



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:07 AM UTC

PDB ID : 7I2B / pdb_00007i2b
Title : Group deposition for crystallographic fragment screening of the NS5 RNA-dependent RNA polymerase from Dengue virus serotype 2 – Crystal structure of the NS5 RNA-dependent RNA polymerase from Dengue virus serotype 2 in complex with Z68404778 (DNV2_NS5A-x0249)
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Deposited on : 2025-03-06
Resolution : 1.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	: 4-5-2 with Phenix2.0
Mogul	: 2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	: 2.0
EDS	: 3.0
Buster-report	: wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	: 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	: 9.0.010 (Gargrove)
Density-Fitness	: 1.0.12
Ideal geometry (proteins)	: Engh & Huber (2001)

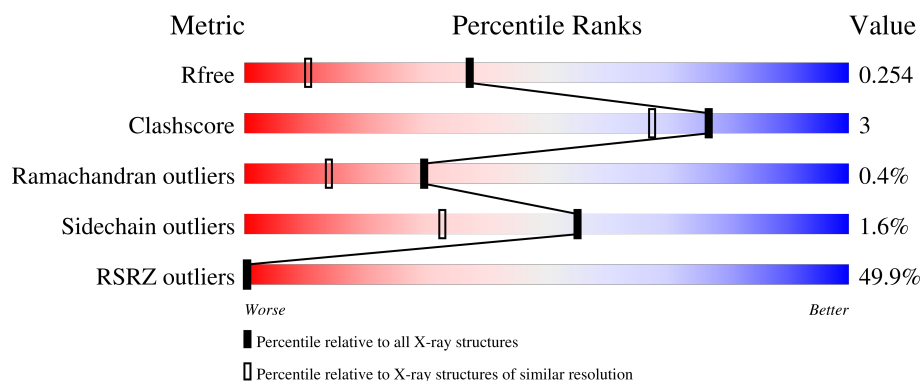
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	637	45% 81% 9% 10%

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:

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	PO4	A	1008	-	X	X	-

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 5223 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 NS5 RNA-dependent RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	573	Total	C	N	O	S	0	7	0
			4734	2981	849	870	34			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	264	GLY	-	expression tag	UNP Q91H74
A	265	PRO	-	expression tag	UNP Q91H74

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

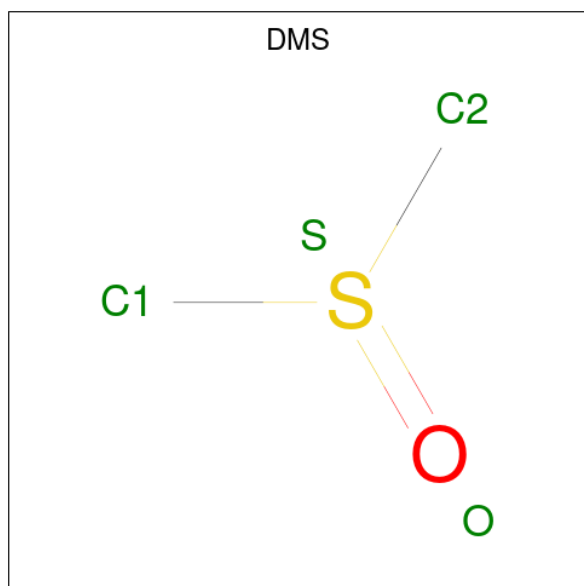
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	1
			24	12	2	8	2		

- Molecule 4 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



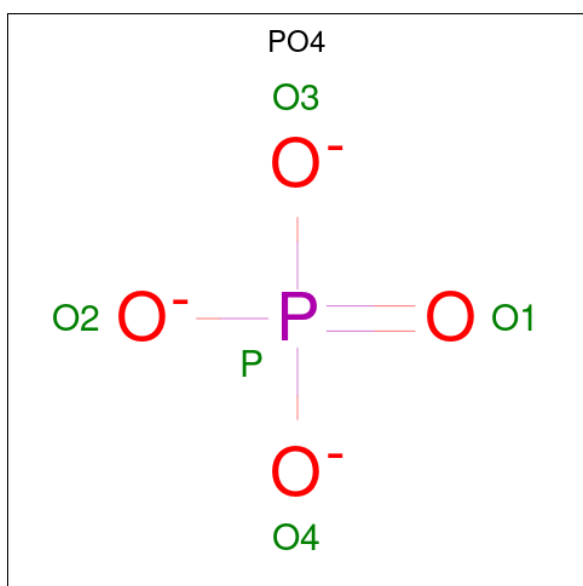
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	S	0	0
			4	2	1	1		
4	A	1	Total	C	O	S	0	0
			4	2	1	1		
4	A	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



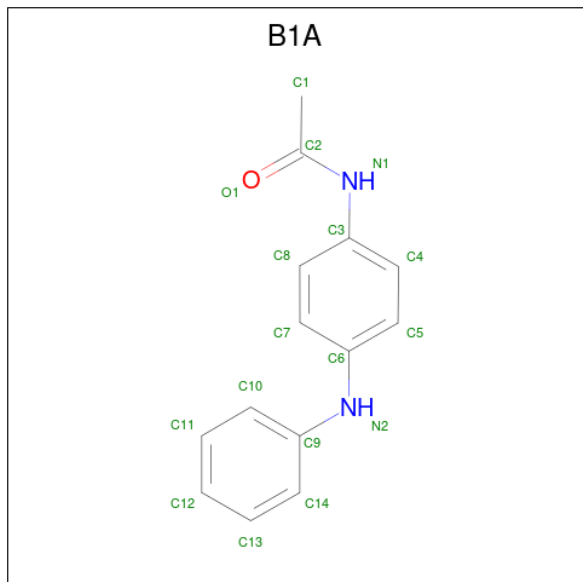
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	P	0	0
			5	4	1		
6	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is {N}-(4-phenylazanylphenyl)ethanamide (CCD ID: B1A) (formula: C₁₄H₁₄N₂O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	1
			34	28	4	2		

- Molecule 8 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Cl	0	0
			1	1		

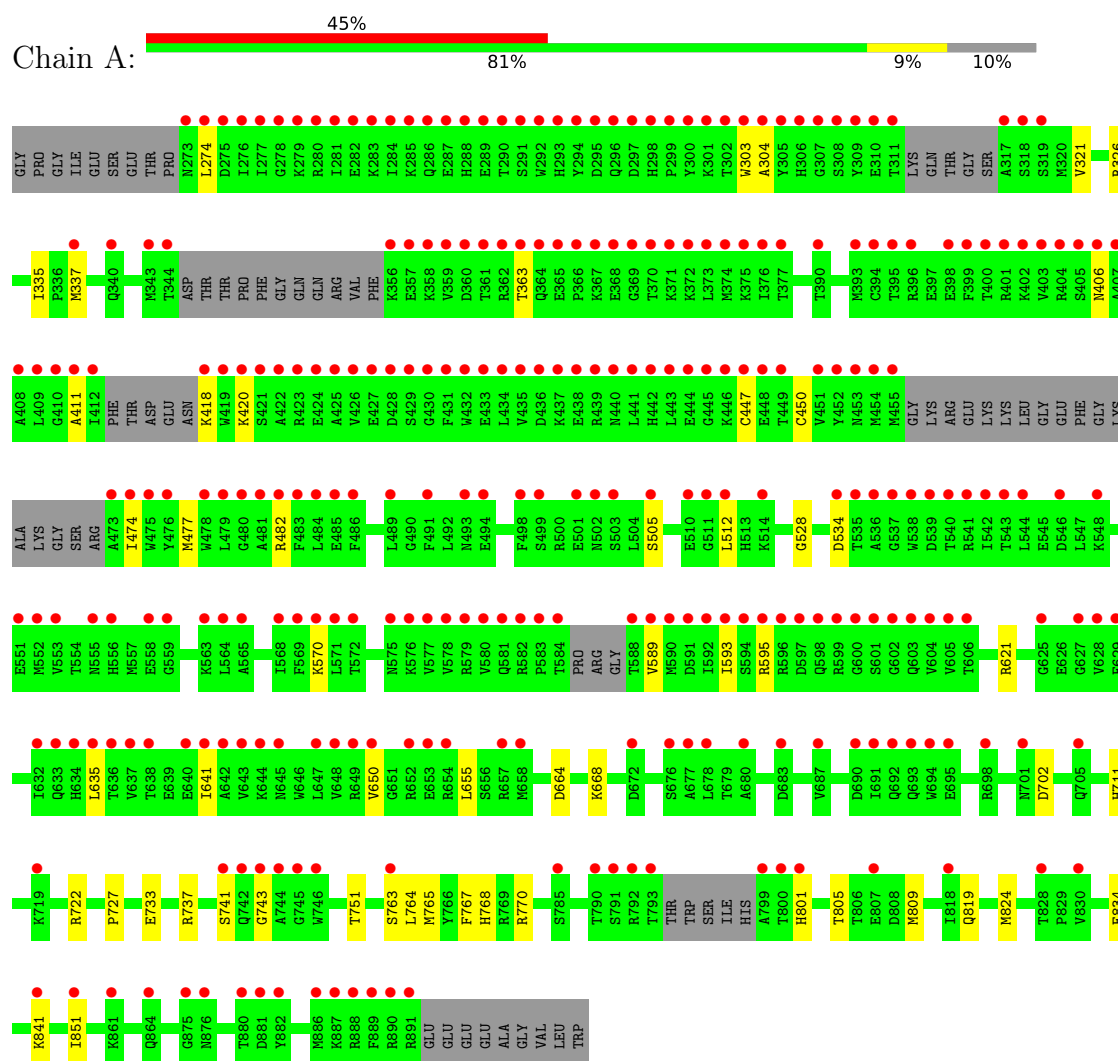
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	392	Total	O	0	0
			392	392		

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: NS5 RNA-dependent RNA polymerase



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	82.48Å 116.86Å 148.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.89 – 1.60 45.89 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.2 (45.89-1.60) 99.2 (45.89-1.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.00 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.8.0267, REFMAC5	Depositor
R, R_{free}	0.193 , 0.220 0.232 , 0.254	Depositor DCC
R_{free} test set	4793 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	28.8	Xtriage
Anisotropy	0.159	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 77.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5223	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.97% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DMS, ZN, PO4, MES, CL, B1A, PEG

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	1.09	3/4839 (0.1%)	1.30	3/6525 (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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	768	HIS	CE1-NE2	6.62	1.39	1.32
1	A	621	ARG	C-O	5.54	1.30	1.24
1	A	751	THR	C-O	5.36	1.30	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	702	ASP	CA-CB-CG	6.24	118.84	112.60
1	A	743	GLY	CA-C-O	-5.62	118.40	122.45
1	A	650	VAL	CA-C-O	-5.17	115.43	119.46

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	741[B]	SER	Mainchain

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	4734	0	4638	27	0
2	A	2	0	0	0	0
3	A	24	0	26	0	0
4	A	12	0	18	1	0
5	A	14	0	20	0	0
6	A	10	0	0	3	0
7	A	34	0	0	0	0
8	A	1	0	0	0	0
9	A	392	0	0	6	1
All	All	5223	0	4702	28	1

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 3.

All (28) 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:664:ASP:OD1	6:A:1008:PO4:O4	1.89	0.91
1:A:664:ASP:OD1	6:A:1008:PO4:P	2.42	0.77
4:A:1004:DMS:H12	9:A:1278:HOH:O	1.94	0.67
1:A:819:GLN:NE2	9:A:1103:HOH:O	2.29	0.65
1:A:801[B]:HIS:H	1:A:801[B]:HIS:CD2	2.14	0.64
1:A:447:CYS:SG	1:A:450:CYS:HB2	2.41	0.60
1:A:841:LYS:NZ	9:A:1102:HOH:O	2.28	0.59
1:A:733:GLU:O	1:A:737:ARG:HG3	2.04	0.58
1:A:505:SER:OG	1:A:655:LEU:O	2.19	0.58
1:A:834:GLU:HG3	9:A:1153:HOH:O	2.05	0.55
1:A:528:GLY:O	1:A:668:LYS:HE3	2.06	0.54
1:A:764:LEU:HG	1:A:765:MET:CE	2.39	0.52
1:A:411:ALA:HA	1:A:477:MET:O	2.13	0.48
1:A:512[A]:LEU:HD21	1:A:711:HIS:NE2	2.31	0.46
1:A:770:ARG:HD2	1:A:851:ILE:HD13	1.98	0.45
1:A:764:LEU:HG	1:A:765:MET:HE2	1.99	0.45
1:A:534:ASP:OD1	6:A:1008:PO4:O4	2.34	0.45
1:A:805:THR:CG2	1:A:809:MET:HE1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:TRP:CZ2	1:A:595:ARG:HD2	2.52	0.44
1:A:337:MET:HG2	9:A:1359:HOH:O	2.19	0.42
1:A:363:THR:HG23	9:A:1384:HOH:O	2.19	0.42
1:A:763[A]:SER:O	1:A:767:PHE:HB3	2.20	0.41
1:A:477:MET:HB2	1:A:482:ARG:NE	2.36	0.41
1:A:512[A]:LEU:HG	1:A:727:PRO:CB	2.51	0.41
1:A:304:ALA:O	1:A:593:ILE:HA	2.21	0.41
1:A:321:VAL:HG11	1:A:326:ARG:CZ	2.51	0.41
1:A:722:ARG:HB3	1:A:824:MET:SD	2.61	0.40
1:A:809:MET:HA	1:A:809:MET:HE2	2.03	0.40

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)
9:A:1139:HOH:O	9:A:1139:HOH:O[2_445]	1.67	0.53

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	566/637 (89%)	547 (97%)	17 (3%)	2 (0%)	30 14

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	420	LYS
1	A	406	ASN

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	508/554 (92%)	500 (98%)	8 (2%)	55 33

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	274	LEU
1	A	335	ILE
1	A	418	LYS
1	A	474	ILE
1	A	570	LYS
1	A	589	VAL
1	A	635	LEU
1	A	641	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	273	ASN
1	A	288	HIS
1	A	575	ASN
1	A	603	GLN
1	A	618	GLN
1	A	786	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 3 are monoatomic - leaving 11 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		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	PO4	A	1008	-	4,4,4	6.66	4 (100%)	6,6,6	1.31	1 (16%)
6	PO4	A	1009	-	4,4,4	1.15	1 (25%)	6,6,6	0.46	0
3	MES	A	1003[B]	-	12,12,12	0.70	0	15,16,16	0.29	0
7	B1A	A	1011[A]	-	18,18,18	0.07	0	23,23,23	0.28	0
7	B1A	A	1011[B]	-	18,18,18	0.09	0	23,23,23	0.32	0
4	DMS	A	1005	-	3,3,3	0.33	0	3,3,3	0.09	0
5	PEG	A	1007	-	6,6,6	0.24	0	5,5,5	0.18	0
4	DMS	A	1006	-	3,3,3	0.18	0	3,3,3	0.47	0
3	MES	A	1003[A]	-	12,12,12	0.85	0	15,16,16	0.77	0
5	PEG	A	1010	-	6,6,6	0.13	0	5,5,5	0.11	0
4	DMS	A	1004	-	3,3,3	0.83	0	3,3,3	0.47	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
7	B1A	A	1011[A]	-	-	0/8/8/8	0/2/2/2
3	MES	A	1003[B]	-	-	5/6/14/14	0/1/1/1
7	B1A	A	1011[B]	-	-	1/8/8/8	0/2/2/2
5	PEG	A	1007	-	-	3/4/4/4	-
3	MES	A	1003[A]	-	-	3/6/14/14	0/1/1/1
5	PEG	A	1010	-	-	2/4/4/4	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1008	PO4	P-O1	10.14	1.74	1.50
6	A	1008	PO4	P-O2	6.73	1.74	1.54
6	A	1008	PO4	P-O3	4.94	1.69	1.54
6	A	1008	PO4	P-O4	-2.16	1.48	1.54
6	A	1009	PO4	P-O1	2.10	1.55	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1008	PO4	O4-P-O2	2.55	115.83	107.91

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1003[A]	MES	C7-C8-S-O1S
3	A	1003[A]	MES	C7-C8-S-O2S
3	A	1003[A]	MES	C7-C8-S-O3S
3	A	1003[B]	MES	C8-C7-N4-C3
3	A	1003[B]	MES	C7-C8-S-O2S
3	A	1003[B]	MES	C7-C8-S-O3S
5	A	1007	PEG	O2-C3-C4-O4
5	A	1010	PEG	O2-C3-C4-O4
3	A	1003[B]	MES	C8-C7-N4-C5
3	A	1003[B]	MES	C7-C8-S-O1S
5	A	1010	PEG	O1-C1-C2-O2
5	A	1007	PEG	O1-C1-C2-O2
5	A	1007	PEG	C4-C3-O2-C2
7	A	1011[B]	B1A	O1-C2-N1-C3

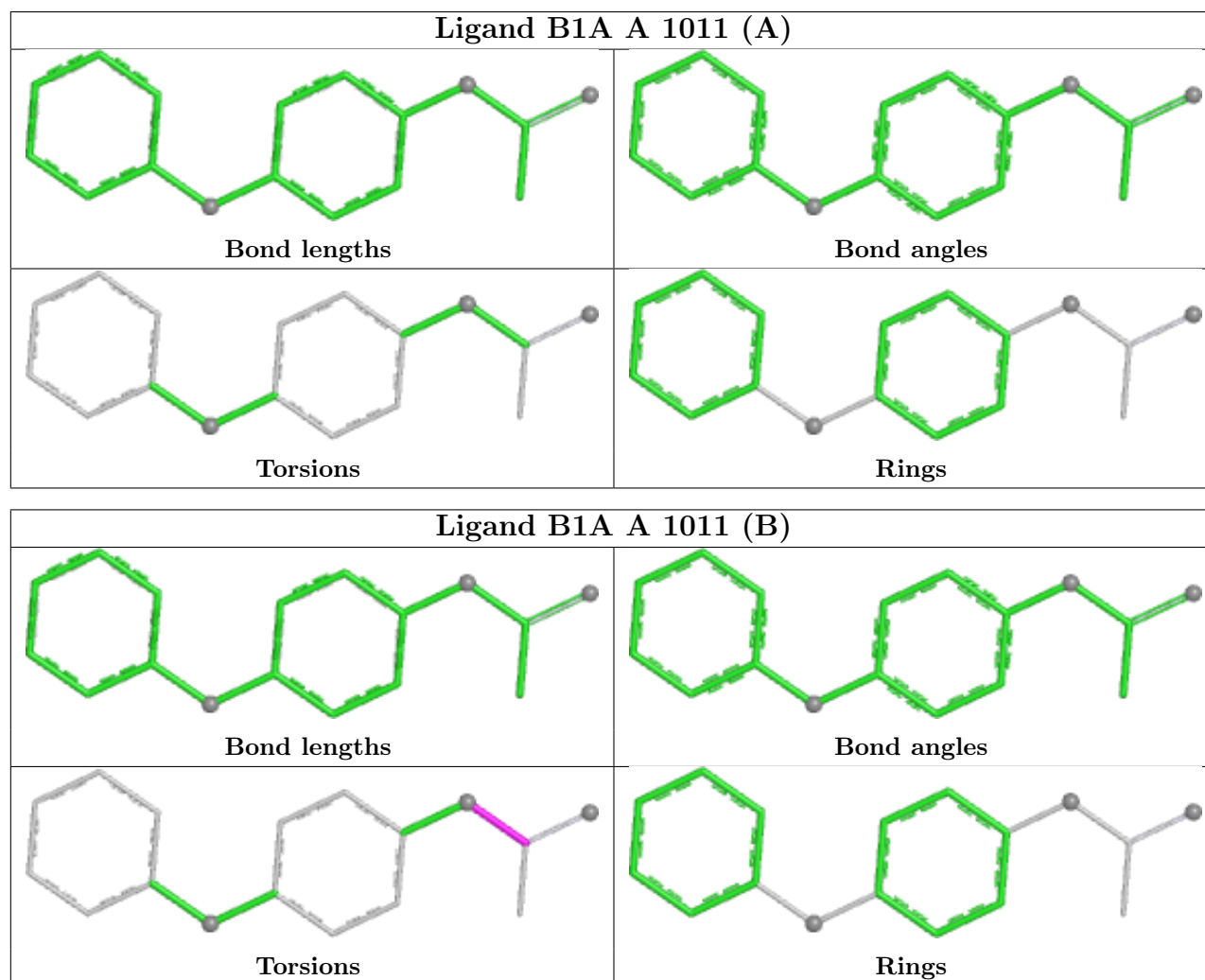
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1008	PO4	3	0
4	A	1004	DMS	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	573/637 (89%)	3.13	286 (49%) 0 0	6, 32, 63, 101	185 (32%)

All (286) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	512[A]	LEU	13.1
1	A	284	ILE	11.9
1	A	637	VAL	11.6
1	A	281	ILE	11.3
1	A	800	THR	11.1
1	A	474	ILE	11.0
1	A	641	ILE	11.0
1	A	593	ILE	10.9
1	A	514	LYS	10.9
1	A	801[A]	HIS	10.8
1	A	632	ILE	10.8
1	A	319	SER	10.6
1	A	705	GLN	10.3
1	A	441	LEU	10.3
1	A	376	ILE	10.3
1	A	635	LEU	10.2
1	A	799	ALA	10.1
1	A	407	ALA	10.0
1	A	412	ILE	9.9
1	A	889	PHE	9.9
1	A	636	THR	9.7
1	A	409	LEU	9.6
1	A	478	TRP	9.5
1	A	373	LEU	9.5
1	A	498	PHE	9.4
1	A	340	GLN	9.4
1	A	426	VAL	9.3

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Mol	Chain	Res	Type	RSRZ
1	A	294	TYR	9.3
1	A	431	PHE	9.3
1	A	876	ASN	9.2
1	A	577	VAL	9.2
1	A	594	SER	9.1
1	A	592	ILE	9.0
1	A	486	PHE	8.9
1	A	292	TRP	8.9
1	A	403	VAL	8.9
1	A	571	LEU	8.9
1	A	719[A]	LYS	8.9
1	A	763[A]	SER	8.8
1	A	343	MET	8.7
1	A	483	PHE	8.7
1	A	480	GLY	8.5
1	A	479	LEU	8.5
1	A	542	ILE	8.4
1	A	638	THR	8.4
1	A	318	SER	8.2
1	A	543	THR	8.2
1	A	430	GLY	8.1
1	A	475	TRP	8.1
1	A	377	THR	8.0
1	A	600	GLY	8.0
1	A	578	VAL	7.9
1	A	317	ALA	7.9
1	A	276	ILE	7.9
1	A	293	HIS	7.9
1	A	511	GLY	7.9
1	A	434	LEU	7.8
1	A	538	TRP	7.8
1	A	283	LYS	7.8
1	A	300	TYR	7.7
1	A	589	VAL	7.7
1	A	400	THR	7.7
1	A	298	HIS	7.7
1	A	301	LYS	7.7
1	A	606	THR	7.6
1	A	305	TYR	7.6
1	A	572	THR	7.6
1	A	399	PHE	7.6
1	A	499	SER	7.5

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Mol	Chain	Res	Type	RSRZ
1	A	452	TYR	7.4
1	A	505	SER	7.4
1	A	411	ALA	7.3
1	A	580	VAL	7.3
1	A	601	SER	7.2
1	A	277	ILE	7.2
1	A	280	ARG	7.2
1	A	448	GLU	7.2
1	A	274	LEU	7.1
1	A	742	GLN	7.1
1	A	694	TRP	7.1
1	A	595	ARG	7.1
1	A	484	LEU	7.0
1	A	864[A]	GLN	7.0
1	A	279	LYS	7.0
1	A	374	MET	7.0
1	A	308	SER	7.0
1	A	311	THR	6.9
1	A	422	ALA	6.9
1	A	375	LYS	6.9
1	A	442	HIS	6.9
1	A	303	TRP	6.9
1	A	449	THR	6.8
1	A	344	THR	6.8
1	A	745	GLY	6.7
1	A	419	TRP	6.7
1	A	405	SER	6.7
1	A	473	ALA	6.7
1	A	425	ALA	6.5
1	A	741[A]	SER	6.5
1	A	657	ARG	6.5
1	A	309	TYR	6.5
1	A	588	THR	6.5
1	A	536	ALA	6.5
1	A	408	ALA	6.4
1	A	476	TYR	6.4
1	A	503	SER	6.3
1	A	359	VAL	6.3
1	A	481	ALA	6.3
1	A	363	THR	6.3
1	A	793	THR	6.2
1	A	485	GLU	6.2

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Mol	Chain	Res	Type	RSRZ
1	A	575	ASN	6.2
1	A	658	MET	6.2
1	A	541	ARG	6.2
1	A	791	SER	6.1
1	A	602	GLY	6.1
1	A	581	GLN	6.1
1	A	358	LYS	6.0
1	A	744	ALA	6.0
1	A	282	GLU	5.9
1	A	634	HIS	5.9
1	A	785[A]	SER	5.9
1	A	295	ASP	5.9
1	A	544	LEU	5.8
1	A	633	GLN	5.8
1	A	535	THR	5.8
1	A	576	LYS	5.7
1	A	306	HIS	5.7
1	A	360	ASP	5.7
1	A	372	LYS	5.7
1	A	278	GLY	5.6
1	A	401	ARG	5.6
1	A	584	THR	5.6
1	A	603	GLN	5.6
1	A	361	THR	5.5
1	A	539	ASP	5.5
1	A	502	ASN	5.5
1	A	534	ASP	5.5
1	A	451	VAL	5.5
1	A	275	ASP	5.4
1	A	302	THR	5.4
1	A	273	ASN	5.4
1	A	693	GLN	5.4
1	A	546	ASP	5.4
1	A	421	SER	5.3
1	A	371	LYS	5.3
1	A	551	GLU	5.3
1	A	698	ARG	5.3
1	A	423	ARG	5.3
1	A	299	PRO	5.2
1	A	564	LEU	5.2
1	A	579	ARG	5.2
1	A	888	ARG	5.2

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Mol	Chain	Res	Type	RSRZ
1	A	365	GLU	5.2
1	A	583	PRO	5.2
1	A	427	GLU	5.1
1	A	482	ARG	5.1
1	A	654	ARG	5.1
1	A	406	ASN	5.1
1	A	304	ALA	5.1
1	A	290	THR	5.1
1	A	629	PHE	5.0
1	A	648	VAL	5.0
1	A	597	ASP	5.0
1	A	429	SER	5.0
1	A	746	TRP	5.0
1	A	402	LYS	4.9
1	A	296	GLN	4.9
1	A	404	ARG	4.9
1	A	677	ALA	4.9
1	A	596	ARG	4.9
1	A	433	GLU	4.9
1	A	364	GLN	4.9
1	A	362	ARG	4.8
1	A	291	SER	4.8
1	A	591	ASP	4.8
1	A	890	ARG	4.8
1	A	297	ASP	4.8
1	A	443	LEU	4.7
1	A	599	ARG	4.7
1	A	598	GLN	4.7
1	A	447	CYS	4.7
1	A	356	LYS	4.7
1	A	570	LYS	4.7
1	A	366	PRO	4.7
1	A	286	GLN	4.6
1	A	653	GLU	4.6
1	A	455	MET	4.6
1	A	548	LYS	4.6
1	A	285	LYS	4.6
1	A	563	LYS	4.6
1	A	501	GLU	4.5
1	A	428	ASP	4.5
1	A	537	GLY	4.5
1	A	590	MET	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	556	HIS	4.5
1	A	390	THR	4.4
1	A	582	ARG	4.4
1	A	887	LYS	4.3
1	A	437	LYS	4.3
1	A	357	GLU	4.2
1	A	440	ASN	4.2
1	A	510	GLU	4.1
1	A	370	THR	4.1
1	A	288	HIS	4.0
1	A	410	GLY	4.0
1	A	891	ARG	4.0
1	A	882	TYR	3.9
1	A	565	ALA	3.9
1	A	627	GLY	3.9
1	A	424	GLU	3.8
1	A	687	VAL	3.8
1	A	445	GLY	3.8
1	A	446	LYS	3.8
1	A	790	THR	3.7
1	A	818	ILE	3.7
1	A	676	SER	3.7
1	A	439	ARG	3.7
1	A	647	LEU	3.6
1	A	792	ARG	3.6
1	A	604	VAL	3.6
1	A	454	MET	3.6
1	A	552	MET	3.6
1	A	310	GLU	3.5
1	A	435	VAL	3.5
1	A	287	GLU	3.5
1	A	453	ASN	3.5
1	A	398	GLU	3.4
1	A	444	GLU	3.4
1	A	830	VAL	3.4
1	A	368	GLU	3.3
1	A	438	GLU	3.3
1	A	649	ARG	3.3
1	A	880	THR	3.3
1	A	650	VAL	3.3
1	A	568	ILE	3.2
1	A	432	TRP	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	851	ILE	3.1
1	A	569	PHE	3.1
1	A	645	ASN	3.1
1	A	644	LYS	3.0
1	A	396	ARG	3.0
1	A	861	LYS	3.0
1	A	553	VAL	3.0
1	A	418	LYS	3.0
1	A	642	ALA	2.9
1	A	540	THR	2.9
1	A	493	ASN	2.9
1	A	555	ASN	2.9
1	A	558	GLU	2.8
1	A	881	ASP	2.8
1	A	605	VAL	2.8
1	A	420	LYS	2.8
1	A	672	ASP	2.8
1	A	680	ALA	2.7
1	A	683	ASP	2.7
1	A	436	ASP	2.7
1	A	625	GLY	2.6
1	A	743	GLY	2.6
1	A	393	MET	2.6
1	A	695	GLU	2.6
1	A	692	GLN	2.5
1	A	559	GLY	2.5
1	A	886	MET	2.5
1	A	307	GLY	2.5
1	A	367	LYS	2.5
1	A	701	ASN	2.4
1	A	489	LEU	2.4
1	A	289	GLU	2.4
1	A	494	GLU	2.4
1	A	875	GLY	2.4
1	A	643	VAL	2.4
1	A	395	THR	2.4
1	A	394	CYS	2.3
1	A	690	ASP	2.3
1	A	369	GLY	2.3
1	A	691	ILE	2.2
1	A	828	THR	2.2
1	A	807	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	491	PHE	2.2
1	A	640	GLU	2.1
1	A	678	LEU	2.1
1	A	337	MET	2.0
1	A	628	VAL	2.0
1	A	652	ARG	2.0
1	A	841	LYS	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 oligosaccharides 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.

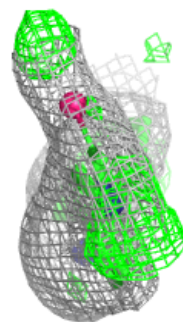
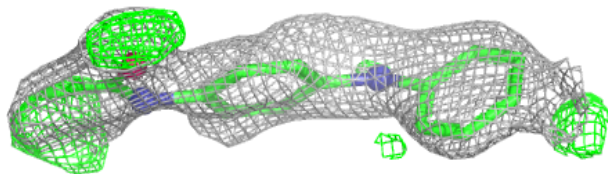
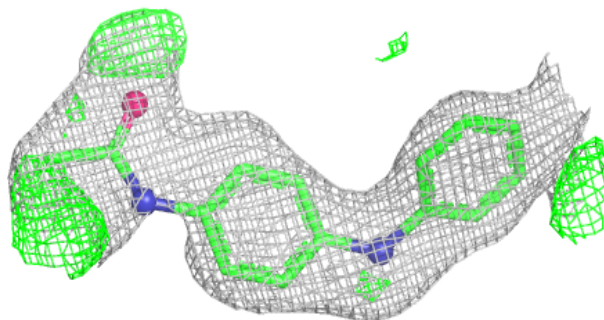
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	B1A	A	1011[A]	17/17	0.57	0.28	32,43,47,47	17
7	B1A	A	1011[B]	17/17	0.57	0.28	26,30,32,33	17
6	PO4	A	1009	5/5	0.63	0.17	72,81,90,109	0
4	DMS	A	1005	4/4	0.70	0.29	74,83,95,107	0
5	PEG	A	1007	7/7	0.78	0.17	88,90,91,94	0
6	PO4	A	1008	5/5	0.80	0.16	30,33,44,62	0
5	PEG	A	1010	7/7	0.83	0.15	57,64,72,76	0
4	DMS	A	1004	4/4	0.92	0.16	39,44,45,45	0
4	DMS	A	1006	4/4	0.93	0.13	47,51,57,59	0
3	MES	A	1003[B]	12/12	0.97	0.33	695,733,806,808	12
3	MES	A	1003[A]	12/12	0.97	0.33	20,25,27,29	12
2	ZN	A	1002	1/1	0.98	0.08	51,51,51,51	0
8	CL	A	1012	1/1	0.99	0.05	37,37,37,37	0
2	ZN	A	1001	1/1	1.00	0.02	20,20,20,20	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.

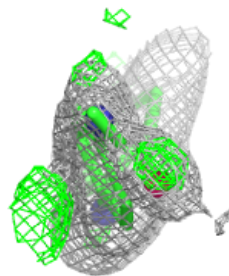
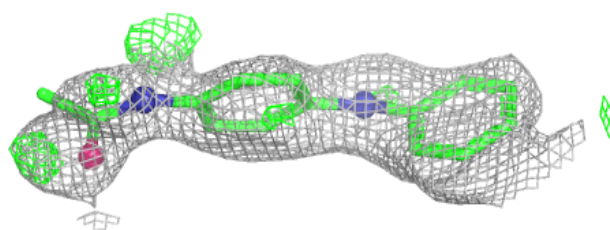
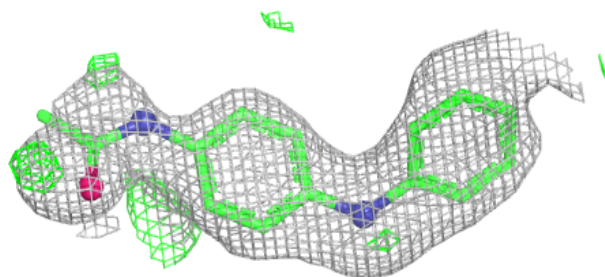
Electron density around B1A A 1011 (A):

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



Electron density around B1A A 1011 (B):

$2mF_o-DF_c$ (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.