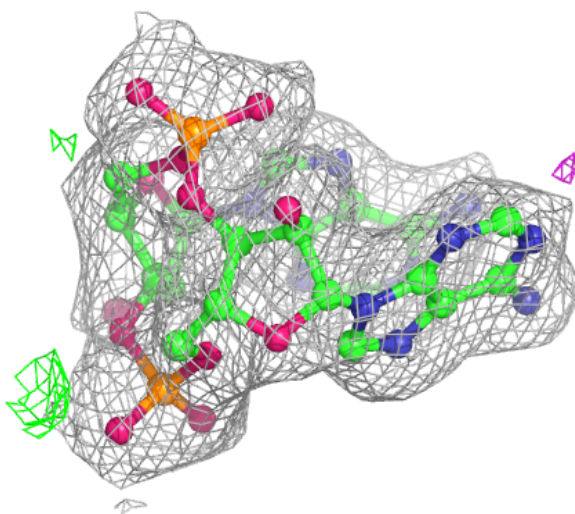
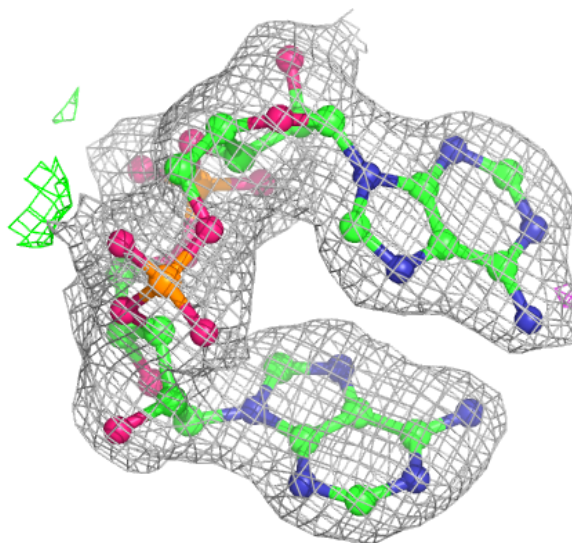
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

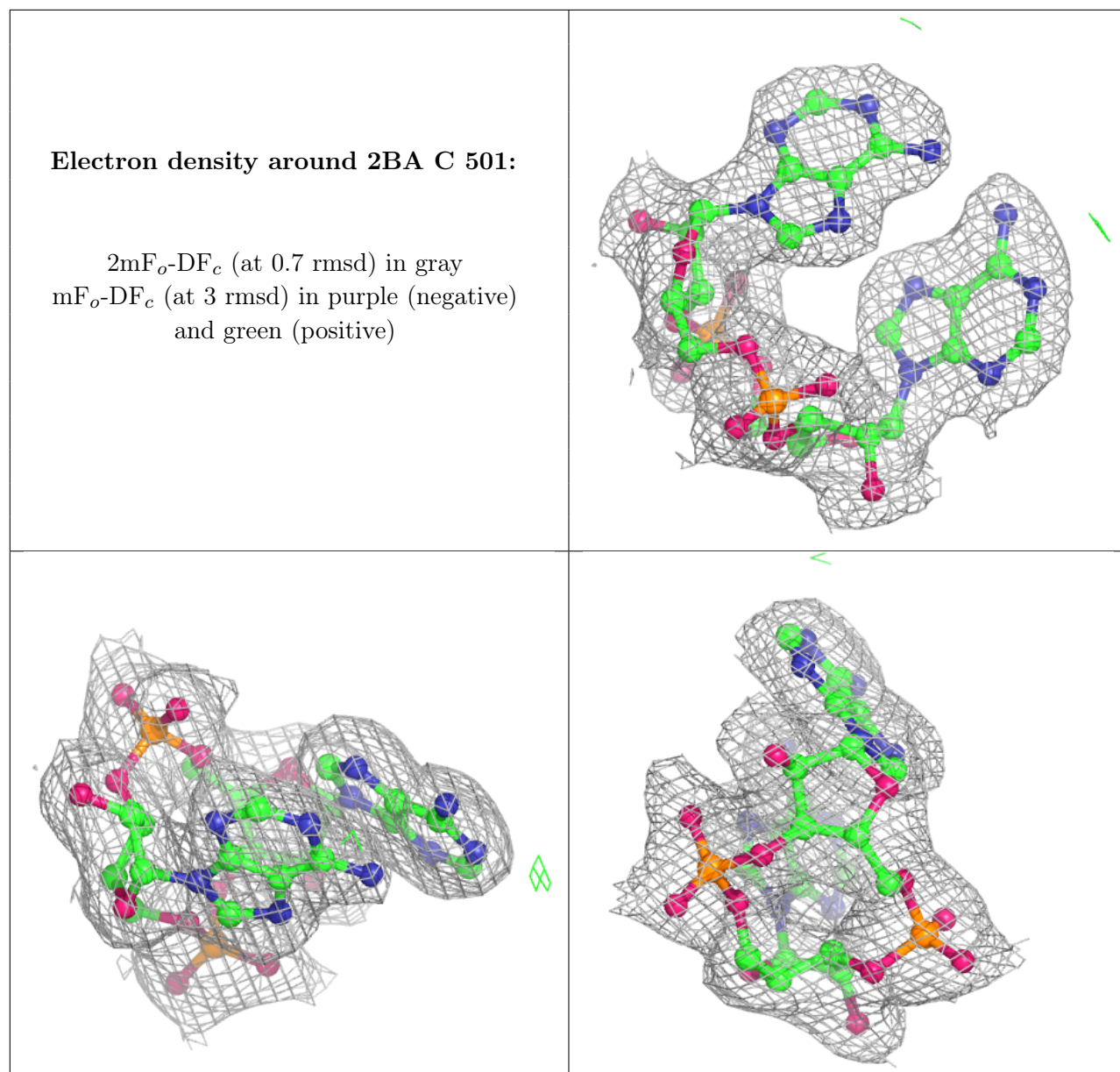
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	2BA	B	501	44/44	0.98	0.14	22,26,32,34	0
2	2BA	C	501	44/44	0.98	0.13	16,22,28,37	0

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 2BA B 501:**

$2mF_o-DF_c$  (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.