



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 02:14 PM UTC

PDB ID : 7HKK / pdb_00007hkk
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 Z802824098 (DNV2_NS5A-x0279)
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Deposited on : 2024-10-15
Resolution : 1.66 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)

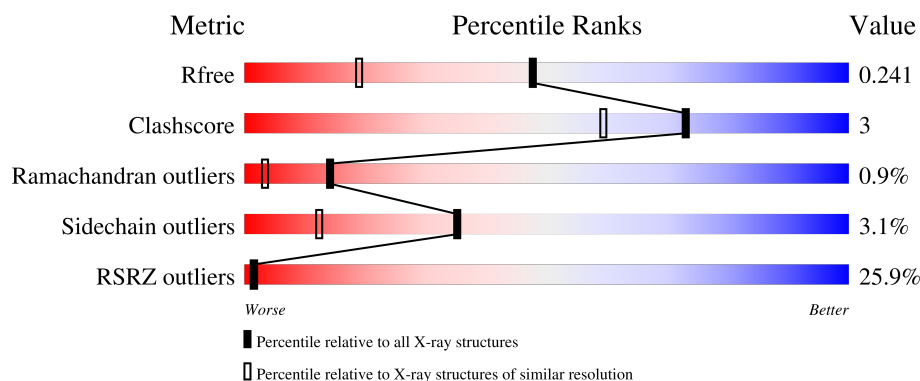
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.66 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	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	24% 82% 9% 9%

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
5	PEG	A	1009	-	-	-	X
6	PO4	A	1008	-	X	X	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 5353 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 Genome polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	582	Total	C	N	O	S	0	8	0
			4822	3036	865	887	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		
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		
5	A	1	Total	C	O	0	0
			7	4	3		

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



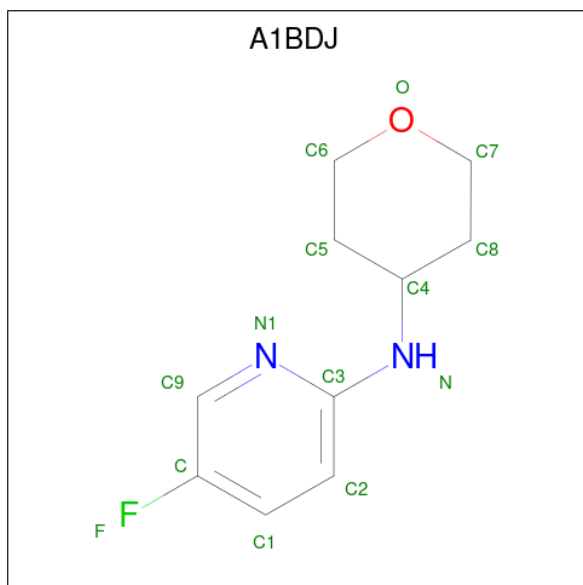
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	P	0	0
			5	4	1		

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

- Molecule 7 is 5-fluoro-N-(oxan-4-yl)pyridin-2-amine (CCD ID: A1BDJ) (formula: C₁₀H₁₃FN₂O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	F	N	O	0	0
			14	10	1	2	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	444	Total	O	0	0
			444	444		

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: Genome polypeptide



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	82.54Å 116.83Å 148.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.30 – 1.66 74.30 – 1.66	Depositor EDS
% Data completeness (in resolution range)	98.4 (74.30-1.66) 98.4 (74.30-1.66)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.98 (at 1.66Å)	Xtriage
Refinement program	REFMAC 5.8.0267, REFMAC5	Depositor
R, R_{free}	0.196 , 0.226 0.218 , 0.241	Depositor DCC
R_{free} test set	4338 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	31.5	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 60.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5353	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% 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: PO4, MES, PEG, DMS, A1BDJ, ZN

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	1.07	3/4929 (0.1%)	1.32	4/6645 (0.1%)

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	751	THR	C-O	5.66	1.30	1.24
1	A	768	HIS	CE1-NE2	5.22	1.37	1.32
1	A	650	VAL	N-CA	5.07	1.50	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	702	ASP	CA-CB-CG	5.61	118.20	112.60
1	A	650	VAL	CA-C-N	5.58	126.30	119.99
1	A	650	VAL	C-N-CA	5.58	126.30	119.99
1	A	702	ASP	CB-CA-C	5.20	118.47	110.14

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	273	ASN	Peptide

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	4822	0	4720	28	0
2	A	2	0	0	0	0
3	A	24	0	26	0	0
4	A	16	0	24	3	0
5	A	21	0	30	0	0
6	A	10	0	0	4	0
7	A	14	0	0	0	0
8	A	444	0	0	7	1
All	All	5353	0	4800	31	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 (31) 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	1.98	0.81
4:A:1004:DMS:H11	8:A:1219:HOH:O	1.91	0.69
1:A:664:ASP:OD1	6:A:1008:PO4:P	2.53	0.66
1:A:733:GLU:O	1:A:737:ARG:HG3	1.97	0.65
1:A:534:ASP:OD1	6:A:1008:PO4:O4	2.18	0.62
1:A:886:MET:HE1	8:A:1245:HOH:O	2.04	0.57
1:A:428:ASP:OD1	1:A:430:GLY:N	2.34	0.57
1:A:638:THR:HA	1:A:641:ILE:HG22	1.87	0.56
1:A:447:CYS:SG	1:A:450:CYS:HB2	2.49	0.53
1:A:819:GLN:NE2	8:A:1108:HOH:O	2.41	0.52
1:A:528:GLY:O	1:A:668:LYS:HE3	2.09	0.51
1:A:406:ASN:OD1	1:A:423:ARG:NH1	2.44	0.51
1:A:580:VAL:HG21	1:A:593:ILE:HD11	1.93	0.51
1:A:303:TRP:CE3	1:A:593:ILE:HD12	2.46	0.51
1:A:534:ASP:OD1	6:A:1008:PO4:P	2.68	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1004:DMS:H12	8:A:1278:HOH:O	2.10	0.50
1:A:418:LYS:HB3	1:A:419:TRP:CE3	2.50	0.47
1:A:886:MET:CE	8:A:1245:HOH:O	2.62	0.46
1:A:394:CYS:HB3	1:A:486:PHE:CE2	2.51	0.46
1:A:411:ALA:HA	1:A:477:MET:O	2.16	0.45
1:A:764:LEU:O	1:A:765:MET:HE2	2.15	0.45
1:A:428:ASP:OD1	1:A:428:ASP:C	2.59	0.45
1:A:321:VAL:HG11	1:A:326:ARG:CZ	2.47	0.44
1:A:475:TRP:CD1	1:A:475:TRP:N	2.84	0.44
1:A:438:GLU:HG3	1:A:449:THR:OG1	2.18	0.44
4:A:1004:DMS:C1	8:A:1219:HOH:O	2.59	0.43
1:A:750:GLU:OE1	8:A:1101:HOH:O	2.22	0.42
1:A:599:ARG:HG2	1:A:606:THR:HG23	2.00	0.42
1:A:764:LEU:C	1:A:765:MET:HE2	2.44	0.42
1:A:746:TRP:CH2	1:A:754:LEU:HD22	2.55	0.42
1:A:514:LYS:HD2	1:A:823:TRP:HZ3	1.87	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)
8:A:1126:HOH:O	8:A:1126:HOH:O[2_445]	1.52	0.68

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	576/637 (90%)	545 (95%)	26 (4%)	5 (1%)	14 3

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	420	LYS
1	A	406	ASN
1	A	418	LYS
1	A	291	SER
1	A	876	ASN

5.3.2 Protein sidechains ⓘ

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	518/554 (94%)	502 (97%)	16 (3%)	35 12

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	273	ASN
1	A	274	LEU
1	A	311	THR
1	A	335	ILE
1	A	356	LYS
1	A	375	LYS
1	A	409	LEU
1	A	426	VAL
1	A	429	SER
1	A	455	MET
1	A	580	VAL
1	A	589	VAL
1	A	634	HIS
1	A	641	ILE
1	A	830	VAL
1	A	887	LYS

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

Mol	Chain	Res	Type
1	A	581	GLN

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Mol	Chain	Res	Type
1	A	603	GLN
1	A	618	GLN
1	A	701	ASN
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, 2 are monoatomic - leaving 12 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	4.53	4 (100%)	6,6,6	0.77	0
7	A1BDJ	A	1012	-	15,15,15	0.29	0	16,19,19	0.26	0
5	PEG	A	1009	-	6,6,6	0.13	0	5,5,5	0.07	0
5	PEG	A	1011	-	6,6,6	0.12	0	5,5,5	0.20	0
3	MES	A	1003[A]	-	12,12,12	0.72	0	15,16,16	0.66	1 (6%)
3	MES	A	1003[B]	-	12,12,12	0.70	0	15,16,16	0.29	0
4	DMS	A	1013	-	3,3,3	0.23	0	3,3,3	0.06	0
4	DMS	A	1004	-	3,3,3	0.48	0	3,3,3	0.36	0
5	PEG	A	1007	-	6,6,6	0.14	0	5,5,5	0.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	PO4	A	1010	-	4,4,4	0.84	0	6,6,6	0.48	0
4	DMS	A	1005	-	3,3,3	0.32	0	3,3,3	0.06	0
4	DMS	A	1006	-	3,3,3	0.12	0	3,3,3	0.23	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	A1BDJ	A	1012	-	-	1/4/12/12	0/2/2/2
5	PEG	A	1009	-	-	2/4/4/4	-
5	PEG	A	1011	-	-	2/4/4/4	-
3	MES	A	1003[A]	-	-	0/6/14/14	0/1/1/1
3	MES	A	1003[B]	-	-	5/6/14/14	0/1/1/1
5	PEG	A	1007	-	-	3/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1008	PO4	P-O1	7.23	1.67	1.50
6	A	1008	PO4	P-O2	4.33	1.67	1.54
6	A	1008	PO4	P-O3	2.57	1.62	1.54
6	A	1008	PO4	P-O4	-2.11	1.48	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1003[A]	MES	O2S-S-C8	-2.21	103.39	106.73

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
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	C4-C3-O2-C2
5	A	1007	PEG	O2-C3-C4-O4
5	A	1009	PEG	O2-C3-C4-O4

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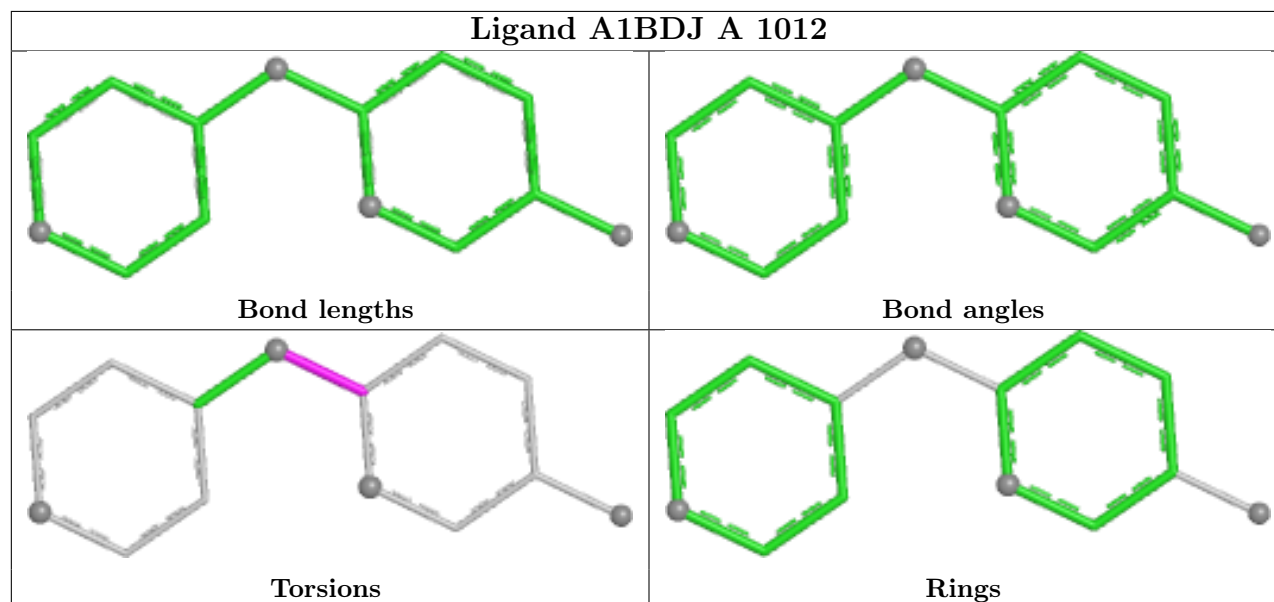
Mol	Chain	Res	Type	Atoms
5	A	1007	PEG	O1-C1-C2-O2
5	A	1009	PEG	O1-C1-C2-O2
5	A	1011	PEG	O2-C3-C4-O4
3	A	1003[B]	MES	C8-C7-N4-C5
3	A	1003[B]	MES	C7-C8-S-O1S
5	A	1011	PEG	C4-C3-O2-C2
7	A	1012	A1BDJ	N1-C3-N-C4

There are no ring outliers.

2 monomers are involved in 7 short contacts:

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

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	582/637 (91%)	1.64	151 (25%) 1 1	6, 42, 110, 151	35 (6%)

All (151) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	512[A]	LEU	15.8
1	A	426	VAL	15.3
1	A	700	TRP	15.2
1	A	800	THR	14.4
1	A	801[A]	HIS	14.4
1	A	511	GLY	13.2
1	A	719[A]	LYS	13.1
1	A	531	TYR	11.9
1	A	400	THR	10.8
1	A	696	PRO	10.5
1	A	697	SER	10.1
1	A	763[A]	SER	9.6
1	A	384	GLU	9.3
1	A	383	LYS	8.9
1	A	864[A]	GLN	8.8
1	A	699	GLY	8.6
1	A	551[A]	GLU	8.6
1	A	741[A]	SER	8.5
1	A	589	VAL	8.4
1	A	698	ARG	8.2
1	A	306	HIS	8.2
1	A	785[A]	SER	8.1
1	A	875	GLY	8.0
1	A	340	GLN	7.8
1	A	851	ILE	7.8
1	A	343	MET	7.8
1	A	533	ASP	7.7

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Mol	Chain	Res	Type	RSRZ
1	A	852	GLY	7.4
1	A	510	GLU	7.3
1	A	705	GLN	7.2
1	A	876	ASN	6.5
1	A	799	ALA	6.4
1	A	600	GLY	6.0
1	A	690	ASP	5.9
1	A	409	LEU	5.6
1	A	413	PHE	5.6
1	A	294	TYR	5.6
1	A	355	PHE	5.4
1	A	841	LYS	5.4
1	A	407	ALA	5.3
1	A	475	TRP	5.0
1	A	412	ILE	4.8
1	A	842	ARG	4.8
1	A	770	ARG	4.7
1	A	637	VAL	4.5
1	A	359	VAL	4.4
1	A	745	GLY	4.4
1	A	845	GLN	4.2
1	A	284	ILE	4.1
1	A	889	PHE	4.0
1	A	307	GLY	4.0
1	A	584	THR	3.9
1	A	363	THR	3.9
1	A	317	ALA	3.9
1	A	419	TRP	3.9
1	A	431	PHE	3.9
1	A	794	THR	3.9
1	A	274	LEU	3.8
1	A	314	THR	3.8
1	A	305	TYR	3.7
1	A	298	HIS	3.7
1	A	597	ASP	3.7
1	A	277	ILE	3.7
1	A	292	TRP	3.7
1	A	593	ILE	3.6
1	A	411	ALA	3.6
1	A	583	PRO	3.5
1	A	281	ILE	3.5
1	A	303	TRP	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	571	LEU	3.5
1	A	473	ALA	3.5
1	A	288	HIS	3.4
1	A	311	THR	3.3
1	A	588	THR	3.3
1	A	642	ALA	3.3
1	A	454	MET	3.2
1	A	435	VAL	3.2
1	A	744	ALA	3.2
1	A	403	VAL	3.2
1	A	344	THR	3.2
1	A	290	THR	3.1
1	A	577	VAL	3.1
1	A	592	ILE	3.0
1	A	319	SER	3.0
1	A	590	MET	3.0
1	A	635	LEU	3.0
1	A	410	GLY	3.0
1	A	293	HIS	2.9
1	A	309	TYR	2.9
1	A	443	LEU	2.9
1	A	455	MET	2.9
1	A	356	LYS	2.9
1	A	428	ASP	2.9
1	A	360	ASP	2.8
1	A	452	TYR	2.8
1	A	361	THR	2.8
1	A	793	THR	2.8
1	A	881	ASP	2.8
1	A	581	GLN	2.8
1	A	432	TRP	2.7
1	A	882	TYR	2.7
1	A	442	HIS	2.7
1	A	476	TYR	2.7
1	A	304	ALA	2.7
1	A	451	VAL	2.7
1	A	478	TRP	2.6
1	A	694	TRP	2.6
1	A	299	PRO	2.6
1	A	746	TRP	2.6
1	A	422	ALA	2.6
1	A	310	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	544	LEU	2.5
1	A	884	PRO	2.5
1	A	638	THR	2.5
1	A	358	LYS	2.5
1	A	471	SER	2.5
1	A	717	ILE	2.5
1	A	300	TYR	2.5
1	A	425	ALA	2.5
1	A	474	ILE	2.5
1	A	830	VAL	2.5
1	A	880	THR	2.5
1	A	634	HIS	2.4
1	A	578	VAL	2.4
1	A	580	VAL	2.4
1	A	558	GLU	2.4
1	A	552	MET	2.4
1	A	399	PHE	2.4
1	A	582	ARG	2.4
1	A	641	ILE	2.3
1	A	308	SER	2.3
1	A	295	ASP	2.3
1	A	408	ALA	2.3
1	A	276	ILE	2.3
1	A	723	VAL	2.3
1	A	891	ARG	2.3
1	A	563	LYS	2.3
1	A	390	THR	2.2
1	A	434	LEU	2.2
1	A	484	LEU	2.2
1	A	275	ASP	2.2
1	A	591	ASP	2.2
1	A	477	MET	2.2
1	A	445	GLY	2.2
1	A	417	ASN	2.2
1	A	418	LYS	2.2
1	A	289	GLU	2.2
1	A	565	ALA	2.1
1	A	441	LEU	2.1
1	A	648	VAL	2.1
1	A	406	ASN	2.1

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](#)

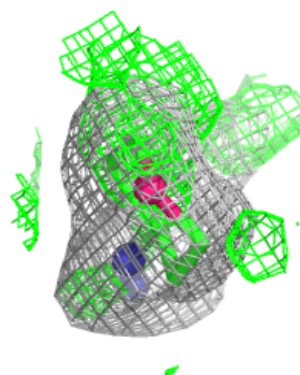
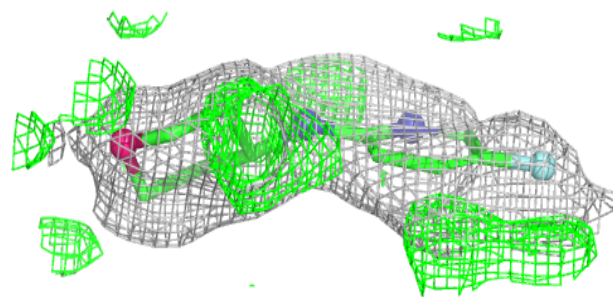
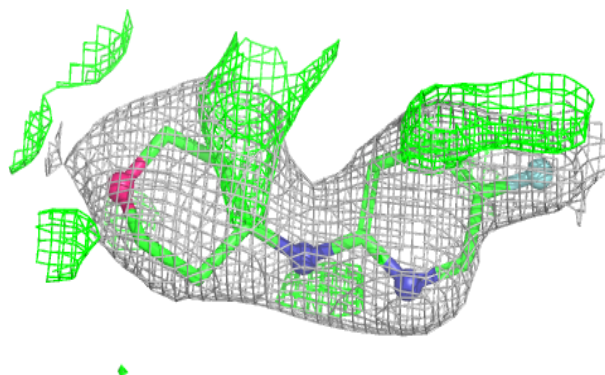
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	PEG	A	1009	7/7	0.63	0.60	194,195,196,197	7
6	PO4	A	1010	5/5	0.64	0.15	80,84,96,107	0
4	DMS	A	1005	4/4	0.72	0.27	80,96,103,113	0
6	PO4	A	1008	5/5	0.73	0.16	36,40,54,57	0
5	PEG	A	1007	7/7	0.73	0.26	49,50,51,51	7
4	DMS	A	1013	4/4	0.76	0.31	106,108,115,119	0
7	A1BDJ	A	1012	14/14	0.79	0.26	52,54,58,58	14
5	PEG	A	1011	7/7	0.85	0.15	63,70,75,77	0
4	DMS	A	1004	4/4	0.92	0.15	50,51,54,54	0
3	MES	A	1003[B]	12/12	0.97	0.35	750,769,810,813	12
4	DMS	A	1006	4/4	0.97	0.10	58,62,62,65	0
3	MES	A	1003[A]	12/12	0.97	0.35	24,28,32,32	12
2	ZN	A	1002	1/1	0.99	0.06	58,58,58,58	0
2	ZN	A	1001	1/1	1.00	0.01	23,23,23,23	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 A1BDJ A 1012:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.