



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 2, 2023 – 07:53 AM EDT

PDB ID : 3HUO  
Title : X-ray crystallographic structure of CTX-M-9 S70G in complex with benzylpenicillin  
Authors : Delmas, J.; Leyssene, D.; Dubois, D.; Robin, F.; Bonnet, R.  
Deposited on : 2009-06-15  
Resolution : 1.50 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

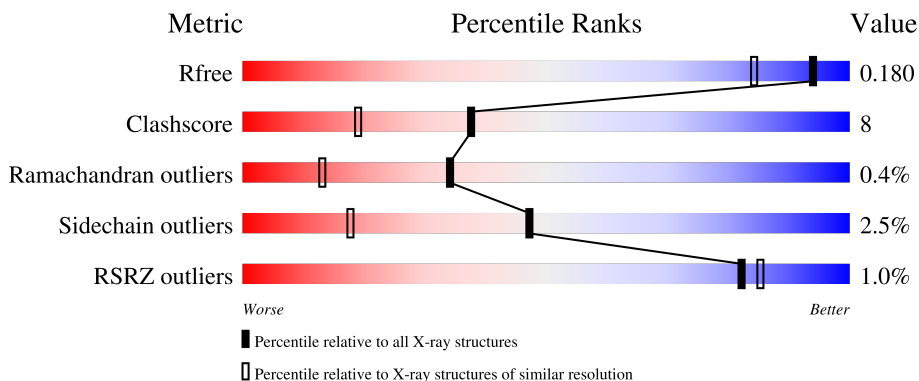
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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	263	 89% 9% .
1	B	263	 91% 6% ..

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4907 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.

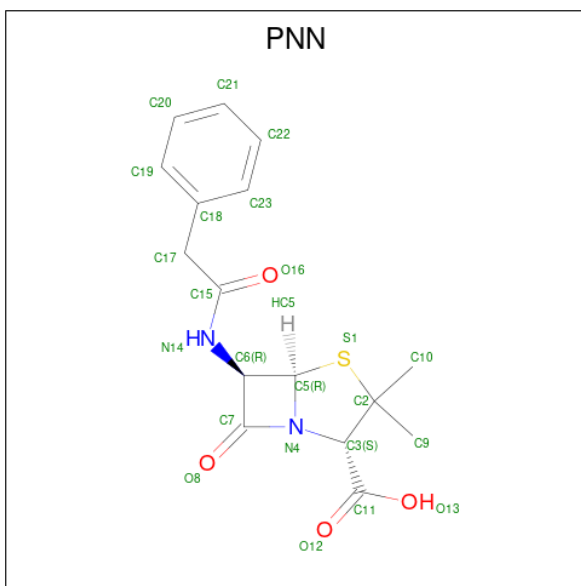
- Molecule 1 is a protein called CTX-M-9 extended-spectrum beta-lactamase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	262	Total	C	N	O	S	0	19	0
			2053	1279	369	398	7			
1	B	260	Total	C	N	O	S	0	16	0
			2025	1266	359	392	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	70	GLY	SER	engineered mutation	UNP Q9L5C8
B	70	GLY	SER	engineered mutation	UNP Q9L5C8

- Molecule 2 is PENICILLIN G (three-letter code: PNN) (formula: C<sub>16</sub>H<sub>18</sub>N<sub>2</sub>O<sub>4</sub>S).



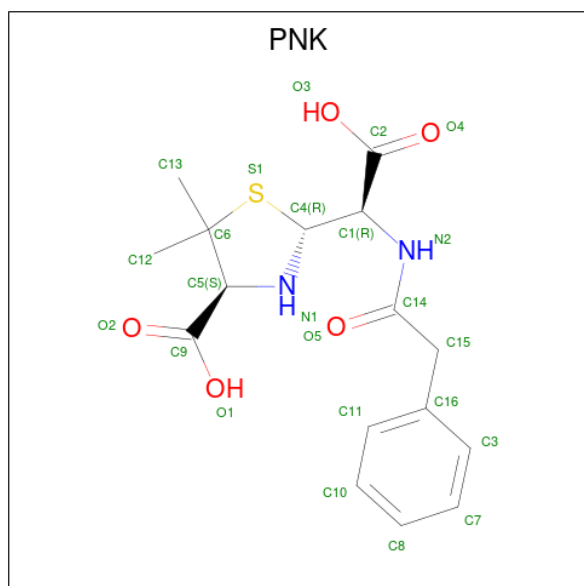
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	Total	C	N	O	S	0	0
			23	16	2	4	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			23	16	2	4	1		
2	A	1	Total	C	N	O	S	0	0
			23	16	2	4	1		
2	A	1	Total	C	N	O	S	0	0
			23	16	2	4	1		
2	B	1	Total	C	N	O	S	0	0
			23	16	2	4	1		

- Molecule 3 is (2R,4S)-2-[(R)-carboxy[(phenylacetyl)amino]methyl]-5,5-dimethyl-1,3-thiazolidine-4-carboxylic acid (three-letter code: PNK) (formula: C<sub>16</sub>H<sub>20</sub>N<sub>2</sub>O<sub>5</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			24	16	2	5	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	327	Total	O	0	7
			334	334		
4	B	354	Total	O	0	2
			356	356		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	45.20Å 106.78Å 47.65Å 90.00° 101.69° 90.00°	Depositor
Resolution (Å)	34.08 – 1.50 34.08 – 1.50	Depositor EDS
% Data completeness (in resolution range)	99.3 (34.08-1.50) 99.3 (34.08-1.50)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.57 (at 1.50Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.148 , 0.181 0.147 , 0.180	Depositor DCC
$R_{free}$ test set	3483 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	8.6	Xtrriage
Anisotropy	0.011	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 52.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4907	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	11.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.25% 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: PNN, PNK

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	0.62	0/2133	0.57	0/2896
1	B	0.65	0/2099	0.57	0/2850
All	All	0.64	0/4232	0.57	0/5746

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	2053	0	2116	34	0
1	B	2025	0	2092	27	0
2	A	92	0	68	6	0
2	B	23	0	17	4	0
3	B	24	0	18	0	0
4	A	334	0	0	16	0
4	B	356	0	0	12	0
All	All	4907	0	4311	66	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 8.

All (66) 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:256[A]:ARG:HH21	1:A:256[A]:ARG:HG2	1.23	1.02
1:B:99:PRO:HG3	1:B:113[A]:VAL:CG2	1.99	0.93
1:B:99:PRO:HG3	1:B:113[A]:VAL:HG21	1.55	0.89
1:A:96[A]:GLU:OE2	1:A:98[A]:LYS:HD3	1.74	0.86
1:A:256[A]:ARG:HG2	1:A:256[A]:ARG:NH2	1.98	0.76
1:A:96[A]:GLU:CD	1:A:98[A]:LYS:HD3	2.06	0.75
2:A:300:PNN:H21	4:A:424:HOH:O	1.88	0.74
2:B:301:PNN:H21	4:B:384:HOH:O	1.89	0.72
1:B:99:PRO:CG	1:B:113[A]:VAL:CG2	2.68	0.71
1:A:188[B]:GLN:HG3	4:A:627:HOH:O	1.92	0.70
1:A:237[A]:SER:OG	2:A:300:PNN:HC93	1.95	0.66
1:A:57:VAL:O	1:A:59[B]:LEU:HD13	1.96	0.65
1:B:252:PRO:HB2	1:B:256:ARG:CD	2.26	0.65
1:B:252:PRO:HB2	1:B:256:ARG:HD2	1.79	0.65
1:A:59[B]:LEU:HD11	4:A:335:HOH:O	1.96	0.64
1:A:256[A]:ARG:HE	1:A:290:LEU:HD13	1.62	0.64
1:B:75[B]:MET:HG2	4:B:328:HOH:O	2.01	0.59
1:B:99:PRO:N	1:B:113[A]:VAL:HG23	2.18	0.58
1:B:256:ARG:NH2	4:B:571:HOH:O	2.31	0.58
1:B:99:PRO:CD	1:B:113[A]:VAL:HG23	2.34	0.58
1:B:99:PRO:CD	1:B:113[A]:VAL:CG2	2.82	0.57
1:A:96[A]:GLU:HG3	4:A:530[A]:HOH:O	2.03	0.57
1:B:99:PRO:CG	1:B:113[A]:VAL:HG21	2.31	0.56
1:A:103:VAL:H	1:A:106:ASN:ND2	2.05	0.55
1:A:111[B]:LYS:HE3	4:A:640:HOH:O	2.07	0.54
1:A:188[B]:GLN:CG	4:A:627:HOH:O	2.53	0.54
1:A:103:VAL:H	1:A:106:ASN:HD21	1.56	0.53
1:B:186[A]:MET:CE	4:B:328:HOH:O	2.56	0.53
1:A:256[A]:ARG:CZ	4:A:310:HOH:O	2.59	0.51
1:A:96[A]:GLU:CG	1:A:98[A]:LYS:HD3	2.41	0.51
1:B:99:PRO:HG3	1:B:113[A]:VAL:HG22	1.89	0.50
1:B:284:ARG:NH2	4:B:455:HOH:O	2.36	0.50
1:A:67:PRO:HD3	4:A:426:HOH:O	2.11	0.50
1:A:96[B]:GLU:HG2	4:A:530[B]:HOH:O	2.10	0.49
1:A:96[B]:GLU:CG	4:A:530[B]:HOH:O	2.61	0.49
2:B:301:PNN:C21	4:B:384:HOH:O	2.57	0.48
1:B:252:PRO:HB2	1:B:256:ARG:HD3	1.95	0.48
1:B:186[A]:MET:HE3	4:B:328:HOH:O	2.14	0.47
1:A:256[A]:ARG:NH1	4:A:518:HOH:O	2.47	0.47
1:B:237[A]:SER:OG	2:B:301:PNN:HC93	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:271[A]:ASN:OD1	4:B:460:HOH:O	2.21	0.46
1:A:256[A]:ARG:NH2	1:A:256[A]:ARG:CG	2.68	0.46
1:B:88[A]:LYS:NZ	4:B:467:HOH:O	2.39	0.45
1:B:237[B]:SER:HB2	2:B:301:PNN:HC3	1.98	0.45
1:B:269:GLN:HG2	4:B:477:HOH:O	2.16	0.45
1:A:91:LEU:HB3	1:A:120:ALA:HB2	1.99	0.45
1:B:98:LYS:HB2	1:B:98:LYS:HE3	1.65	0.45
1:A:26:THR:HG22	1:A:31:GLN:HG3	2.00	0.44
1:A:197:HIS:HB2	2:A:303:PNN:HC92	2.00	0.44
1:A:259:LEU:HD11	1:A:290:LEU:HD11	2.00	0.44
1:B:75[B]:MET:HG3	1:B:160:PHE:CE2	2.53	0.44
1:B:103:VAL:H	1:B:106:ASN:HD21	1.66	0.43
1:A:197:HIS:HB2	2:A:303:PNN:C9	2.48	0.43
2:A:303:PNN:HC92	2:A:303:PNN:O12	2.18	0.43
2:A:300:PNN:C21	4:A:424:HOH:O	2.59	0.42
1:A:256[A]:ARG:NH1	4:A:310:HOH:O	2.53	0.42
1:B:271[A]:ASN:CG	4:B:460:HOH:O	2.58	0.41
1:A:186[A]:MET:CE	4:A:350:HOH:O	2.67	0.41
1:A:111[A]:LYS:HD2	4:A:640:HOH:O	2.20	0.41
1:B:276[B]:ARG:HG3	4:B:350:HOH:O	2.20	0.41
1:A:93:GLN:O	1:A:118:THR:HA	2.21	0.40
1:A:184:ARG:O	1:A:188[B]:GLN:HG3	2.21	0.40
1:A:98[B]:LYS:HD2	4:A:505:HOH:O	2.21	0.40
1:A:194:THR:HG21	1:A:249[B]:VAL:HG21	2.03	0.40
1:B:91:LEU:HB3	1:B:120:ALA:HB2	2.04	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	279/263 (106%)	274 (98%)	4 (1%)	1 (0%)	34 13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	275/263 (105%)	270 (98%)	4 (2%)	1 (0%)	34	13
All	All	554/526 (105%)	544 (98%)	8 (1%)	2 (0%)	34	13

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	103	VAL
1	B	103	VAL

### 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	219/204 (107%)	213 (97%)	6 (3%)	44	15
1	B	217/204 (106%)	210 (97%)	7 (3%)	39	10
All	All	436/408 (107%)	423 (97%)	13 (3%)	47	12

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	ASN
1	A	111[A]	LYS
1	A	111[B]	LYS
1	A	130	SER
1	A	227[A]	THR
1	A	227[B]	THR
1	B	88[A]	LYS
1	B	88[B]	LYS
1	B	106	ASN
1	B	130	SER
1	B	256	ARG
1	B	273	GLU
1	B	290	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	GLN
1	A	106	ASN
1	A	206	GLN
1	A	254	GLN
1	A	269	GLN
1	B	89	GLN
1	B	106	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](#)

6 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	PNN	A	302	-	25,25,25	1.68	4 (16%)	37,38,38	1.67	5 (13%)
2	PNN	A	303	-	25,25,25	1.87	6 (24%)	37,38,38	2.08	10 (27%)
2	PNN	B	301	-	25,25,25	1.28	3 (12%)	37,38,38	1.77	6 (16%)
2	PNN	A	300	-	25,25,25	1.25	3 (12%)	37,38,38	1.69	9 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	PNN	A	304	-	25,25,25	1.54	6 (24%)	37,38,38	1.93	9 (24%)
3	PNK	B	305	-	21,25,25	0.74	0	27,36,36	0.73	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
2	PNN	A	302	-	-	0/12/43/43	0/3/3/3
2	PNN	A	303	-	-	0/12/43/43	0/3/3/3
2	PNN	B	301	-	-	4/12/43/43	0/3/3/3
2	PNN	A	300	-	-	4/12/43/43	0/3/3/3
2	PNN	A	304	-	-	0/12/43/43	0/3/3/3
3	PNK	B	305	-	-	4/16/35/35	0/2/2/2

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	303	PNN	C2-S1	-4.65	1.75	1.85
2	A	302	PNN	C7-N4	-4.48	1.27	1.37
2	A	302	PNN	C2-S1	-4.28	1.76	1.85
2	B	301	PNN	C7-N4	-3.96	1.28	1.37
2	A	303	PNN	C7-N4	-3.87	1.29	1.37
2	A	300	PNN	C7-N4	-3.81	1.29	1.37
2	A	302	PNN	C5-S1	-3.81	1.75	1.81
2	A	303	PNN	C5-S1	-3.63	1.75	1.81
2	A	304	PNN	C2-S1	-3.59	1.78	1.85
2	A	304	PNN	C7-N4	-3.38	1.30	1.37
2	B	301	PNN	C2-S1	-3.16	1.78	1.85
2	A	300	PNN	C2-S1	-3.07	1.79	1.85
2	A	303	PNN	C6-C7	-3.05	1.46	1.54
2	A	304	PNN	C5-S1	-2.96	1.76	1.81
2	A	304	PNN	C6-C7	-2.90	1.47	1.54
2	A	303	PNN	C3-N4	-2.76	1.41	1.46
2	A	304	PNN	C3-N4	-2.55	1.41	1.46
2	A	302	PNN	C6-C7	-2.47	1.48	1.54
2	A	300	PNN	C5-S1	-2.41	1.77	1.81
2	A	303	PNN	C5-N4	-2.37	1.42	1.47
2	B	301	PNN	C6-C7	-2.10	1.48	1.54
2	A	304	PNN	C5-N4	-2.06	1.42	1.47

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	303	PNN	C5-N4-C3	6.23	125.02	117.26
2	A	304	PNN	C5-N4-C3	5.99	124.73	117.26
2	A	303	PNN	S1-C5-N4	-5.78	97.34	105.10
2	A	302	PNN	S1-C5-N4	-5.75	97.37	105.10
2	A	303	PNN	C2-C3-C11	-4.98	105.12	112.86
2	A	304	PNN	S1-C5-N4	-4.92	98.49	105.10
2	B	301	PNN	S1-C5-N4	-4.86	98.56	105.10
2	A	304	PNN	C2-C3-C11	-4.79	105.41	112.86
2	B	301	PNN	C6-C5-N4	-4.71	81.91	87.98
2	A	300	PNN	C6-C5-N4	-4.53	82.14	87.98
2	A	300	PNN	C5-N4-C7	4.48	99.71	93.93
2	B	301	PNN	C5-N4-C7	4.28	99.45	93.93
2	A	302	PNN	C5-N4-C3	4.18	122.46	117.26
2	A	300	PNN	S1-C5-N4	-3.83	99.95	105.10
2	A	302	PNN	C6-C5-N4	-3.37	83.64	87.98
2	B	301	PNN	C5-N4-C3	3.28	121.35	117.26
2	A	303	PNN	C2-S1-C5	3.18	101.05	94.08
2	A	302	PNN	C5-N4-C7	3.15	97.99	93.93
2	A	304	PNN	C5-C6-N14	-3.00	111.72	118.27
2	A	304	PNN	C2-S1-C5	2.83	100.28	94.08
2	A	303	PNN	C5-C6-N14	-2.63	112.53	118.27
2	A	303	PNN	C5-N4-C7	2.62	97.31	93.93
2	A	303	PNN	C6-C5-N4	-2.61	84.62	87.98
2	A	300	PNN	C5-N4-C3	2.61	120.51	117.26
2	A	300	PNN	C2-C3-C11	2.56	116.86	112.86
2	A	300	PNN	O13-C11-C3	2.46	120.41	112.55
2	B	301	PNN	O13-C11-C3	2.43	120.31	112.55
2	A	304	PNN	C6-C5-N4	-2.35	84.96	87.98
2	A	304	PNN	O8-C7-C6	-2.32	129.82	136.31
2	B	301	PNN	O8-C7-N4	2.27	134.95	131.75
2	A	303	PNN	C6-N14-C15	-2.25	117.52	121.83
2	A	304	PNN	C5-N4-C7	2.24	96.82	93.93
2	A	302	PNN	O13-C11-C3	2.17	119.49	112.55
2	A	303	PNN	O13-C11-C3	2.17	119.48	112.55
2	A	300	PNN	O8-C7-C6	-2.16	130.26	136.31
2	A	300	PNN	O8-C7-N4	2.11	134.73	131.75
2	A	300	PNN	C17-C18-C19	-2.07	117.93	120.89
2	A	304	PNN	O13-C11-C3	2.07	119.15	112.55
2	A	303	PNN	O8-C7-C6	-2.02	130.66	136.31

There are no chirality outliers.

All (12) torsion outliers are listed below:

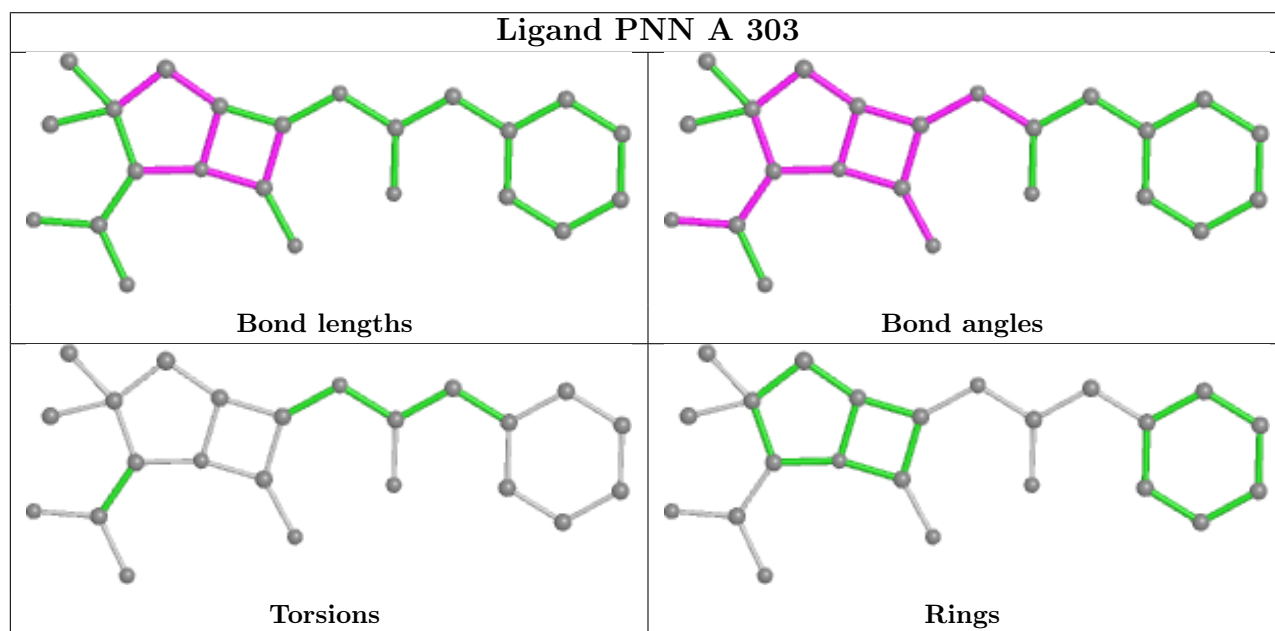
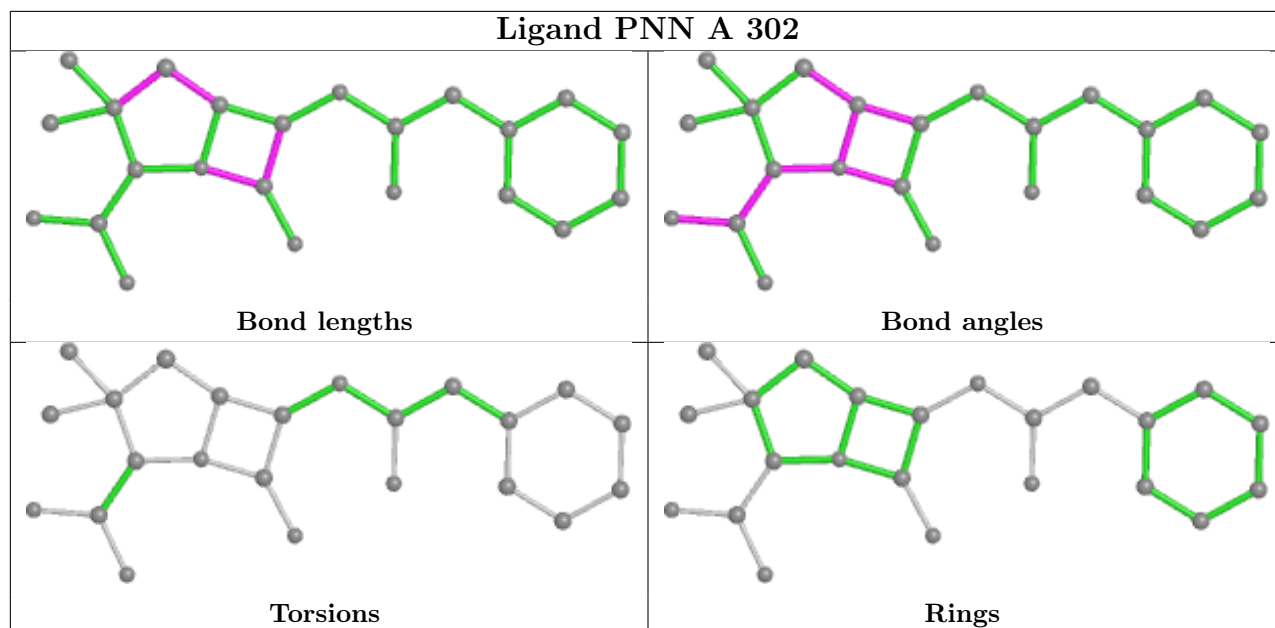
Mol	Chain	Res	Type	Atoms
2	A	300	PNN	C15-C17-C18-C19
2	A	300	PNN	C15-C17-C18-C23
2	B	301	PNN	C15-C17-C18-C19
2	B	301	PNN	C15-C17-C18-C23
3	B	305	PNK	C4-C1-N2-C14
3	B	305	PNK	C4-C1-C2-O4
3	B	305	PNK	C2-C1-N2-C14
2	A	300	PNN	O16-C15-C17-C18
2	B	301	PNN	O16-C15-C17-C18
3	B	305	PNK	C4-C1-C2-O3
2	A	300	PNN	N14-C15-C17-C18
2	B	301	PNN	N14-C15-C17-C18

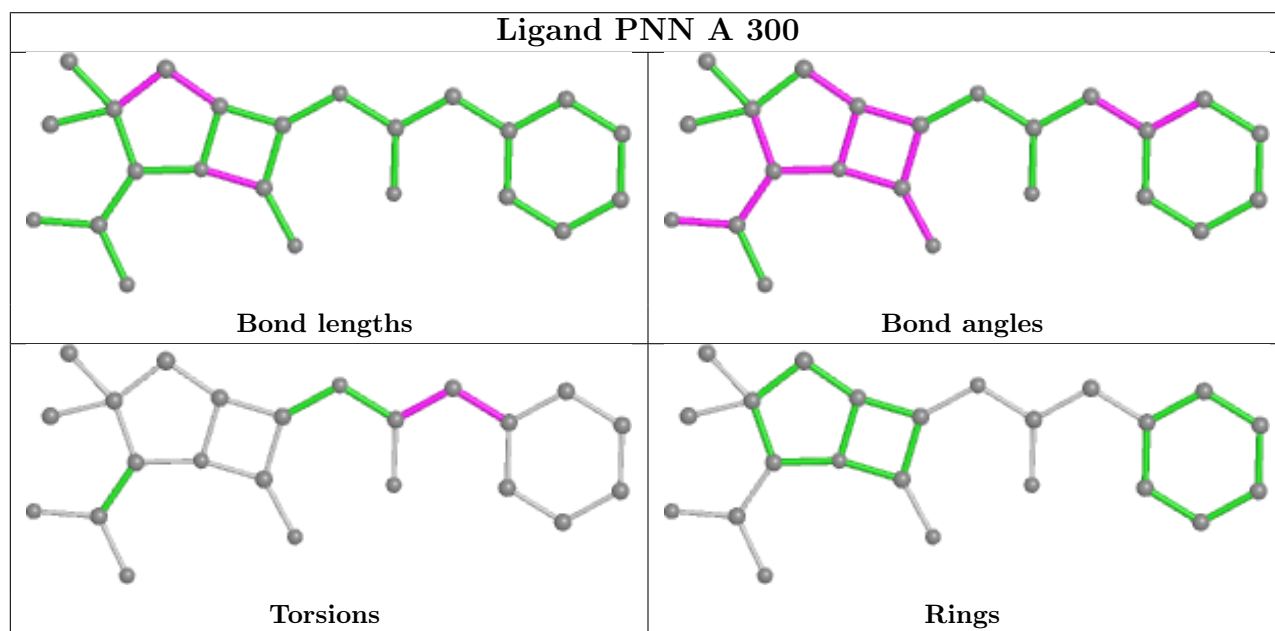
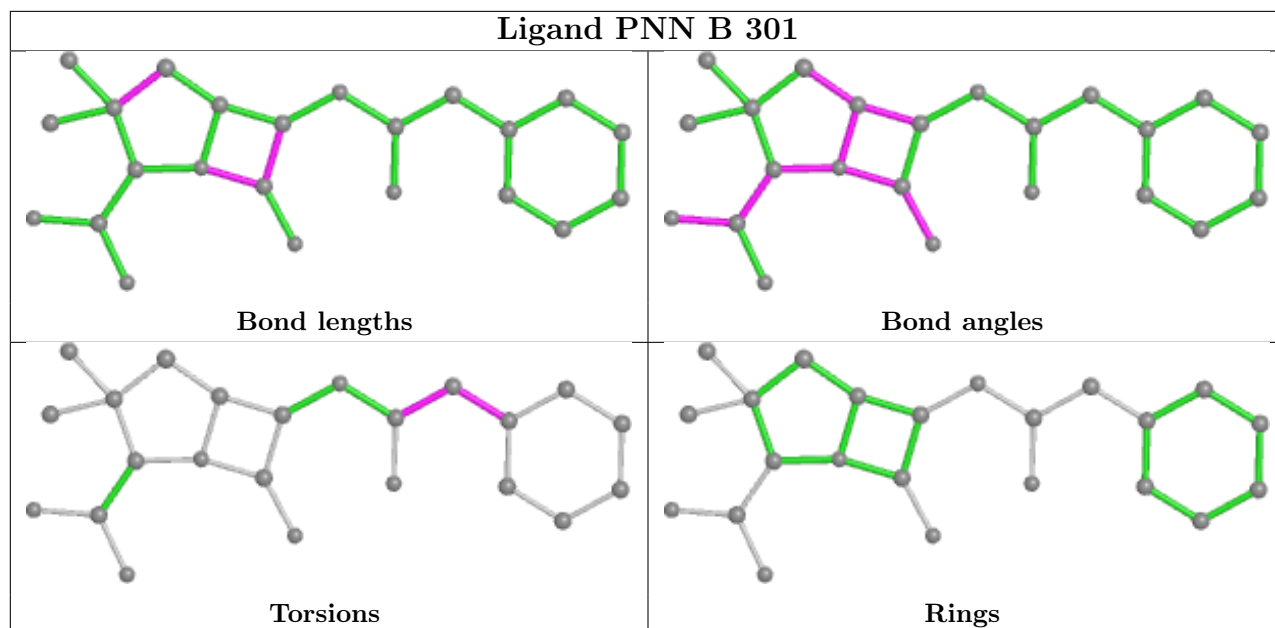
There are no ring outliers.

3 monomers are involved in 10 short contacts:

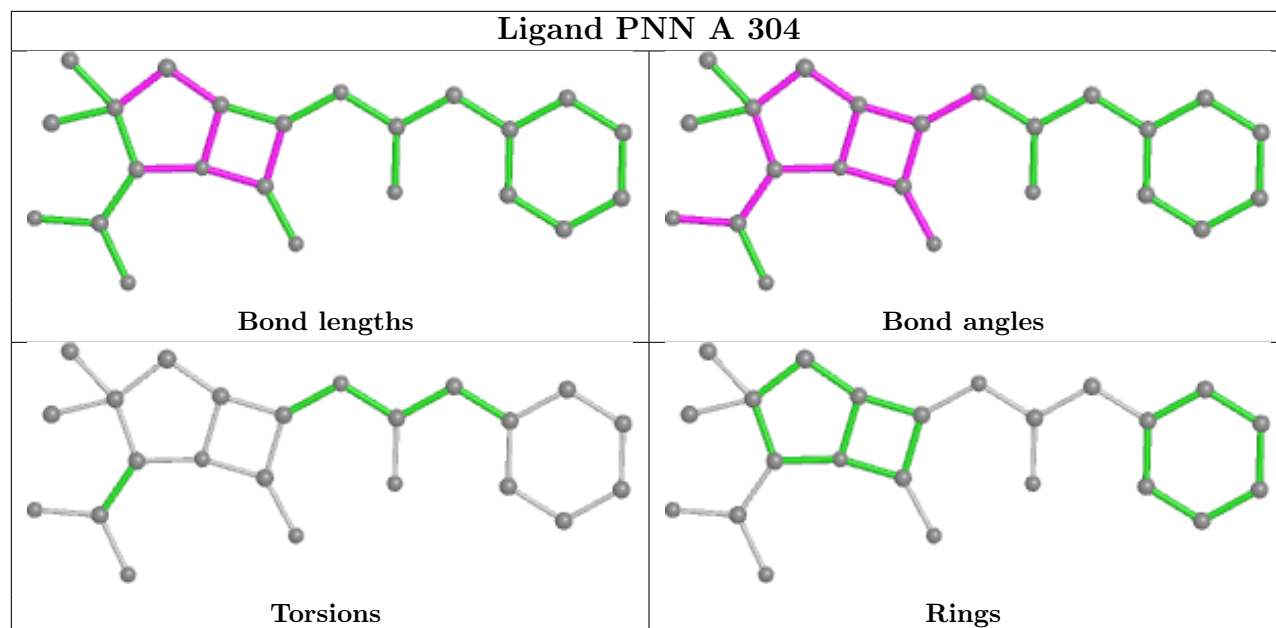
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	303	PNN	3	0
2	B	301	PNN	4	0
2	A	300	PNN	3	0

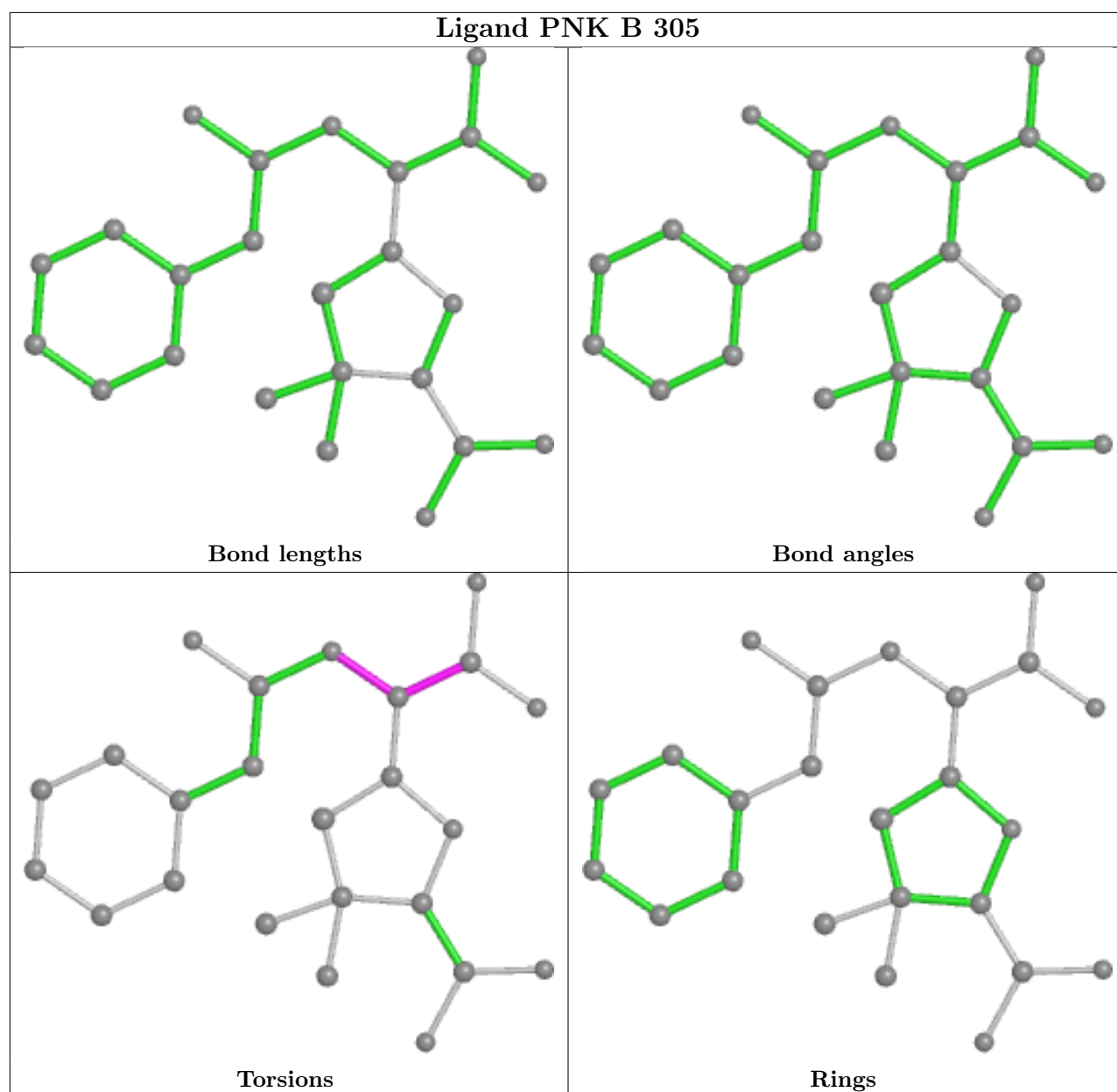
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	262/263 (99%)	-0.29	2 (0%) 86 89	4, 7, 18, 33	0
1	B	260/263 (98%)	-0.24	3 (1%) 79 82	4, 8, 20, 37	0
All	All	522/526 (99%)	-0.26	5 (0%) 82 85	4, 8, 19, 37	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	28	ALA	3.3
1	B	290	LEU	3.0
1	A	26	THR	2.1
1	A	227[A]	THR	2.1
1	B	271[A]	ASN	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](#)

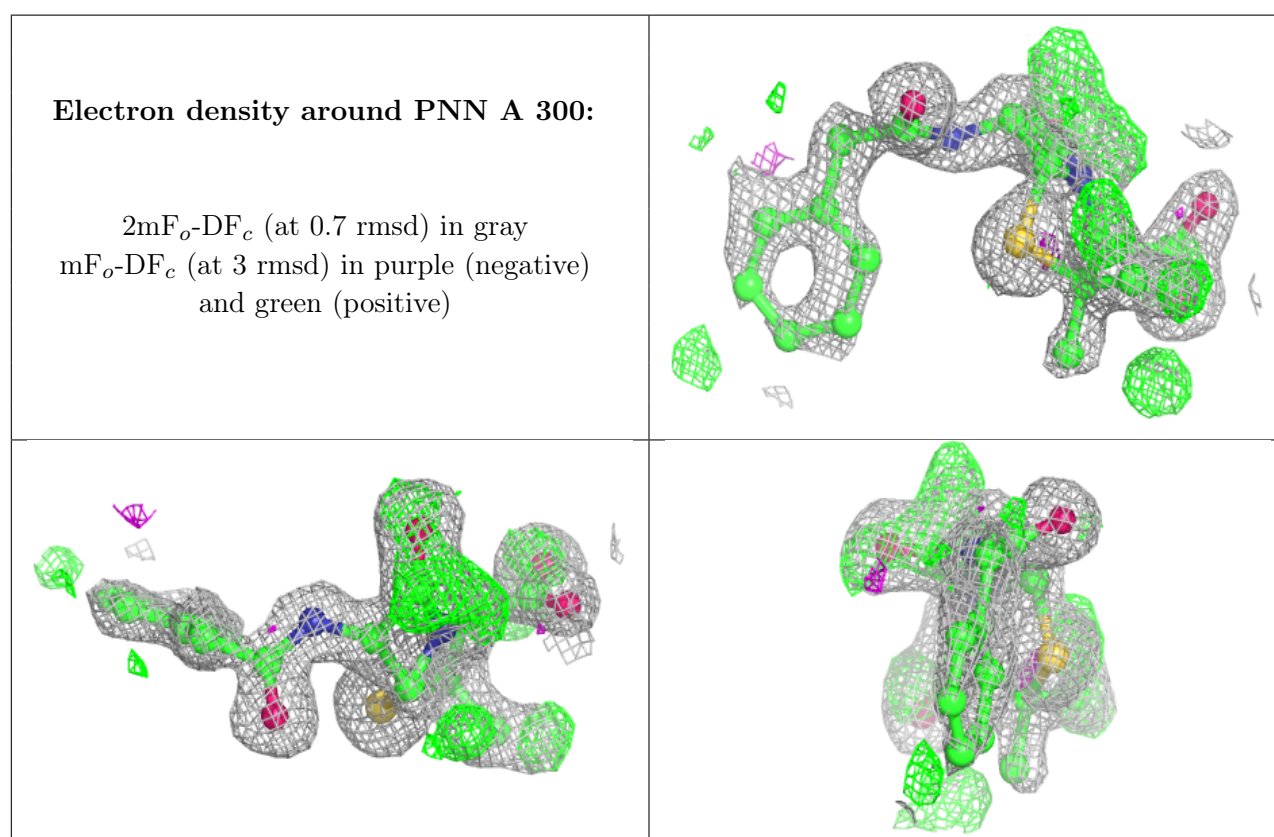
There are no monosaccharides in this entry.

### 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.

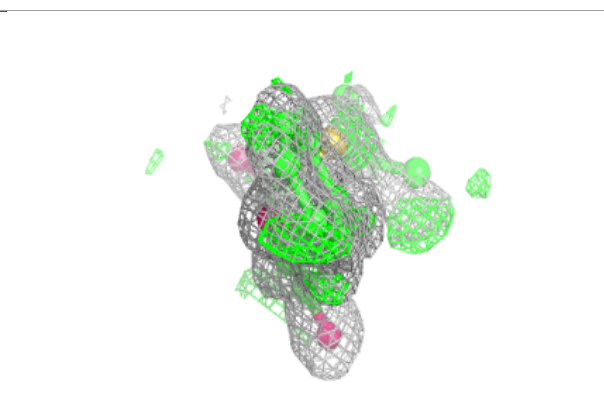
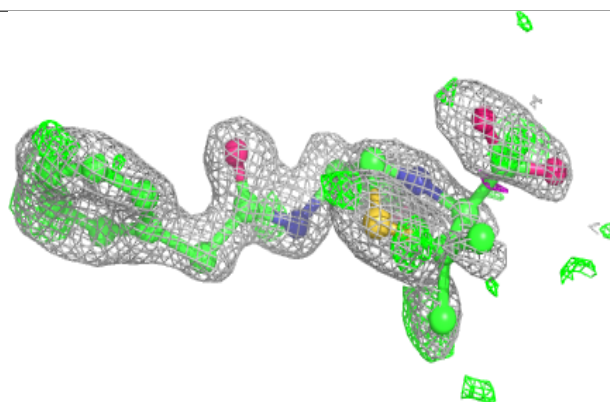
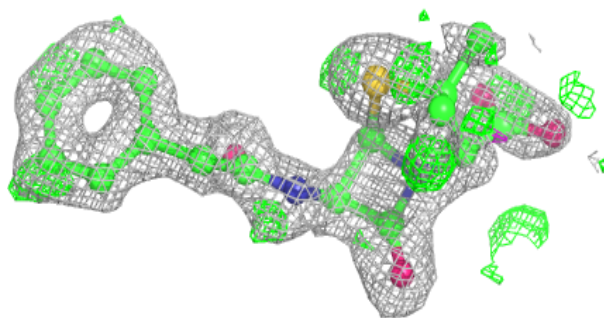
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PNN	A	300	23/23	0.87	0.20	2,11,17,18	23
2	PNN	A	303	23/23	0.87	0.21	5,9,17,17	23
2	PNN	A	304	23/23	0.90	0.16	3,9,13,16	23
2	PNN	A	302	23/23	0.91	0.23	4,9,16,17	23
2	PNN	B	301	23/23	0.92	0.12	3,11,18,18	23
3	PNK	B	305	24/24	0.92	0.14	6,8,10,14	24

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.

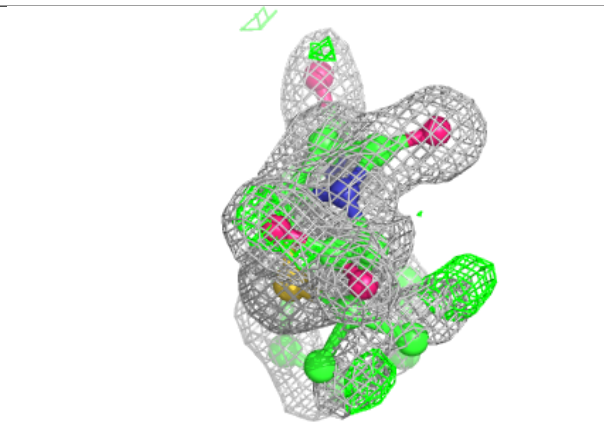
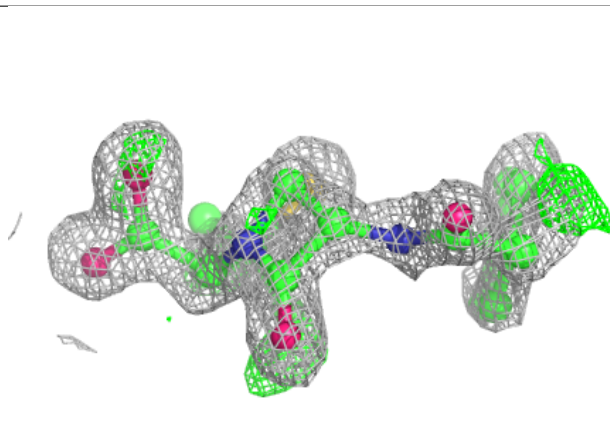
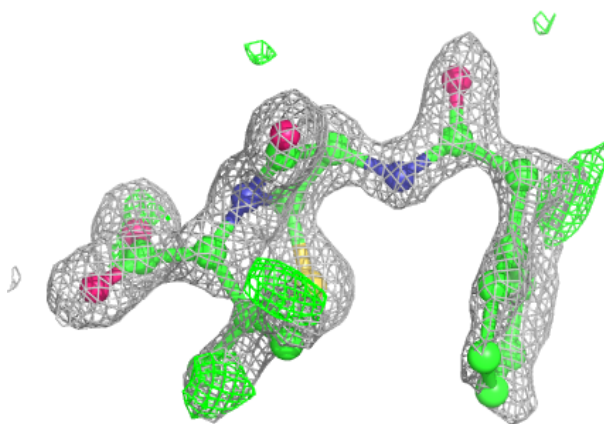


**Electron density around PNN A 303:**

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

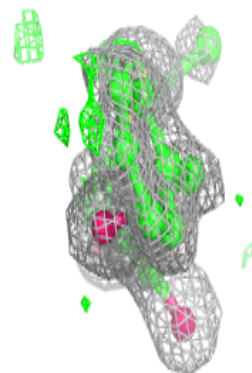
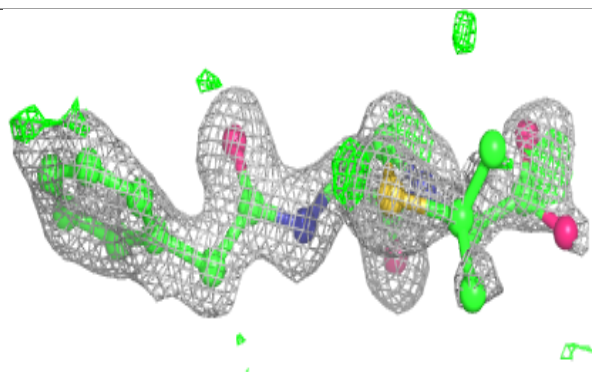
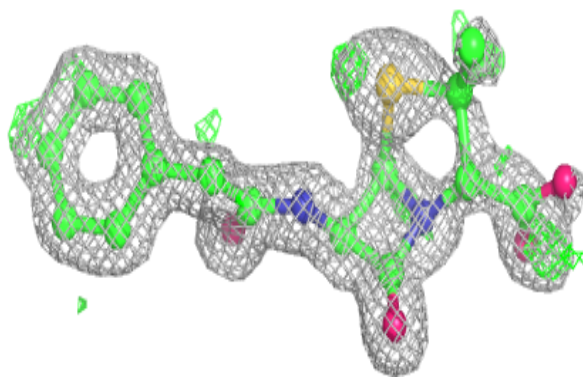
**Electron density around PNN A 304:**

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

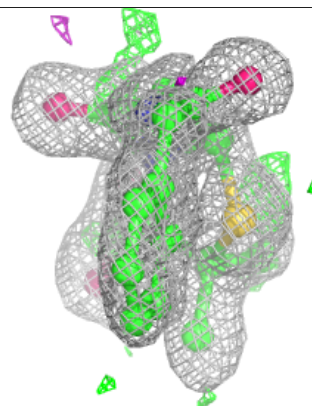
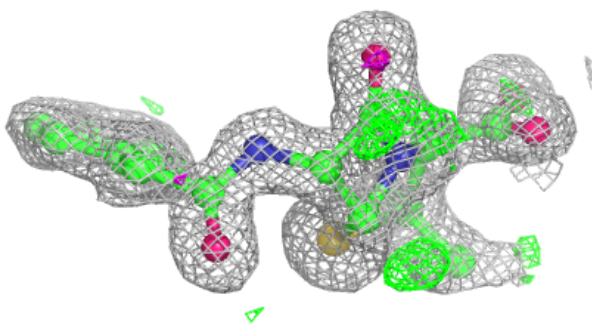
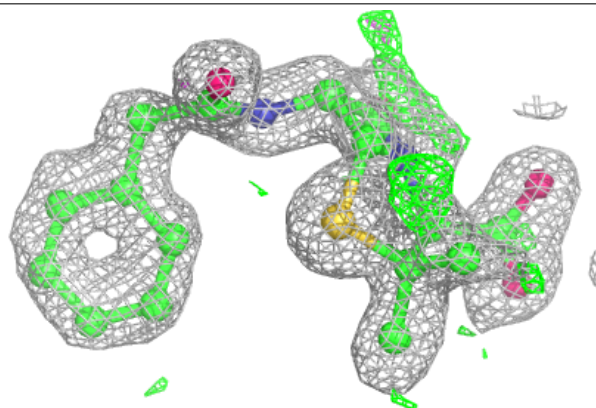


**Electron density around PNN A 302:**

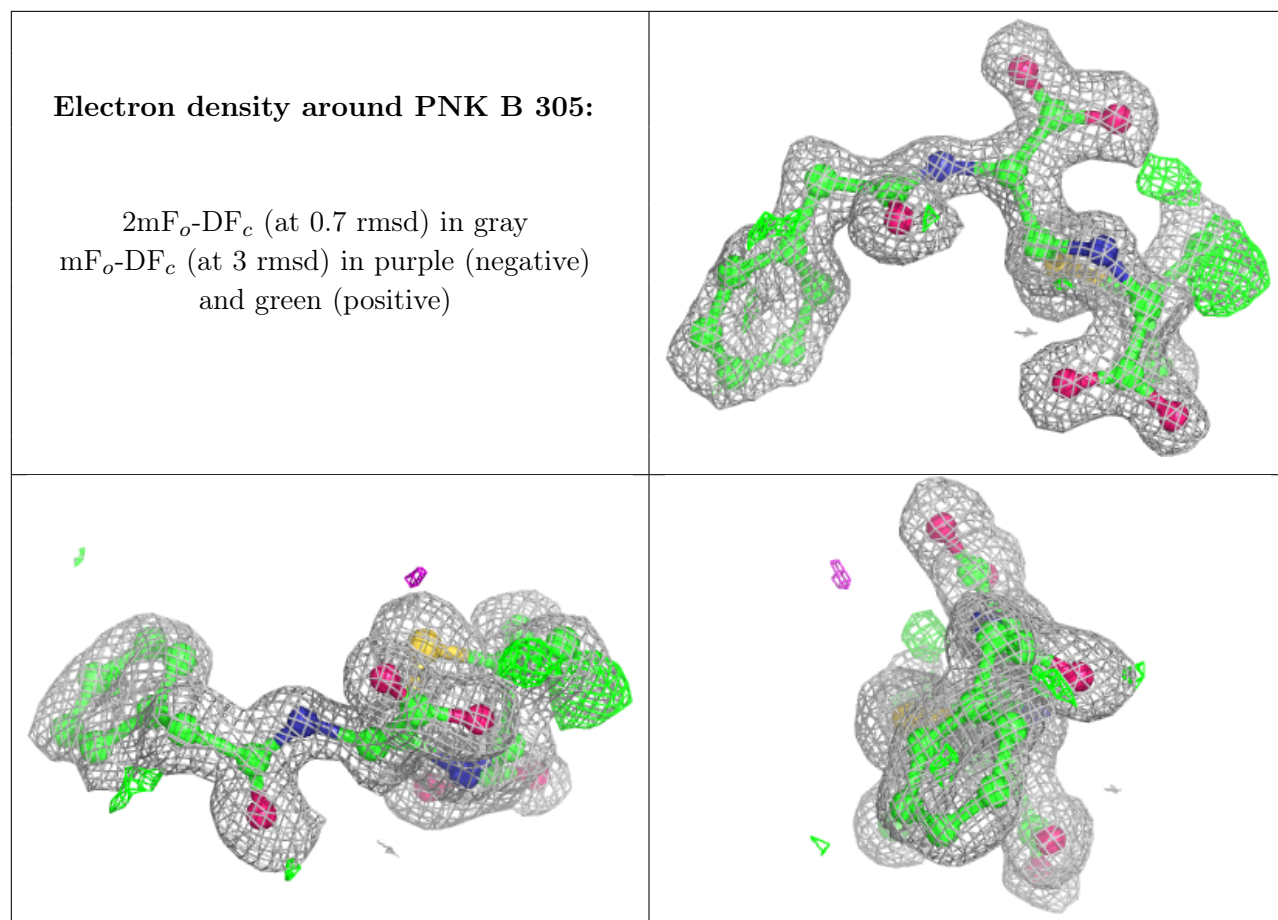
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around PNN B 301:**

$2mF_o-DF_c$  (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.