wwPDB X-ray Structure Validation Summary Report (i)

Aug 8, 2020 – 12:52 PM BST

PDB ID	:	4QTN
Title	:	Crystal structure of the Vitamin B3 transporter PnuC
Authors	:	Guskov, A.; Jaehme, M.; Slotboom, D.J.
Deposited on	:	2014-07-08
Resolution	:	2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i)) were used in the production of this report:

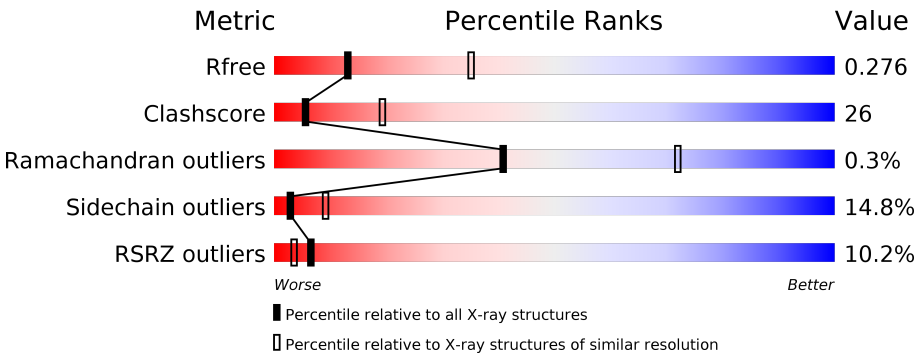
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 on 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	A	244	10% 57% 32% 7% •
1	B	244	9% 48% 39% 10% •
1	C	244	9% 59% 34% • •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5808 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 Nicotinamide riboside transporter PnuC.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	235	1887	1269	298	310	2	8	0	0	0
1	B	235	1887	1269	298	310	2	8	0	0	0
1	C	237	1900	1276	301	313	2	8	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	expression tag	UNP D2ZZC1
A	2	GLY	-	expression tag	UNP D2ZZC1
A	239	HIS	-	expression tag	UNP D2ZZC1
A	240	HIS	-	expression tag	UNP D2ZZC1
A	241	HIS	-	expression tag	UNP D2ZZC1
A	242	HIS	-	expression tag	UNP D2ZZC1
A	243	HIS	-	expression tag	UNP D2ZZC1
A	244	HIS	-	expression tag	UNP D2ZZC1
B	1	MSE	-	expression tag	UNP D2ZZC1
B	2	GLY	-	expression tag	UNP D2ZZC1
B	239	HIS	-	expression tag	UNP D2ZZC1
B	240	HIS	-	expression tag	UNP D2ZZC1
B	241	HIS	-	expression tag	UNP D2ZZC1
B	242	HIS	-	expression tag	UNP D2ZZC1
B	243	HIS	-	expression tag	UNP D2ZZC1
B	244	HIS	-	expression tag	UNP D2ZZC1
C	1	MSE	-	expression tag	UNP D2ZZC1
C	2	GLY	-	expression tag	UNP D2ZZC1
C	239	HIS	-	expression tag	UNP D2ZZC1
C	240	HIS	-	expression tag	UNP D2ZZC1
C	241	HIS	-	expression tag	UNP D2ZZC1
C	242	HIS	-	expression tag	UNP D2ZZC1
C	243	HIS	-	expression tag	UNP D2ZZC1

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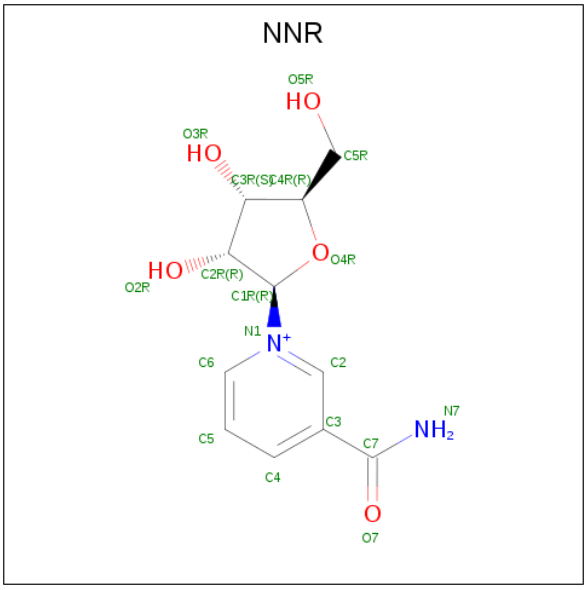
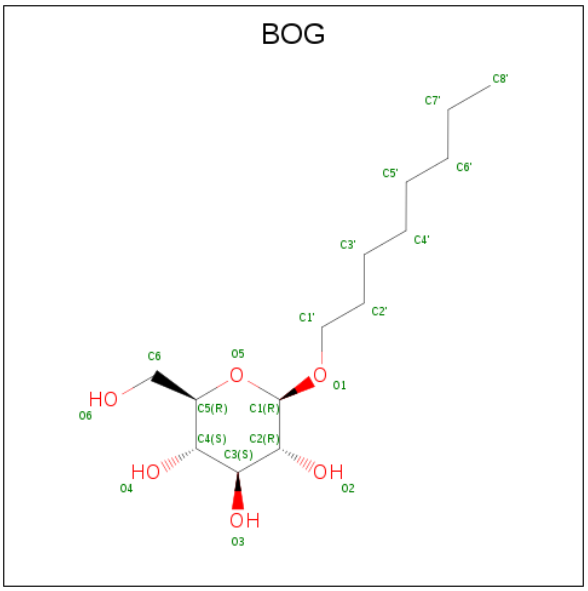
Chain	Residue	Modelled	Actual	Comment	Reference
C	244	HIS	-	expression tag	UNP D2ZZC1

- Molecule 2 is Nicotinamide riboside (three-letter code: NNR) (formula: $C_{11}H_{15}N_2O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			18	11	2	5		
2	B	1	Total	C	N	O	0	0
			18	11	2	5		
2	C	1	Total	C	N	O	0	0
			18	11	2	5		

- Molecule 3 is octyl beta-D-glucopyranoside (three-letter code: BOG) (formula: $C_{14}H_{28}O_6$).



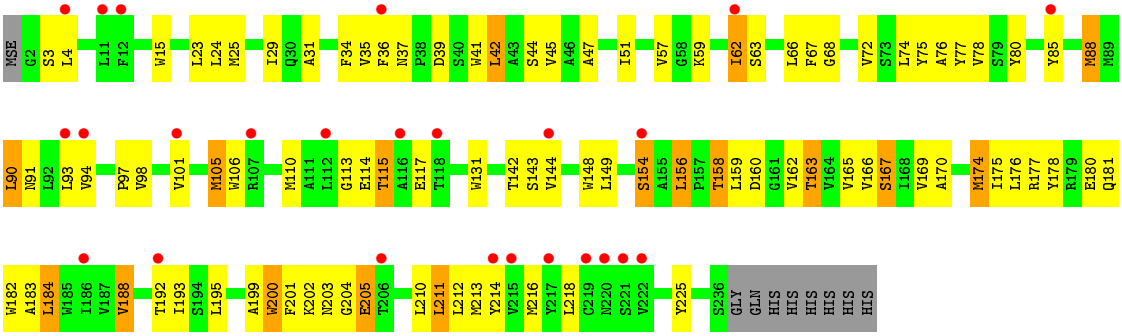
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	20	14	6	0	0
			Total	C	O		
3	B	1	20	14	6	0	0
			Total	C	O		
3	B	1	20	14	6	0	0
			Total	C	O		
3	C	1	20	14	6	0	0

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.

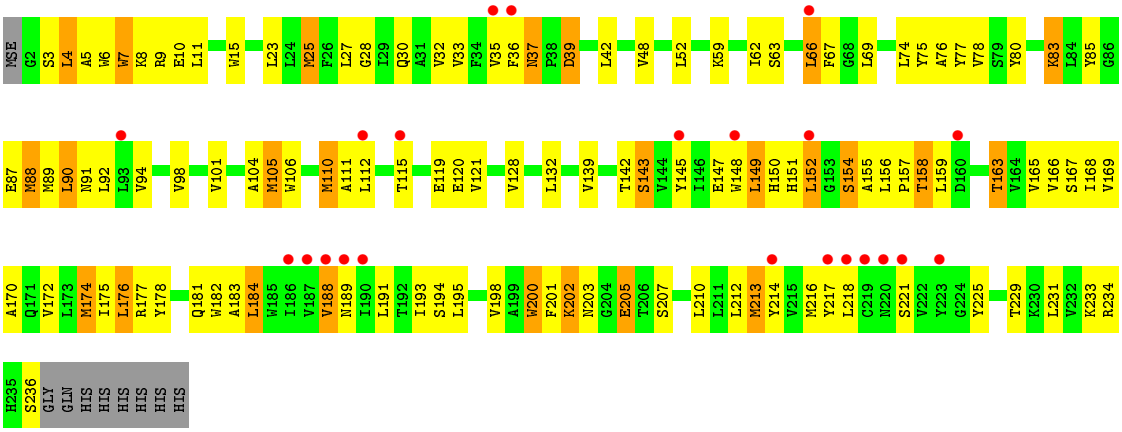
- Molecule 1: Nicotinamide riboside transporter PnuC

Chain A:



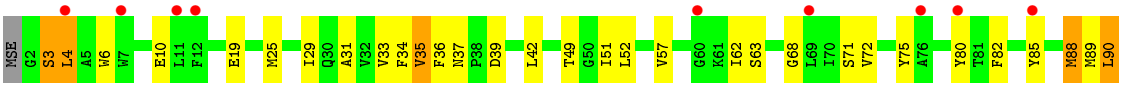
- Molecule 1: Nicotinamide riboside transporter PnuC

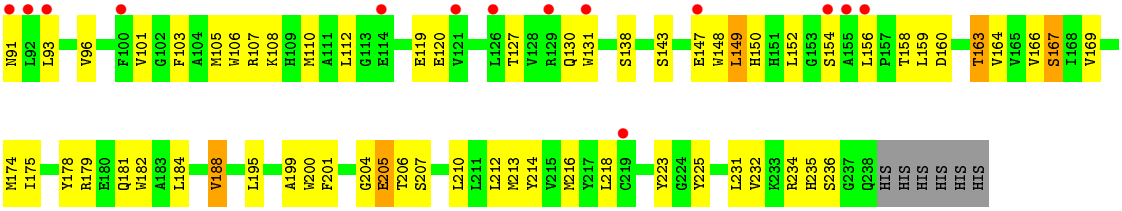
Chain B:



- Molecule 1: Nicotinamide riboside transporter PnuC

Chain C:




N91
L92
L93
V96
F100
V101
G102
F103
A104
M105
W106
R107
K108
H109
M110
A111
L112
G113
E114
E119
E120
V121
L126
T127
V128
R129
Q130
W131
S138
S143
E147
W148
L149
H150
H151
L152
G153
S154
A155
L156
P157
T158
L159
D160
T163
V164
V165
V166
S167
I168
V169
M174
I175
Y178
R179
E180
Q181
W182
A183
L184
V188
L195
A199
W200
F201
G204
E205
T206
S207
L210
L211
L212
M213
Y214
V215
M216
Y217
L218
C219
Y223
G224
Y225
L231
V232
K233
R234
H235
S236
G237
Q238
HIS
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	93.32Å 112.93Å 120.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.31 – 2.80 48.31 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.31-2.80) 99.8 (48.31-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.01 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.244 , 0.276 0.245 , 0.276	Depositor DCC
R_{free} test set	1597 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	102.7	Xtriage
Anisotropy	0.259	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 79.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	5808	wwPDB-VP
Average B, all atoms (Å^2)	117.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: NNR, BOG

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	0.61	0/1936	0.57	0/2633
1	B	0.63	0/1936	0.62	1/2633 (0.0%)
1	C	0.56	0/1949	0.58	1/2650 (0.0%)
All	All	0.60	0/5821	0.59	2/7916 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	110	MSE	CA-CB-CG	-5.94	103.20	113.30
1	C	231	LEU	CA-CB-CG	5.36	127.62	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	113	GLY	Peptide

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	1887	0	1931	109	0
1	B	1887	0	1931	120	0
1	C	1900	0	1942	107	0
2	A	18	0	14	1	0
2	B	18	0	14	0	0
2	C	18	0	14	1	0
3	A	20	0	28	1	0
3	B	40	0	56	2	0
3	C	20	0	28	0	0
All	All	5808	0	5958	302	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 26.

The worst 5 of 302 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:25:MSE:HE1	1:C:184:LEU:CD1	1.67	1.22
1:A:154:SER:HB2	1:A:156:LEU:CD2	1.74	1.15
1:C:62:ILE:HD12	1:C:110:MSE:HE3	1.33	1.10
1:C:200:TRP:CD1	1:C:201:PHE:HE1	1.70	1.08
1:B:154:SER:HB2	1:B:156:LEU:HD22	1.31	1.08

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	233/244 (96%)	220 (94%)	13 (6%)	0	100	100
1	B	233/244 (96%)	214 (92%)	18 (8%)	1 (0%)	34	66
1	C	235/244 (96%)	217 (92%)	17 (7%)	1 (0%)	34	66
All	All	701/732 (96%)	651 (93%)	48 (7%)	2 (0%)	41	72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	7	TRP
1	C	35	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	200/199 (100%)	173 (86%)	27 (14%)	4	11
1	B	200/199 (100%)	159 (80%)	41 (20%)	1	3
1	C	201/199 (101%)	180 (90%)	21 (10%)	7	21
All	All	601/597 (101%)	512 (85%)	89 (15%)	3	9

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	98	VAL
1	B	154	SER
1	C	163	THR
1	B	105	MSE
1	B	139	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	ASN

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Mol	Chain	Res	Type
1	A	171	GLN
1	B	37	ASN
1	C	37	ASN
1	C	235	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)

7 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	NNR	C	301	-	18,19,19	5.75	9 (50%)	23,27,27	1.31	2 (8%)
3	BOG	B	303	-	20,20,20	1.44	2 (10%)	25,25,25	0.88	0
3	BOG	B	302	-	20,20,20	1.55	2 (10%)	25,25,25	1.23	3 (12%)
3	BOG	C	302	-	20,20,20	1.35	3 (15%)	25,25,25	1.19	3 (12%)
3	BOG	A	302	-	20,20,20	1.24	2 (10%)	25,25,25	1.11	3 (12%)
2	NNR	A	301	-	18,19,19	5.53	9 (50%)	23,27,27	1.42	4 (17%)
2	NNR	B	301	-	18,19,19	5.76	9 (50%)	23,27,27	1.39	4 (17%)

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	NNR	C	301	-	-	0/10/26/26	0/2/2/2
3	BOG	B	303	-	-	6/11/31/31	0/1/1/1
3	BOG	B	302	-	-	7/11/31/31	0/1/1/1
3	BOG	C	302	-	-	5/11/31/31	0/1/1/1
3	BOG	A	302	-	-	6/11/31/31	0/1/1/1
2	NNR	A	301	-	-	6/10/26/26	0/2/2/2
2	NNR	B	301	-	-	3/10/26/26	0/2/2/2

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	NNR	O4R-C1R	15.73	1.63	1.41
2	C	301	NNR	C2R-C1R	-15.43	1.30	1.53
2	A	301	NNR	O4R-C1R	15.19	1.62	1.41
2	C	301	NNR	O4R-C1R	14.43	1.61	1.41
2	B	301	NNR	C2R-C1R	-14.00	1.32	1.53

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	301	NNR	C6-N1-C2	-3.80	118.51	121.97
2	C	301	NNR	C3R-C2R-C1R	3.46	106.19	100.98
3	C	302	BOG	O5-C5-C4	3.41	115.89	109.69
3	B	302	BOG	O1-C1-C2	3.25	113.38	108.30
2	C	301	NNR	C6-N1-C2	-3.06	119.18	121.97

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	303	BOG	O5-C1-O1-C1'
3	B	302	BOG	C2-C1-O1-C1'
3	B	302	BOG	O5-C1-O1-C1'
3	B	302	BOG	C2'-C1'-O1-C1
3	C	302	BOG	C2-C1-O1-C1'

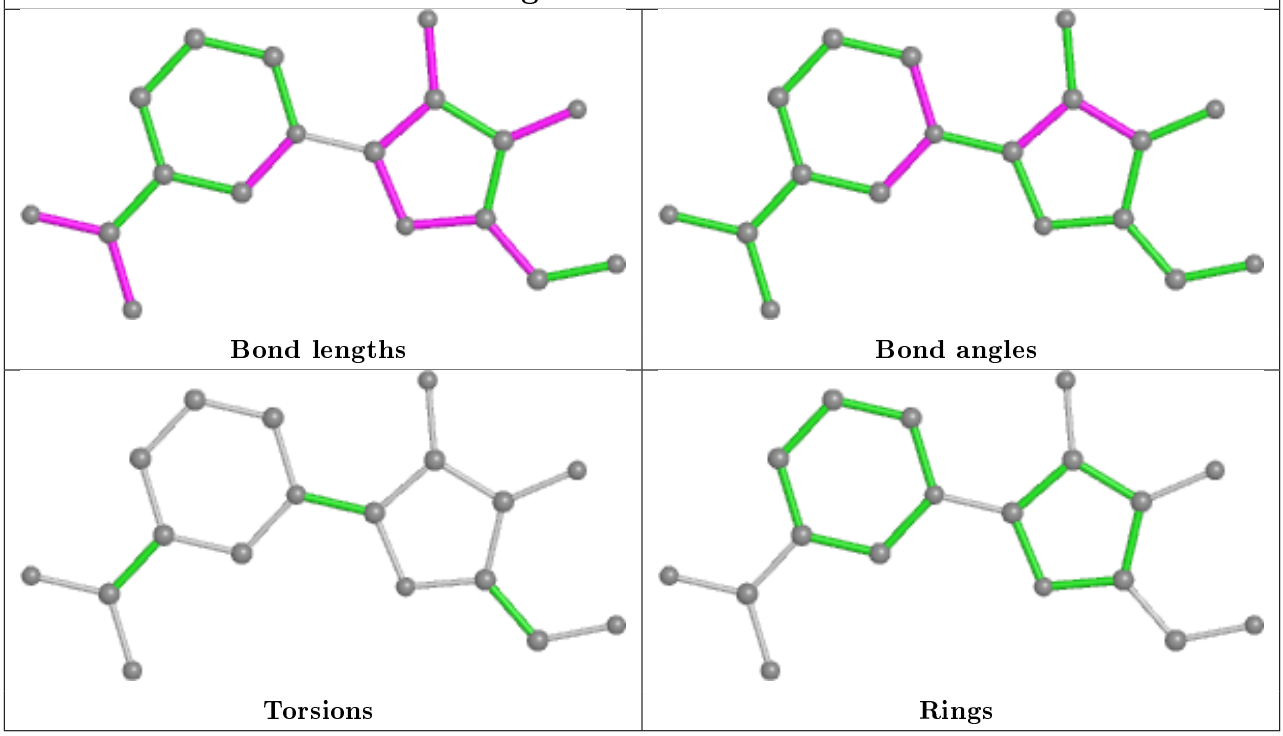
There are no ring outliers.

4 monomers are involved in 5 short contacts:

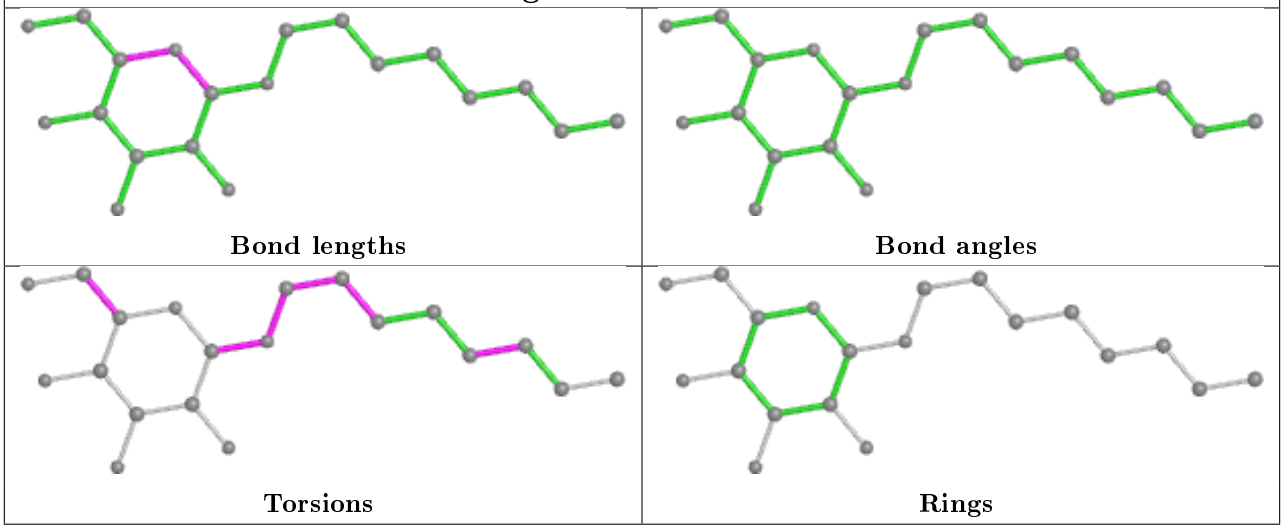
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	301	NNR	1	0
3	B	303	BOG	2	0
3	A	302	BOG	1	0
2	A	301	NNR	1	0

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 then 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.

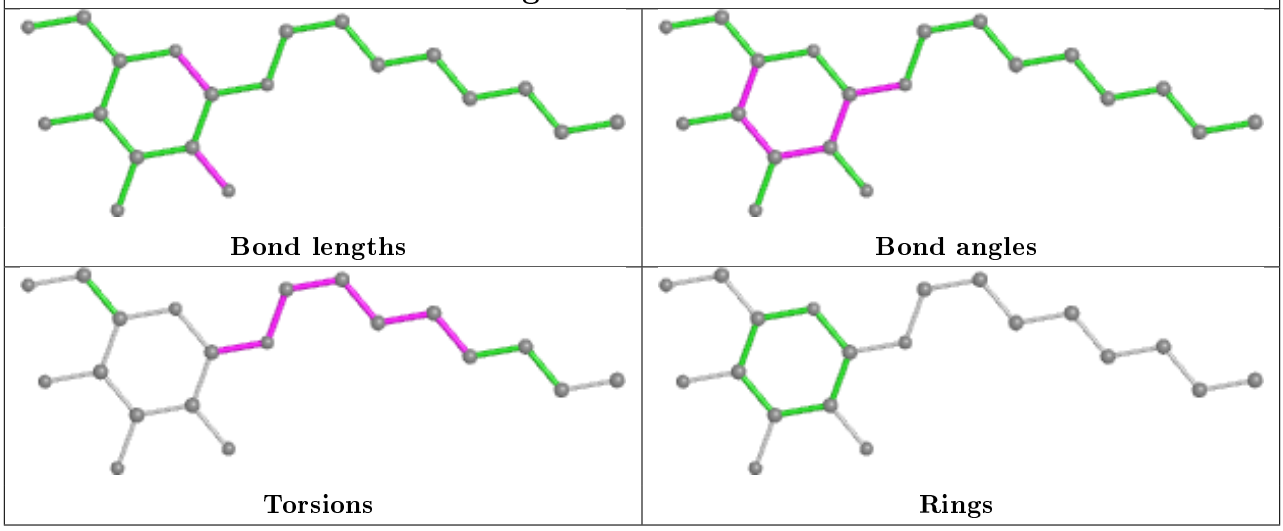
Ligand NNR C 301



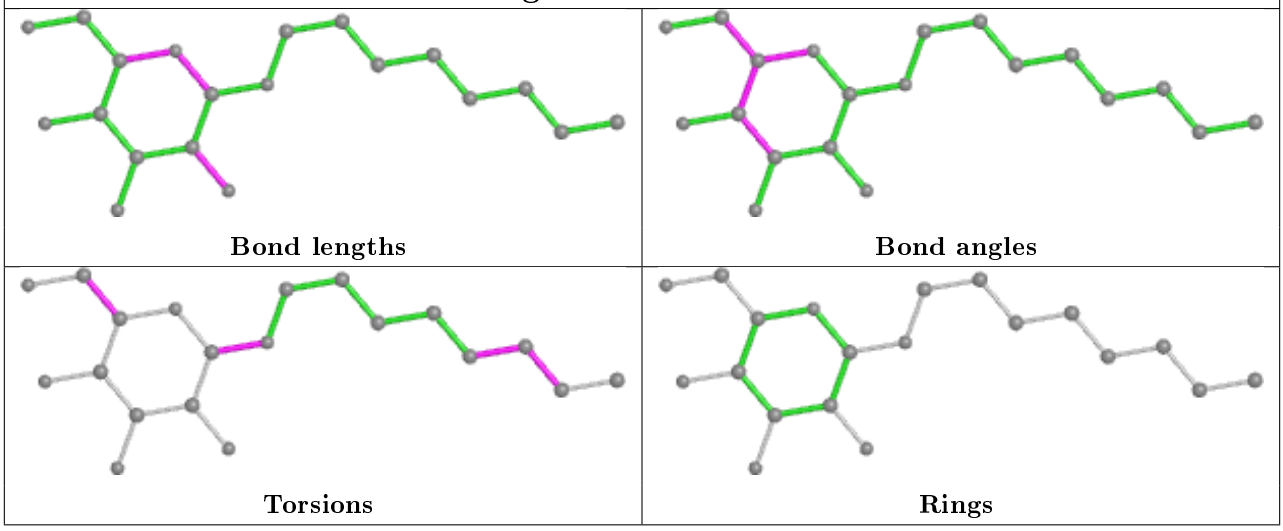
Ligand BOG B 303



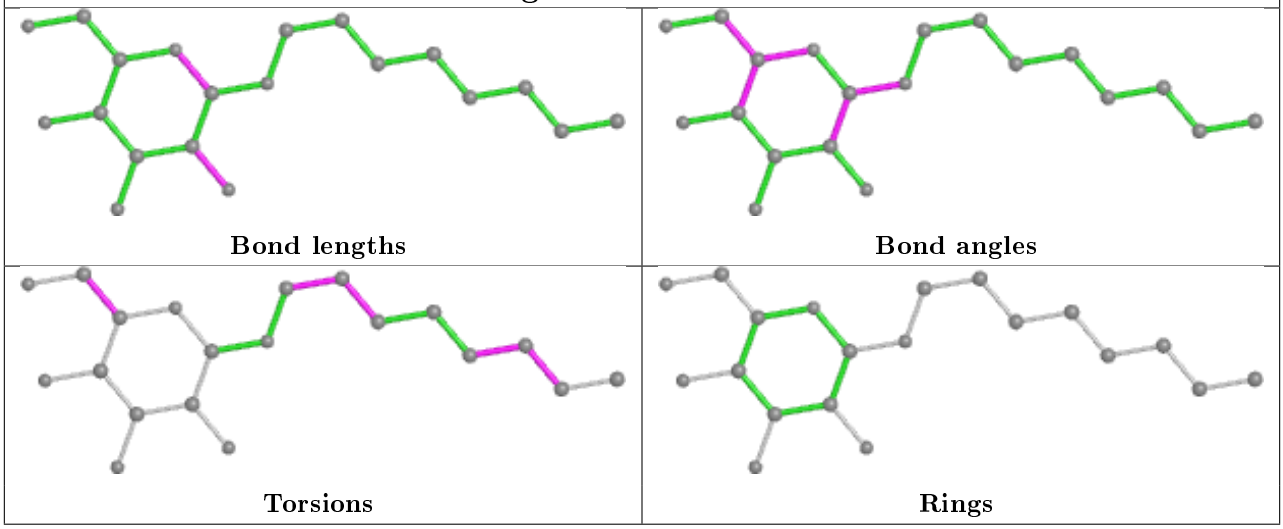
Ligand BOG B 302



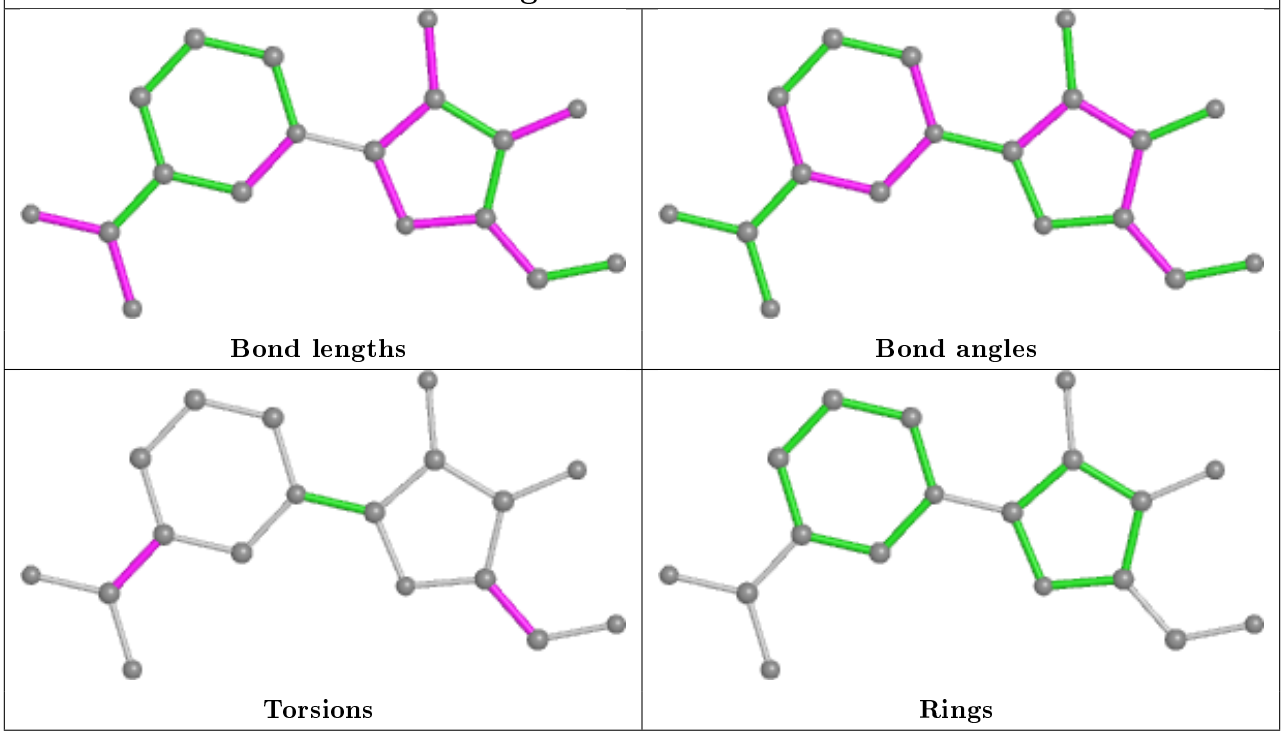
Ligand BOG C 302

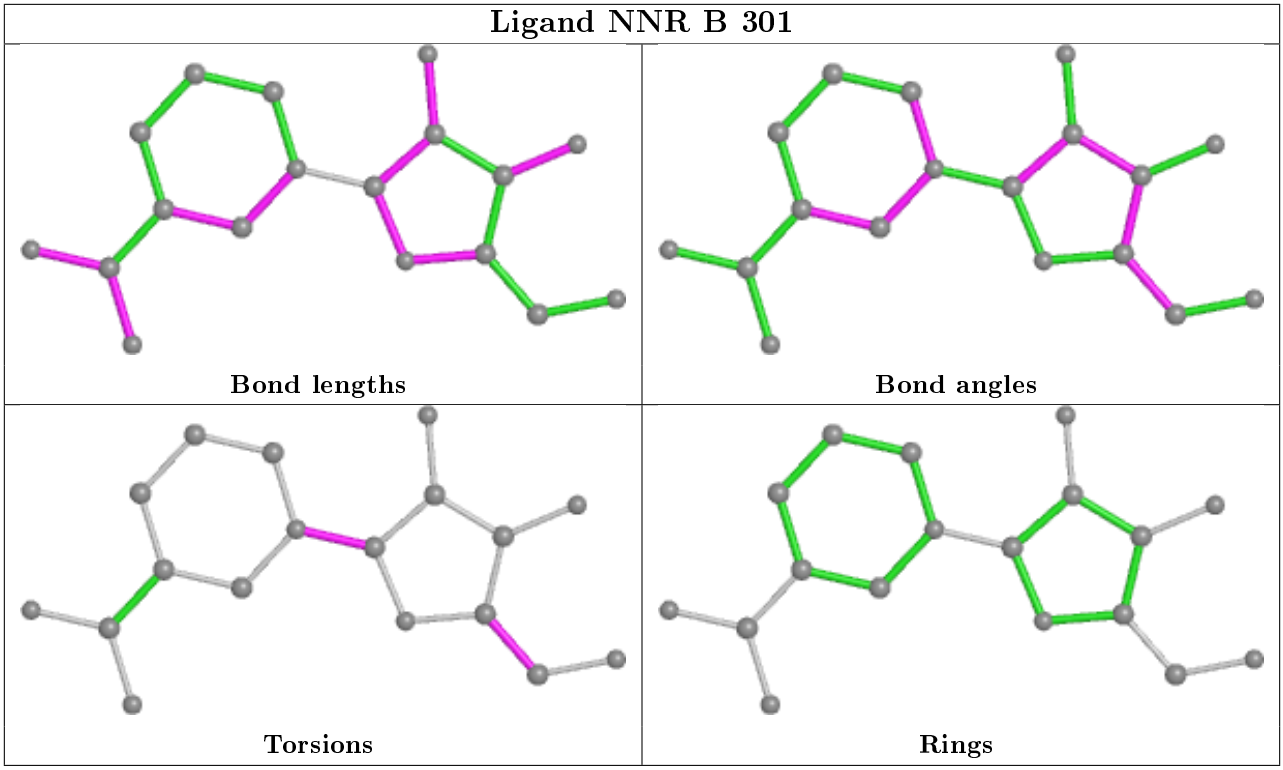


Ligand BOG A 302



Ligand NNR A 301





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, 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	A	227/244 (93%)	0.56	25 (11%)	5	3	70, 112, 168, 196	0
1	B	227/244 (93%)	0.35	22 (9%)	7	4	72, 108, 174, 211	0
1	C	229/244 (93%)	0.47	23 (10%)	7	4	72, 115, 179, 210	0
All	All	683/732 (93%)	0.46	70 (10%)	6	3	70, 112, 175, 211	0

The worst 5 of 70 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	155	ALA	5.0
1	C	85	TYR	4.9
1	B	112	LEU	4.8
1	C	147	GLU	4.7
1	B	152	LEU	4.7

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)

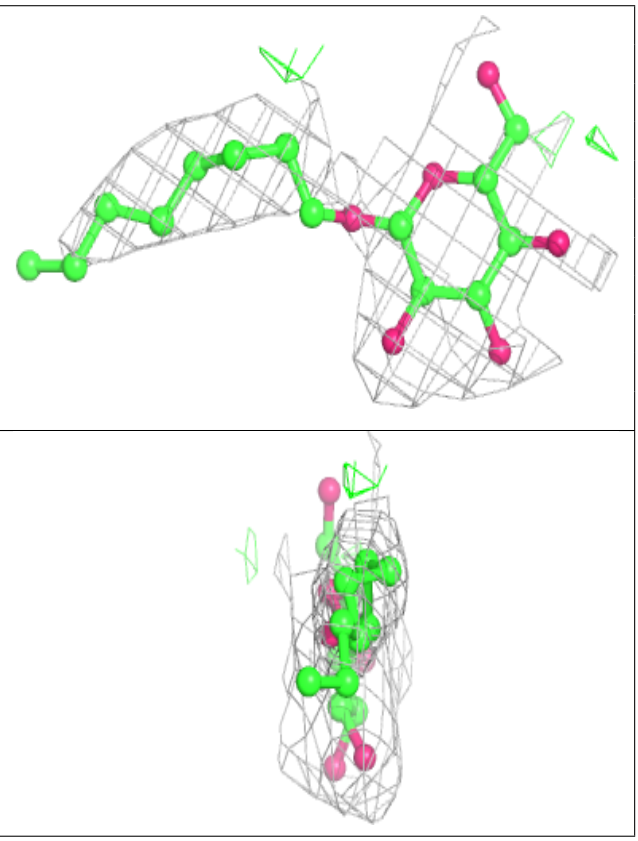
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	BOG	B	302	20/20	0.88	0.26	76,100,122,135	0
3	BOG	C	302	20/20	0.93	0.25	81,124,153,158	0
2	NNR	B	301	18/18	0.93	0.24	80,95,109,111	0
3	BOG	B	303	20/20	0.94	0.34	92,99,116,126	0
2	NNR	C	301	18/18	0.94	0.19	77,99,117,125	0
2	NNR	A	301	18/18	0.95	0.28	97,105,122,129	0
3	BOG	A	302	20/20	0.95	0.31	72,102,127,142	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.

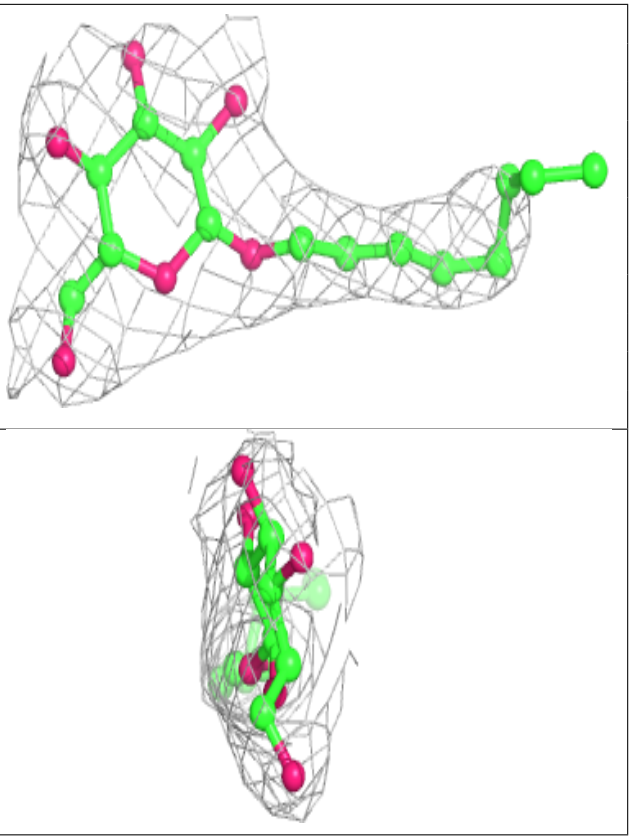
Electron density around BOG B 302:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)



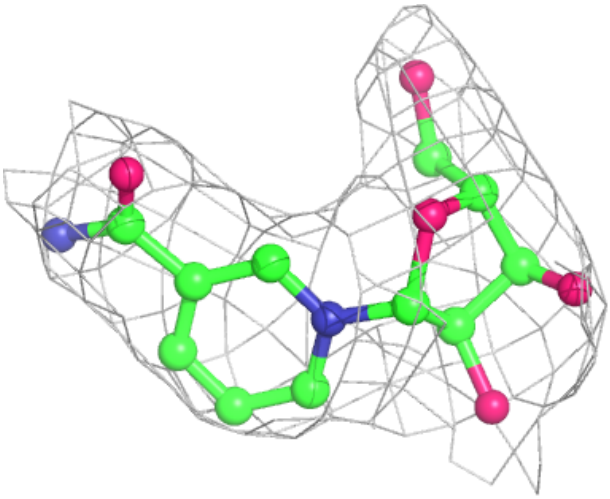
Electron density around BOG C 302:

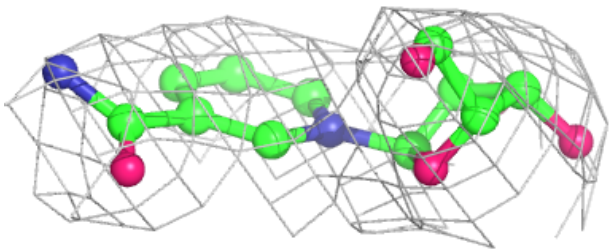
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

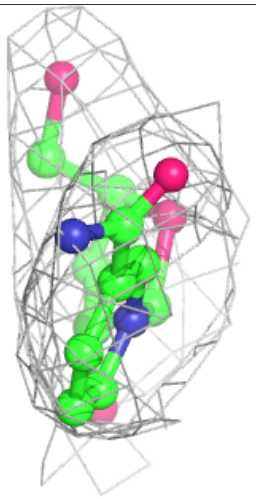


Electron density around NNR B 301:

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

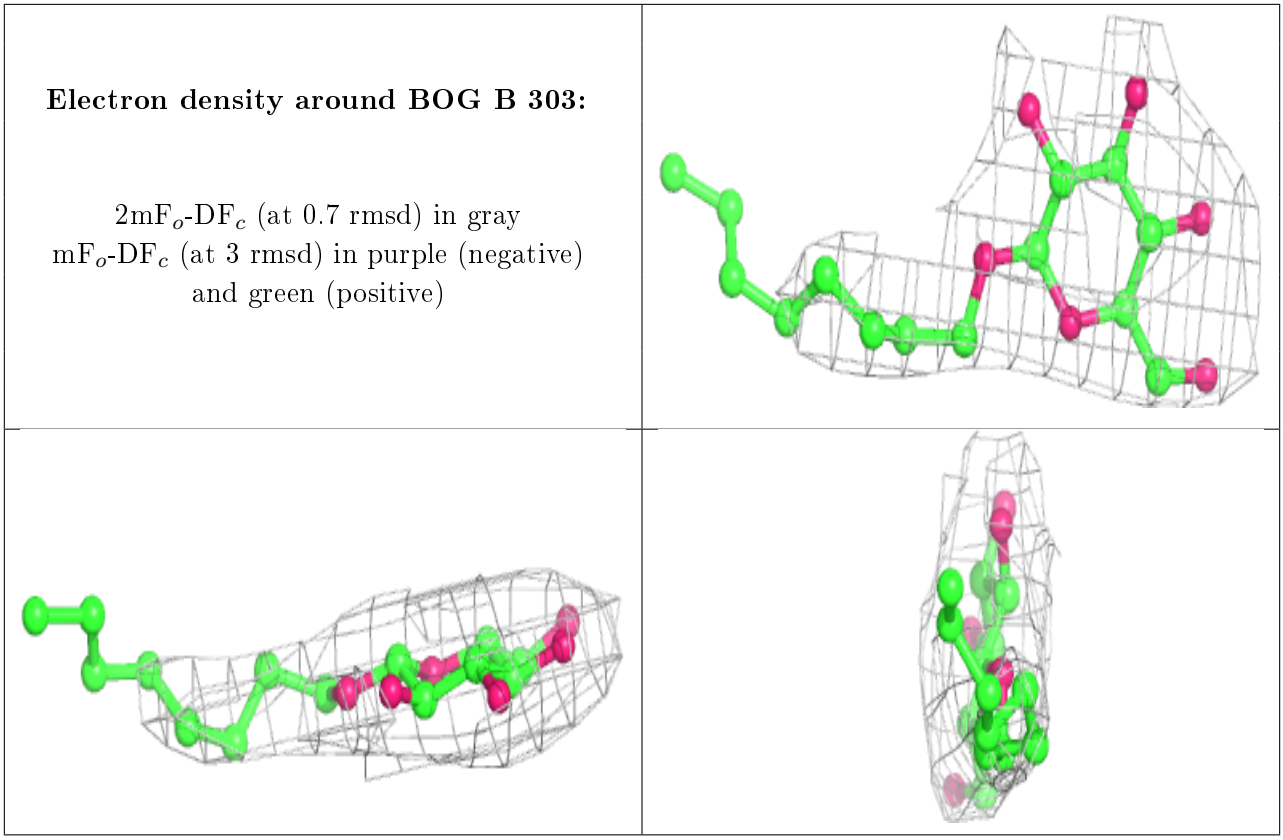






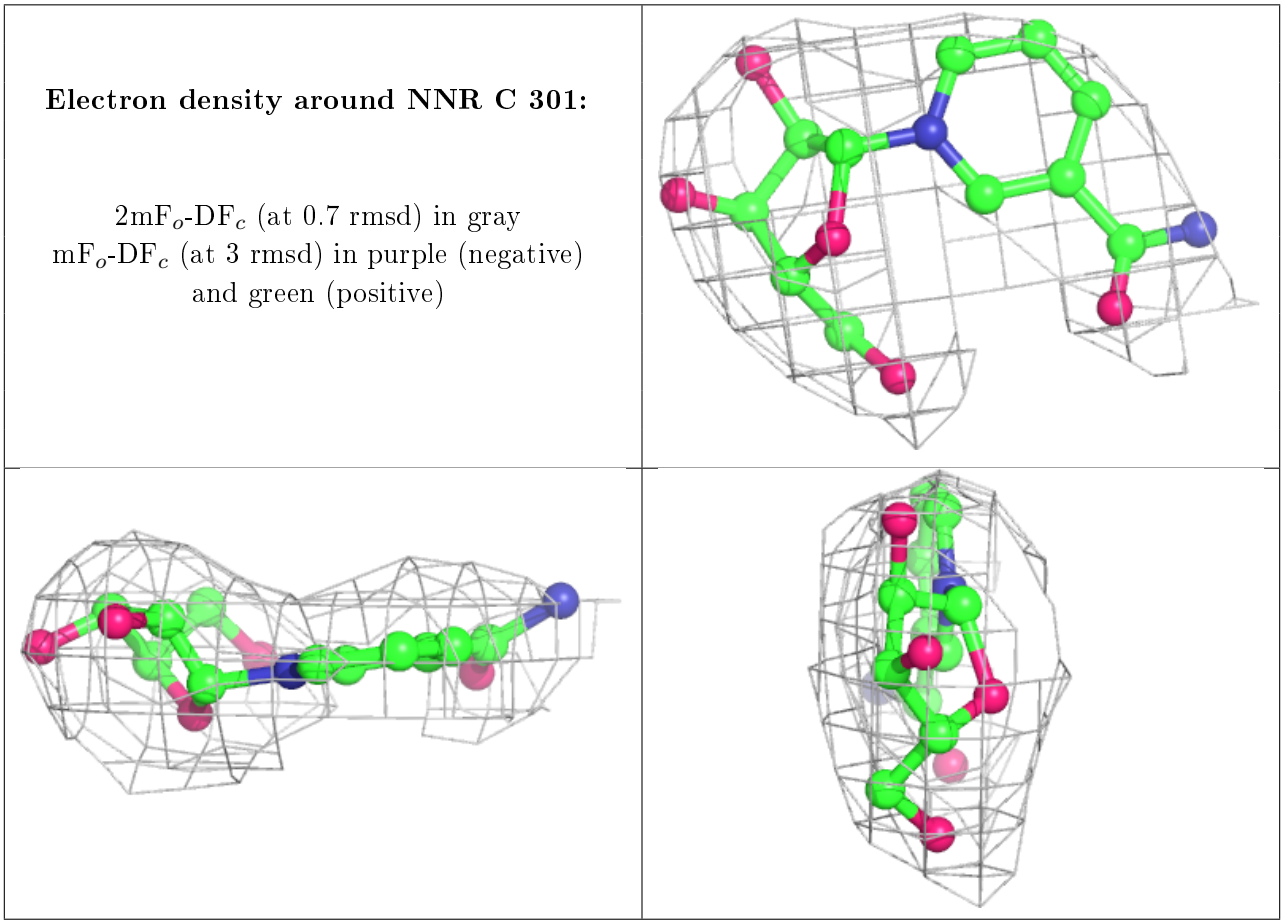
Electron density around BOG B 303:

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



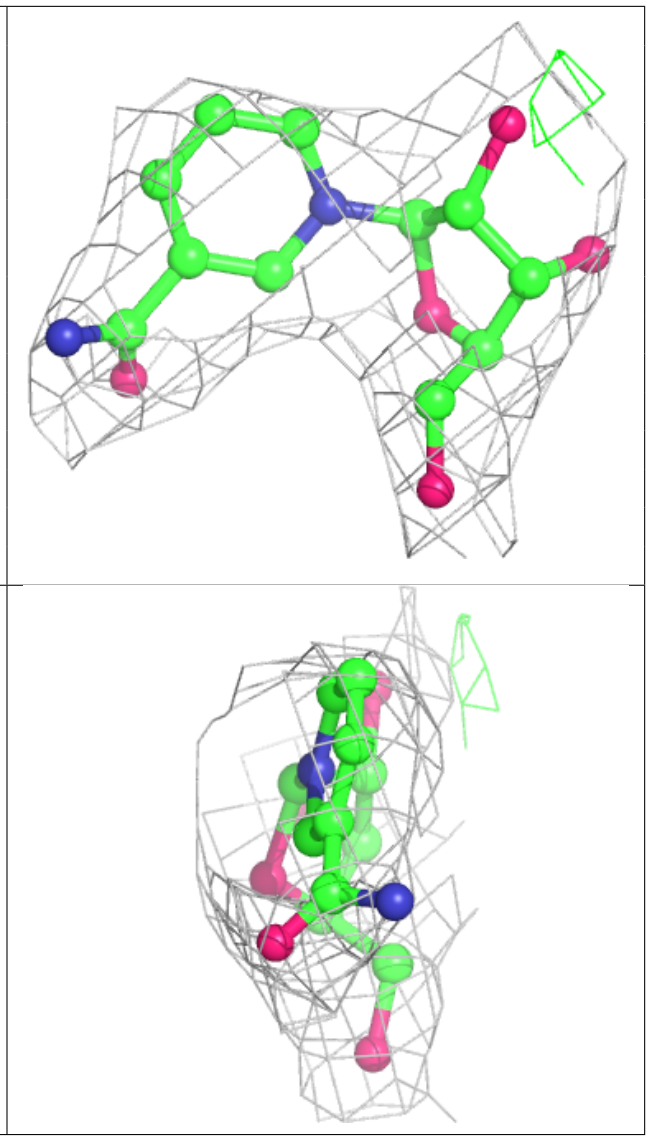
Electron density around NNR C 301:

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



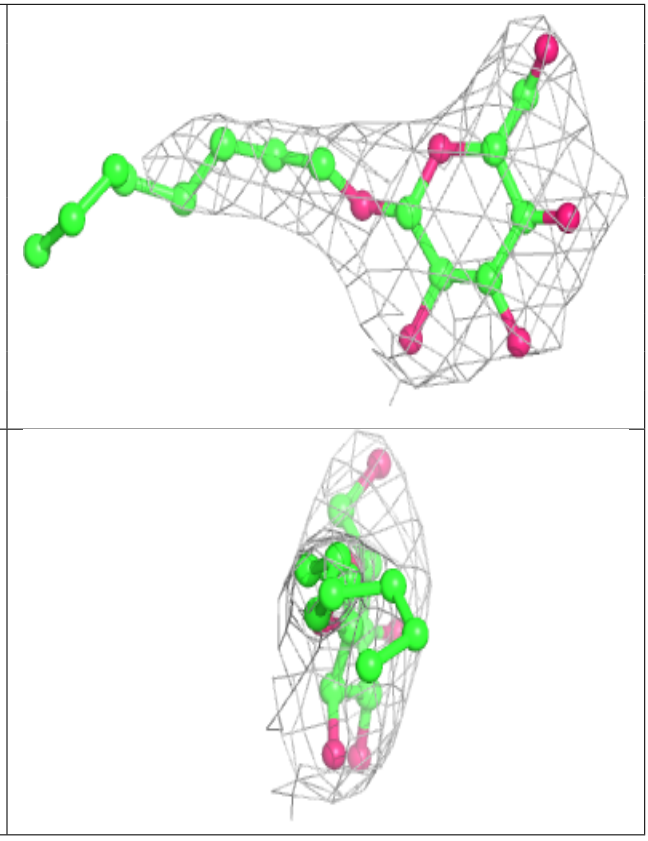
Electron density around NNR A 301:

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



Electron density around BOG 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)



6.5 Other polymers (i)

There are no such residues in this entry.