

# Full wwPDB X-ray Structure Validation Report (i)

#### Jan 28, 2021 – 12:07 AM GMT

PDB ID	:	6Y75
Title	:	BIL2 domain from T.thermophila BUBL1 locus (C1A-N143A)
Authors	:	Ilari, A.; Chiarini, V.
Deposited on		
Resolution	:	2.30  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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

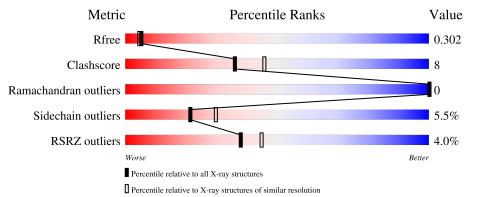
9	:	4.02b-467 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.16
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.16

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	5042(2.30-2.30)
Clashscore	141614	5643(2.30-2.30)
Ramachandran outliers	138981	5575(2.30-2.30)
Sidechain outliers	138945	5575(2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 <=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	А	153	85%	13%	•				
1	С	153	86%	12%	•				
2	В	150	84%	13%	•				
2	D	150	9%	15%	•				

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
3	PEG	А	501	-	-	Х	Х



# 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 5178 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Δ	153	Total	С	Ν	0	S	0	0	0
	А	100	1232	784	211	232	5	0	0	0
1	C	153	Total	С	Ν	0	S	0	0	0
		100	1232	784	211	232	5		0	U

• Molecule 1 is a protein called NAD(P)(+)-arginine ADP-ribosyltransferase.

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	CYS	$\operatorname{conflict}$	UNP $Q236S9$
A	143	ALA	ASN	$\operatorname{conflict}$	UNP $Q236S9$
С	1	ALA	CYS	$\operatorname{conflict}$	UNP $Q236S9$
С	143	ALA	ASN	$\operatorname{conflict}$	UNP $Q236S9$

• Molecule 2 is a protein called NAD(P)(+)-arginine ADP-ribosyltransferase.

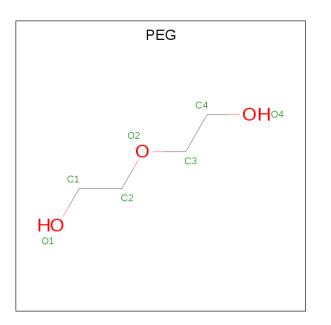
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
0	D	150	Total	С	Ν	Ο	S	0	0	0
	D	150	1211	770	208	228	5	0	0	0
0	п	150	Total	С	Ν	Ο	S	0	0	0
		150	1211	770	208	228	5	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	1	ALA	CYS	$\operatorname{conflict}$	UNP Q236S9
В	143	ALA	ASN	conflict	UNP $Q236S9$
D	1	ALA	CYS	conflict	UNP $Q236S9$
D	143	ALA	ASN	$\operatorname{conflict}$	UNP $Q236S9$

• Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).





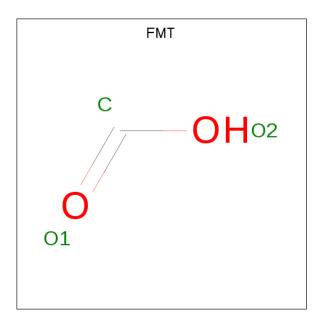
Mo	bl	Chain	Residues	Atoms	ZeroOcc	AltConf
3		А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 7  4  3 \end{array}$	0	0
3		В	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 7  4  3 \end{array}$	0	0

• Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total Zn 1 1	0	0
4	А	1	Total Zn 1 1	0	0
4	D	1	Total Zn 1 1	0	0
4	С	1	Total Zn 1 1	0	0

• Molecule 5 is FORMIC ACID (three-letter code: FMT) (formula:  $CH_2O_2$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 3  1  2 \end{array}$	0	0
5	В	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 3  1  2 \end{array}$	0	0

• Molecule 6 is water.

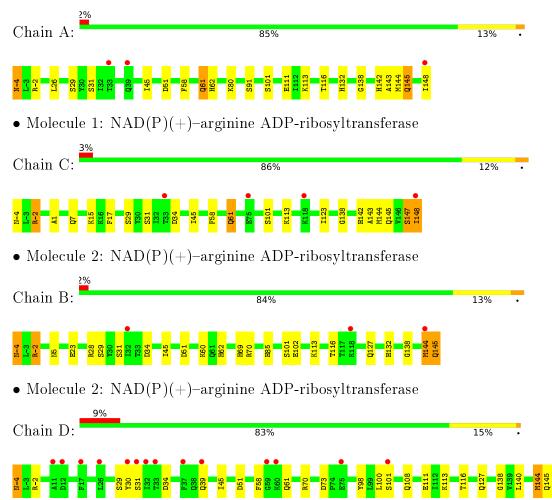
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	81	Total O 81 81	0	0
6	В	77	Total O 77 77	0	0
6	С	75	Total         O           75         75	0	0
6	D	35	$\begin{array}{cc} {\rm Total} & {\rm O} \\ 35 & 35 \end{array}$	0	0



# 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: NAD(P)(+)-arginine ADP-ribosyltransferase





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	76.82Å 67.61Å 82.44Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $114.58^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	47.57 - 2.30	Depositor
	47.52 - 2.30	EDS
% Data completeness	99.8 (47.57 - 2.30)	Depositor
(in resolution range)	99.8(47.52-2.30)	EDS
R <sub>merge</sub>	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.75 (at 2.29 \text{\AA})$	Xtriage
Refinement program	REFMAC $5.8.0258$	Depositor
$R, R_{free}$	0.254 , $0.302$	Depositor
It, It free	0.254 , $0.302$	DCC
$R_{free}$ test set	1662 reflections $(4.84\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	32.2	Xtriage
Anisotropy	0.143	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.31, $33.0$	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.50, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	5178	wwPDB-VP
Average B, all atoms $(Å^2)$	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 14.96% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: ZN, PEG, FMT

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	
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.26	0/1259	0.57	0/1701
1	С	0.26	0/1259	0.57	0/1701
2	В	0.26	0/1238	0.61	0/1672
2	D	0.25	0/1238	0.57	0/1672
All	All	0.26	0/4994	0.58	0/6746

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 (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	А	1232	0	1209	22	0
1	С	1232	0	1209	20	0
2	В	1211	0	1184	26	1
2	D	1211	0	1184	16	0
3	А	7	0	10	4	0
3	В	7	0	10	0	0
4	А	1	0	0	0	0
4	В	1	0	0	0	0
4	С	1	0	0	0	1



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1	0	0	0	0
5	В	6	0	2	0	0
6	А	81	0	0	8	0
6	В	77	0	0	7	0
6	С	75	0	0	3	0
6	D	35	0	0	2	0
All	All	5178	0	4808	78	1

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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 8.

All (78) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A 4 1	A 4 5 55 D	Interatomic	Clash
Atom-1	Atom-2	${ m distance}~({ m \AA})$	overlap (Å)
1:C:-2:ARG:HH11	1:C:-2:ARG:HG2	1.33	0.90
2:B:5:ASN:HD22	1:C:7:GLN:HE21	1.22	0.87
2:B:-4:ASN:OD1	2:B:-2:ARG:HD3	1.78	0.82
1:C:-2:ARG:HG2	1:C:-2:ARG:NH1	2.02	0.71
2:D:30:TYR:CE2	2:D:100:LEU:CD2	2.75	0.69
2:B:5:ASN:HA	1:C:17:PHE:CZ	2.29	0.68
2:B:145:GLN:HE21	2:B:145:GLN:HA	1.58	0.66
2:D:30:TYR:CE2	2:D:100:LEU:HD21	2.32	0.65
2:B:5:ASN:ND2	1:C:7:GLN:HE21	1.92	0.65
1:A:132:HIS:HE1	3:A:501:PEG:O2	1.80	0.65
1:A:61:GLN:HG2	6:A:603:HOH:O	2.01	0.60
1:C:142:HIS:HD2	1:C:143:ALA:O	1.84	0.59
2:B:102:GLU:HA	6:B:606:HOH:O	2.02	0.58
1:C:31:SER:HB2	6:C:448:HOH:O	2.03	0.57
1:A:145:GLN:HB2	1:A:148:ILE:HG13	1.86	0.57
2:B:70:ARG:HD2	6:B:609:HOH:O	2.05	0.56
1:C:-2:ARG:HD3	1:C:148:ILE:HG21	1.88	0.56
2:B:145:GLN:CA	2:B:145:GLN:HE21	2.15	0.56
2:B:-4:ASN:OD1	2:B:-2:ARG:CD	2.51	0.56
1:A:61:GLN:HG3	6:A:664:HOH:O	2.06	0.54
2:D:30:TYR:HD2	2:D:140:LEU:HD22	1.73	0.54
1:C:147:SER:O	1:C:148:ILE:C	2.46	0.54
1:A:148:ILE:HG12	6:A:666:HOH:O	2.07	0.54
2:B:132:HIS:HE1	6:B:661:HOH:O	1.92	0.53
1:A:132:HIS:HE1	3:A:501:PEG:H12	1.74	0.53
2:D:70:ARG:HD2	6:D:402:HOH:O	2.09	0.51
1:A:132:HIS:CE1	3:A:501:PEG:O2	2.62	0.51



Continued from prev		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:132:HIS:CE1	3:A:501:PEG:H12	2.45	0.51
1:A:-4:ASN:N	1:A:-4:ASN:HD22	2.10	0.49
2:D:30:TYR:HE2	2:D:100:LEU:CD2	2.23	0.49
1:A:132:HIS:HD2	6:A:638:HOH:O	1.95	0.49
2:B:31:SER:OG	2:B:34:ASP:HB2	2.12	0.48
1:A:111:GLU:HG2	1:A:113:LYS:HE3	1.95	0.48
2:B:5:ASN:HB3	1:C:17:PHE:CE2	2.50	0.47
1:A:-2:ARG:HE	1:A:148:ILE:HB	1.79	0.47
1:A:-4:ASN:HD21	1:A:-2:ARG:NH1	2.12	0.47
1:C:58:PHE:CE2	1:C:61:GLN:HB3	2.49	0.47
2:B:62:HIS:HE1	6:C:441:HOH:O	1.98	0.47
2:D:58:PHE:CE2	2:D:61:GLN:HG3	2.50	0.47
1:A:101:SER:HA	1:A:138:GLY:O	2.15	0.46
1:A:80:LYS:HG2	1:A:91:SER:HB2	1.98	0.46
1:C:101:SER:HA	1:C:138:GLY:O	2.16	0.46
1:C:-2:ARG:CD	1:C:148:ILE:HG12	2.46	0.46
2:B:101:SER:HA	2:B:138:GLY:O	2.16	0.45
2:B:60:LYS:HE2	6:B:662:HOH:O	2.16	0.45
2:B:145:GLN:NE2	2:B:145:GLN:HA	2.29	0.45
2:D:-4:ASN:N	2:D:-4:ASN:HD22	2.15	0.45
2:B:60:LYS:CE	6:B:662:HOH:O	2.65	0.44
1:C:142:HIS:CD2	1:C:143:ALA:O	2.69	0.44
1:A:111:GLU:CG	1:A:113:LYS:HE3	2.49	0.43
1:A:142:HIS:HD2	1:A:143:ALA:O	2.00	0.43
1:A:62:HIS:HE1	6:A:669:HOH:O	2.01	0.43
2:B:-4:ASN:N	2:B:-4:ASN:HD22	2.15	0.43
2:B:127:GLN:HG2	2:B:144:MET:O	2.19	0.43
2:D:-4:ASN:OD1	2:D:-2:ARG:HG3	2.19	0.43
2:D:39:GLN:HG3	6:D:401:HOH:O	2.19	0.42
1:C:31:SER:OG	1:C:34:ASP:HB2	2.19	0.42
2:B:102:GLU:CA	6:B:606:HOH:O	2.63	0.42
6:A:633:HOH:O	2:B:85:HIS:HE1	2.02	0.42
2:D:73:ASP:HA	2:D:98:TYR:O	2.20	0.42
2:D:31:SER:OG	2:D:34:ASP:HB2	2.20	0.42
1:A:58:PHE:CE2	1:A:61:GLN:HB3	2.55	0.42
1:C:1:ALA:HB3	1:C:123:ILE:HD12	2.02	0.42
1:A:31:SER:HA	6:A:656:HOH:O	2.20	0.41
2:D:127:GLN:HG2	2:D:144:MET:O	2.20	0.41
2:B:51:ASP:O	2:B:116:THR:HA	2.21	0.41
1:A:113:LYS:HD2	6:A:616:HOH:O	2.20	0.41
2:B:5:ASN:CB	1:C:17:PHE:CZ	3.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:101:SER:HA	2:D:138:GLY:O	2.19	0.41
2:D:111:GLU:HG2	2:D:113:LYS:HE3	2.03	0.41
2:D:51:ASP:O	2:D:116:THR:HA	2.20	0.41
2:B:5:ASN:HB3	1:C:17:PHE:CZ	2.56	0.41
2:B:28:ARG:NE	6:B:606:HOH:O	2.51	0.41
1:C:15:LYS:HE3	6:C:460:HOH:O	2.20	0.41
1:C:-2:ARG:HD3	1:C:148:ILE:HG12	2.02	0.40
2:B:-4:ASN:OD1	2:B:-2:ARG:HG2	2.21	0.40
2:D:98:TYR:CE1	2:D:108:GLN:HB2	2.57	0.40
1:A:51:ASP:O	1:A:116:THR:HA	2.22	0.40

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All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:23:GLU:OE1	4:C:301:ZN:ZN[2_647]	1.69	0.51

### 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	Perce	ntiles
1	А	151/153~(99%)	148 (98%)	3(2%)	0	100	100
1	С	151/153~(99%)	148 (98%)	3 (2%)	0	100	100
2	В	148/150~(99%)	143~(97%)	5(3%)	0	100	100
2	D	148/150~(99%)	145~(98%)	3 (2%)	0	100	100
All	All	598/606~(99%)	584 (98%)	14 (2%)	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	А	138/138~(100%)	131~(95%)	7~(5%)	24 33
1	С	138/138~(100%)	128~(93%)	10 (7%)	14 18
2	В	135/135~(100%)	127 (94%)	8 (6%)	19 27
2	D	135/135~(100%)	130~(96%)	5 (4%)	34 48
All	All	546/546~(100%)	516~(94%)	30 (6%)	21 30

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	-4	ASN
1	А	26	LEU
1	А	29	SER
1	A A A A	45	ILE
1	А	61	GLN
1	A	144	MET
1	А	145	GLN
2	В	-4	ASN
2	В	-2	ARG
2	В	29	SER
2	В	45	ILE
2	В	69	HIS
2	В	113	LYS
$\begin{array}{c} 2\\ 2 \end{array}$	В	144	MET
2	В	145	GLN
1	С	-4	ASN
1	С	-2	ARG
1	С	29	SER
1	C C C C C C C C C	45	ILE
1	С	61	GLN
1	С	113	LYS
1	С	144	MET
1	С	145	GLN
1	C	147	SER



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Mol	Chain	Res	Type
1	С	148	ILE
2	D	-4	ASN
2	D	29	SER
2	D	45	ILE
2	D	144	MET
2	D	145	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	-4	ASN
1	А	40	ASN
1	А	52	GLN
1	А	85	HIS
1	А	127	GLN
1	А	130	ASN
1	A A A A A	131	ASN
1	А	132	HIS
1	А	142	HIS
1	А	145	GLN
2	В	52	GLN
$\begin{array}{c} 2\\ 2 \end{array}$	В	62	HIS
	В	85	HIS
2	В	131	ASN
2	В	132	HIS
2	В	142	HIS
2	В	145	GLN
1	C C C C C C D	7	GLN
1	С	52	GLN
1	С	85	HIS
1	С	127	GLN
1	С	131	ASN
1	С	142	HIS
2		7	GLN
2	D	52	GLN
2	D	85	HIS
2	D	127	GLN
2	D	131	ASN
$\frac{2}{2}$	D	132	HIS
2	D	142	HIS



#### 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)

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				
	туре	Cham	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	FMT	В	504	-	0,2,2	0.00	-	$_{0,1,1}$	0.00	-
3	PEG	В	501	-	$6,\!6,\!6$	0.12	0	$5,\!5,\!5$	0.16	0
5	FMT	В	502	-	0,2,2	0.00	-	$_{0,1,1}$	0.00	-
3	PEG	А	501	-	$6,\!6,\!6$	0.20	0	$5,\!5,\!5$	0.13	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	PEG	В	501	-	-	1/4/4/4	-
3	PEG	А	501	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.



There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	501	PEG	O1-C1-C2-O2
3	А	501	PEG	C4-C3-O2-C2
3	В	501	PEG	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	А	501	PEG	4	0

#### 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,  $95^{th}$  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 $>$	$\# RSRZ {>}2$	$\mathbf{OWAB}(\mathbf{A}^2)$	$\mathbf{Q}{<}0.9$
1	А	153/153~(100%)	0.29	3 (1%) 65 71	18, 29, 46, 56	0
1	С	153/153~(100%)	0.30	4 (2%) 56 63	21, 32, 51, 69	0
2	В	150/150~(100%)	0.29	3 (2%) 65 71	20, 29, 47, 72	0
2	D	150/150~(100%)	0.59	14 (9%) 8 11	25, 38, 63, 74	0
All	All	606/606~(100%)	0.37	24 (3%) 38 45	18, 32, 54, 74	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	32	ILE	4.5
1	С	148	ILE	4.5
1	А	148	ILE	4.0
2	D	60	LYS	3.8
2	D	39	GLN	3.7
2	В	144	MET	3.2
2	D	31	SER	2.9
2	В	118	LYS	2.8
1	А	39	GLN	2.7
2	D	11	ALA	2.7
1	А	33	THR	2.7
2	В	32	ILE	2.7
1	С	118	LYS	2.6
1	С	33	THR	2.6
2	D	37	PHE	2.4
1	С	75	GLU	2.4
2	D	30	TYR	2.3
2	D	75	GLU	2.2
2	D	26	LEU	2.2
2	D	12	ASP	2.2
2	D	17	PHE	2.1



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Mol	Chain	Res	Type	RSRZ
2	D	33	THR	2.1
2	D	101	SER	2.0
2	D	59	GLY	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.

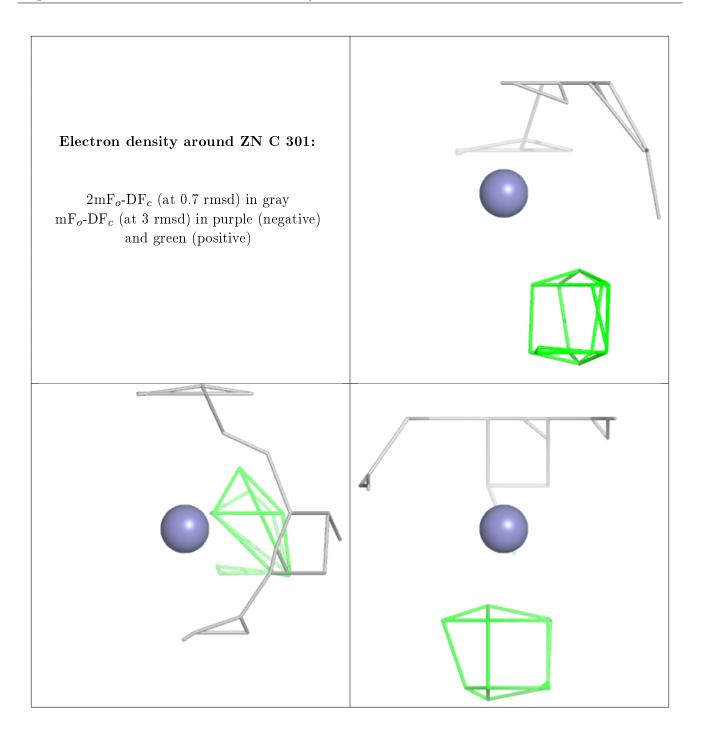
### 6.4 Ligands (i)

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,  $95^{th}$  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.

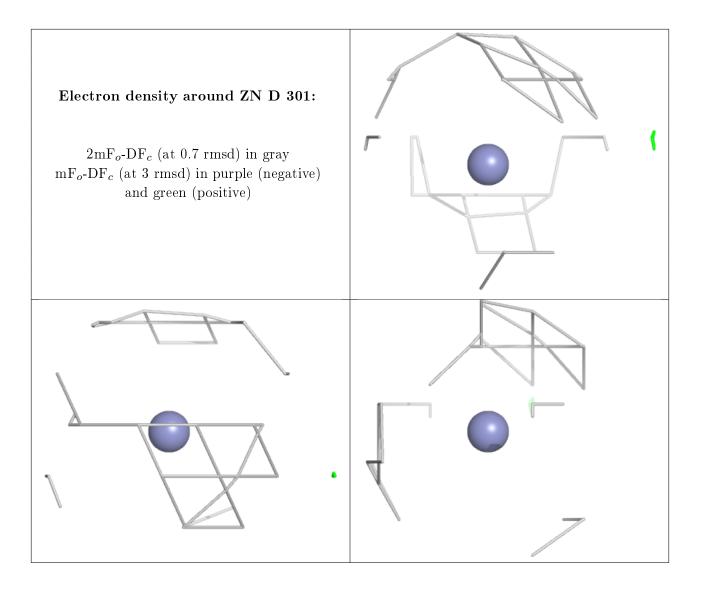
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{\AA}^2)$	Q<0.9
3	PEG	А	501	7/7	0.43	0.41	$48,\!54,\!61,\!62$	0
5	FMT	В	504	3/3	0.75	0.23	$56,\!56,\!56,\!56$	0
3	PEG	В	501	7/7	0.83	0.33	$58,\!64,\!70,\!72$	0
5	FMT	В	502	3/3	0.85	0.12	$52,\!52,\!54,\!55$	0
4	ZN	С	301	1/1	0.97	0.10	$33,\!33,\!33,\!33$	0
4	ZN	D	301	1/1	0.99	0.08	$33,\!33,\!33,\!33$	0
4	ZN	А	502	1/1	0.99	0.09	$29,\!29,\!29,\!29$	0
4	ZN	В	503	1/1	1.00	0.08	$36,\!36,\!36,\!36$	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.

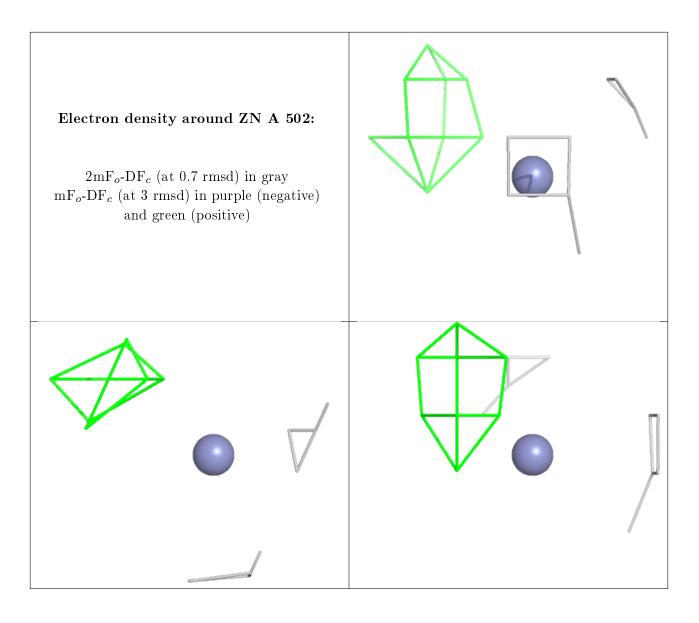




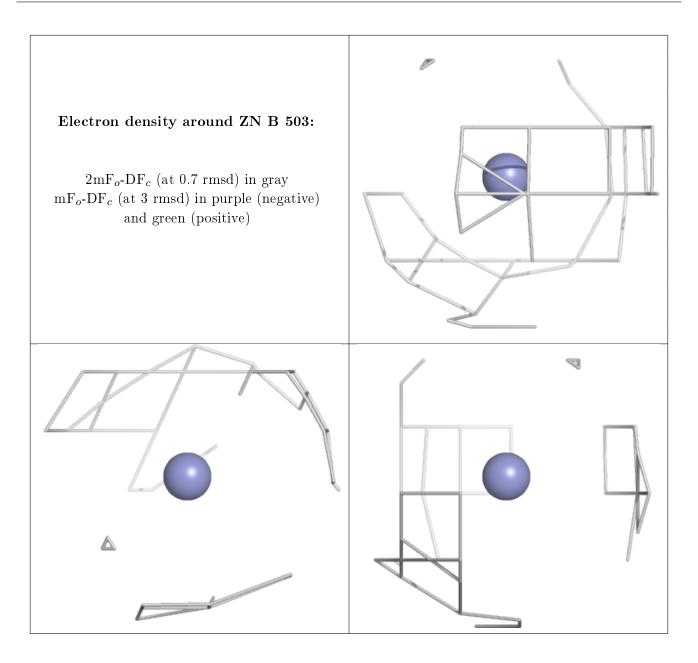












## 6.5 Other polymers (i)

There are no such residues in this entry.

