



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 03:28 AM UTC

PDB ID : 7I2H / pdb_00007i2h
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 Z1198177230 (DENV2_NS5A-x0411)
Authors : Aschenbrenner, J.C.; Saini, M.; Chopra, A.; Marples, P.G.; Balcomb, B.H.; Lithgo, R.M.; Fearon, D.; von Delft, F.; Ruiz, F.X.; Arnold, E.
Deposited on : 2025-03-06
Resolution : 1.84 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)

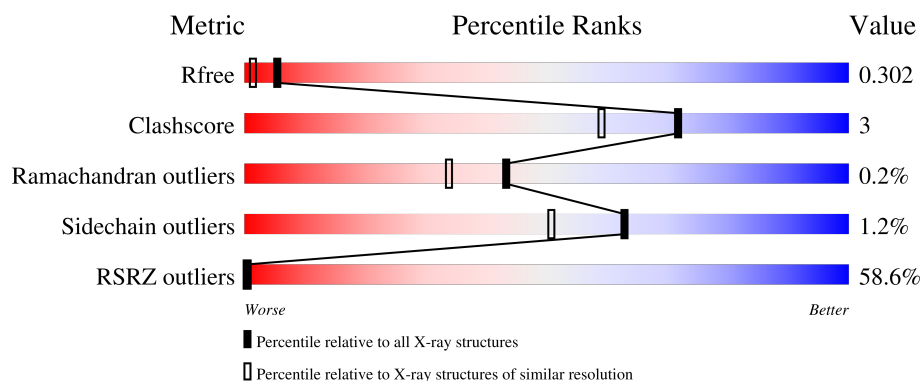
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.84 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	1296 (1.84-1.84)
Clashscore	190562	1329 (1.84-1.84)
Ramachandran outliers	187476	1318 (1.84-1.84)
Sidechain outliers	187428	1318 (1.84-1.84)
RSRZ outliers	180081	1296 (1.84-1.84)

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	52% 82% 7% 11%

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	PO4	A	1007	-	-	X	-
7	K6U	A	1010	-	-	-	X

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 5078 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	567	Total	C	N	O	S	0	7	0
			4690	2953	841	862	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).



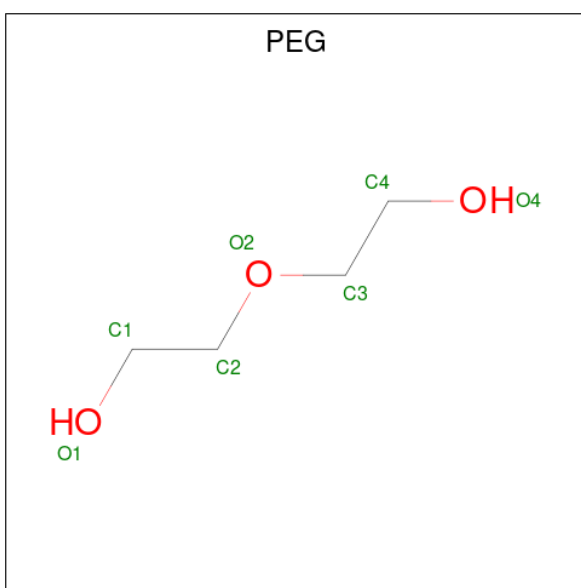
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	S	0	0
			4	2	1	1		
4	A	1	Total	C	O	S	0	0
			4	2	1	1		
4	A	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



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

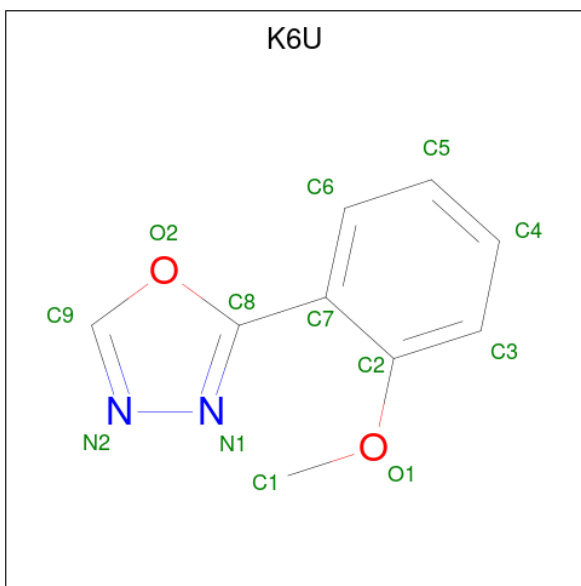
- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

- Molecule 7 is (2M)-2-(2-methoxyphenyl)-1,3,4-oxadiazole (CCD ID: K6U) (formula:

C₉H₈N₂O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			13	9	2	2		
7	A	1	Total	C	N	O	0	0
			13	9	2	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		

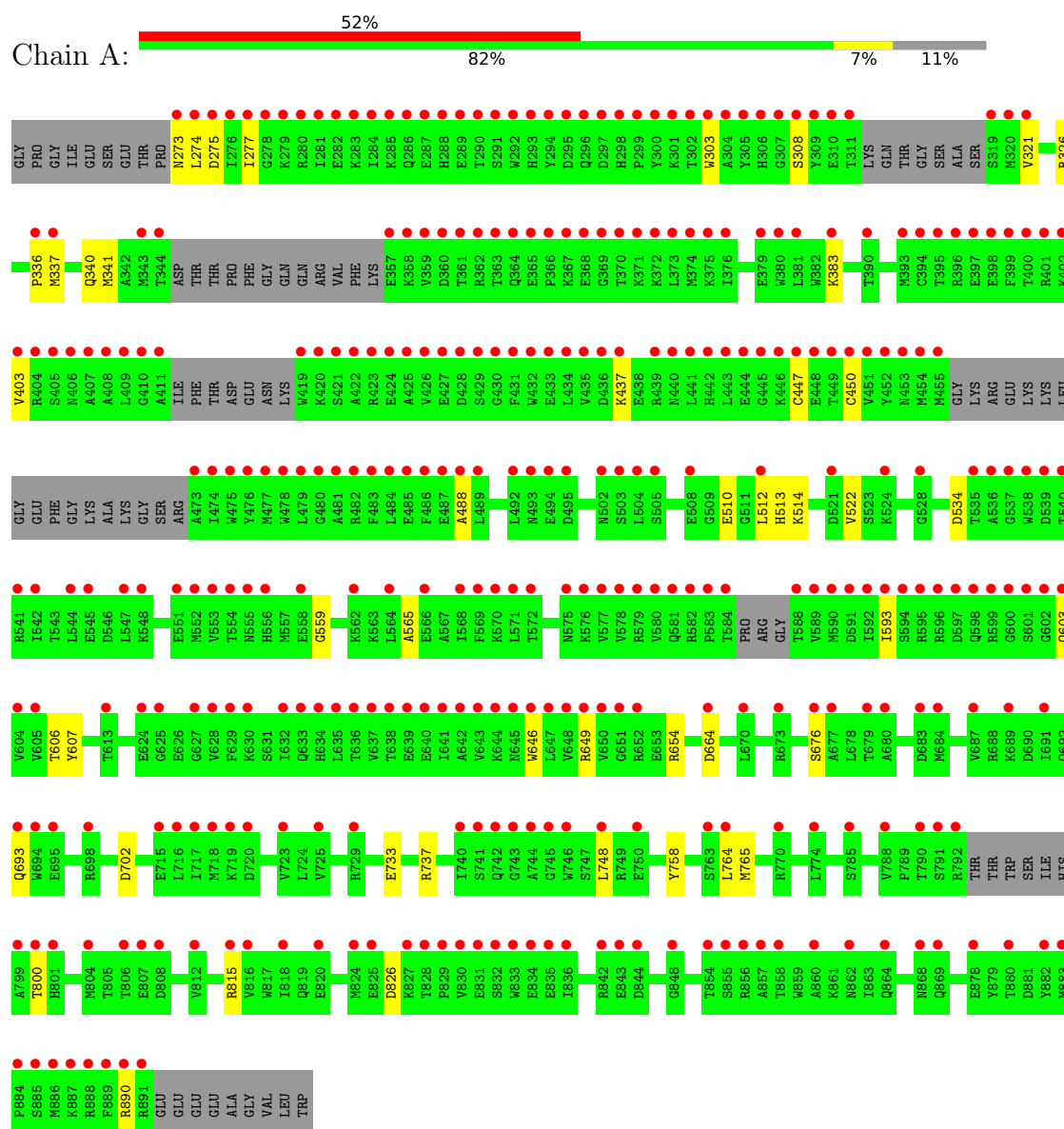
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	306	Total	O	0	0
			306	306		

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	82.38Å 115.50Å 146.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.50 – 1.84 37.50 – 1.84	Depositor EDS
% Data completeness (in resolution range)	95.7 (37.50-1.84) 95.7 (37.50-1.84)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 1.84Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.203 , 0.244 0.284 , 0.302	Depositor DCC
R_{free} test set	3160 reflections (5.19%)	wwPDB-VP
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.278	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 149.2	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	0.86	EDS
Total number of atoms	5078	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.07% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, CL, MES, ZN, K6U, DMS, PO4

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	1.08	2/4795 (0.0%)	1.38	4/6467 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	815	ARG	C-O	5.57	1.30	1.24
1	A	522	VAL	C-O	-5.05	1.18	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	702	ASP	CA-CB-CG	5.79	118.39	112.60
1	A	559	GLY	CA-C-N	5.55	127.72	120.28
1	A	559	GLY	C-N-CA	5.55	127.72	120.28
1	A	437	LYS	N-CA-C	-5.50	104.97	110.97

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4690	0	4584	28	0
2	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	24	0	26	1	0
4	A	12	0	18	4	0
5	A	10	0	0	3	0
6	A	7	0	10	0	0
7	A	26	0	0	1	0
8	A	1	0	0	0	0
9	A	306	0	0	6	3
All	All	5078	0	4638	31	3

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	5:A:1007:PO4:O4	2.06	0.73
1:A:607:TYR:H	7:A:1010:K6U:C9	2.04	0.71
4:A:1004:DMS:H11	9:A:1192:HOH:O	1.89	0.71
1:A:510:GLU:O	1:A:514:LYS:HG3	1.92	0.69
1:A:336:PRO:O	1:A:340:GLN:HG2	1.96	0.66
1:A:534:ASP:OD1	5:A:1007:PO4:O4	2.18	0.61
1:A:800:THR:HG21	9:A:1102:HOH:O	2.04	0.57
4:A:1004:DMS:H12	9:A:1256:HOH:O	2.05	0.56
4:A:1004:DMS:C1	9:A:1192:HOH:O	2.51	0.53
1:A:337:MET:HG2	9:A:1295:HOH:O	2.10	0.52
1:A:603:GLN:HB2	1:A:606:THR:OG1	2.11	0.51
1:A:513:HIS:HB3	1:A:765:MET:HE1	1.96	0.48
1:A:664:ASP:OD1	5:A:1007:PO4:P	2.71	0.48
1:A:733:GLU:O	1:A:737:ARG:HG3	2.15	0.46
1:A:447:CYS:SG	1:A:450:CYS:HB2	2.55	0.46
1:A:764:LEU:HG	1:A:765:MET:HE3	1.98	0.46
1:A:748:LEU:HD13	3:A:1003[B]:MES:H61	1.98	0.46
1:A:826:ASP:OD1	1:A:826:ASP:C	2.60	0.44
1:A:764:LEU:O	1:A:765:MET:HE2	2.16	0.44
1:A:488:ALA:HB1	1:A:565:ALA:HA	2.00	0.44
1:A:758:TYR:CD1	4:A:1006:DMS:H21	2.54	0.43
1:A:274:LEU:HA	1:A:277:ILE:HG12	2.00	0.43
1:A:275:ASP:OD1	1:A:275:ASP:N	2.52	0.42
1:A:321:VAL:HG11	1:A:326:ARG:CZ	2.50	0.41
1:A:273:ASN:N	1:A:275:ASP:OD1	2.52	0.41
1:A:737:ARG:HB3	9:A:1343:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:TRP:CD2	1:A:593:ILE:HD12	2.55	0.41
1:A:341:MET:HE1	1:A:737:ARG:HG3	2.03	0.41
1:A:512[B]:LEU:HD23	1:A:512[B]:LEU:HA	1.90	0.41
1:A:336:PRO:O	1:A:340:GLN:CG	2.67	0.41
1:A:646:TRP:CZ2	1:A:654:ARG:HG3	2.56	0.40

All (3) 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:1105:HOH:O	9:A:1105:HOH:O[2_445]	1.75	0.45
9:A:1251:HOH:O	9:A:1368:HOH:O[2_445]	2.09	0.11
9:A:1247:HOH:O	9:A:1344:HOH:O[2_545]	2.18	0.02

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	560/637 (88%)	535 (96%)	24 (4%)	1 (0%)	43	34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	890	ARG

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	503/554 (91%)	497 (99%)	6 (1%)	63	51

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	308	SER
1	A	383	LYS
1	A	403	VAL
1	A	649	ARG
1	A	676	SER
1	A	693	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	288	HIS
1	A	493	ASN
1	A	645	ASN
1	A	869	GLN

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 13 ligands modelled in this entry, 3 are monoatomic - leaving 10 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
3	MES	A	1003[A]	-	12,12,12	0.82	0	15,16,16	0.52	0
3	MES	A	1003[B]	-	12,12,12	0.87	0	15,16,16	0.62	0
6	PEG	A	1009	-	6,6,6	0.14	0	5,5,5	0.10	0
4	DMS	A	1005	-	3,3,3	0.24	0	3,3,3	0.02	0
5	PO4	A	1007	-	4,4,4	3.49	3 (75%)	6,6,6	0.71	0
7	K6U	A	1011	-	13,14,14	0.24	0	13,18,18	0.59	0
4	DMS	A	1004	-	3,3,3	0.47	0	3,3,3	0.39	0
7	K6U	A	1010	-	13,14,14	0.18	0	13,18,18	0.45	0
4	DMS	A	1006	-	3,3,3	0.12	0	3,3,3	0.40	0
5	PO4	A	1008	-	4,4,4	1.04	0	6,6,6	0.42	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MES	A	1003[A]	-	-	3/6/14/14	0/1/1/1
3	MES	A	1003[B]	-	-	4/6/14/14	0/1/1/1
6	PEG	A	1009	-	-	2/4/4/4	-
7	K6U	A	1011	-	-	3/6/6/6	0/2/2/2
7	K6U	A	1010	-	-	3/6/6/6	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1007	PO4	P-O1	6.04	1.64	1.50
5	A	1007	PO4	P-O2	2.40	1.61	1.54
5	A	1007	PO4	P-O3	2.14	1.60	1.54

There are no bond angle outliers.

There are no chirality outliers.

All (15) 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-O3S
3	A	1003[B]	MES	C8-C7-N4-C3
6	A	1009	PEG	O2-C3-C4-O4
7	A	1011	K6U	C3-C2-O1-C1
7	A	1011	K6U	C7-C2-O1-C1
7	A	1010	K6U	C2-C7-C8-N1
3	A	1003[A]	MES	C7-C8-S-O2S
7	A	1011	K6U	C2-C7-C8-N1
7	A	1010	K6U	C3-C2-O1-C1
3	A	1003[B]	MES	C8-C7-N4-C5
7	A	1010	K6U	C7-C2-O1-C1
3	A	1003[B]	MES	C7-C8-S-O3S
3	A	1003[B]	MES	C7-C8-S-O2S
6	A	1009	PEG	C4-C3-O2-C2

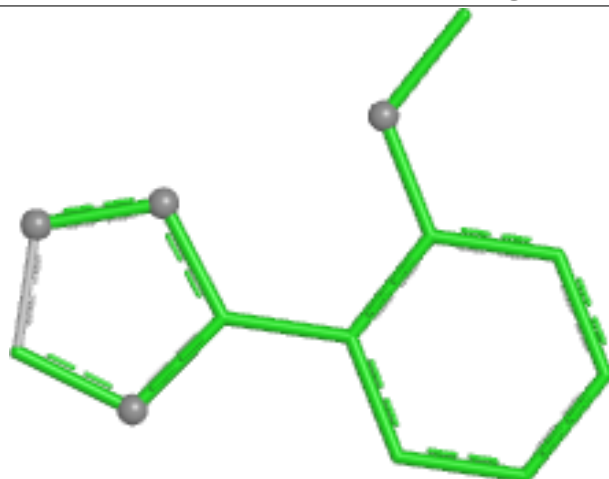
There are no ring outliers.

5 monomers are involved in 9 short contacts:

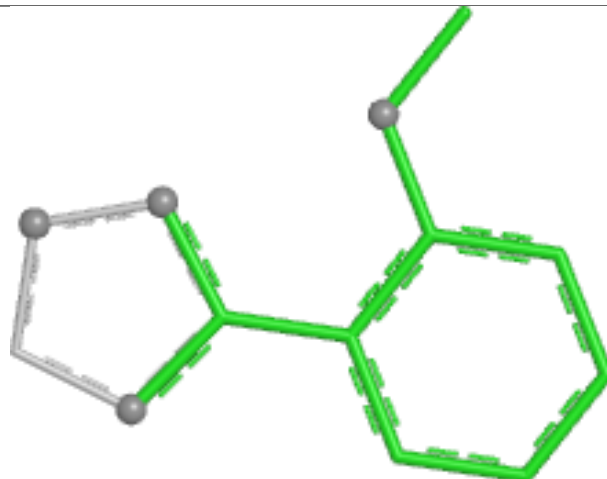
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1003[B]	MES	1	0
5	A	1007	PO4	3	0
4	A	1004	DMS	3	0
7	A	1010	K6U	1	0
4	A	1006	DMS	1	0

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.

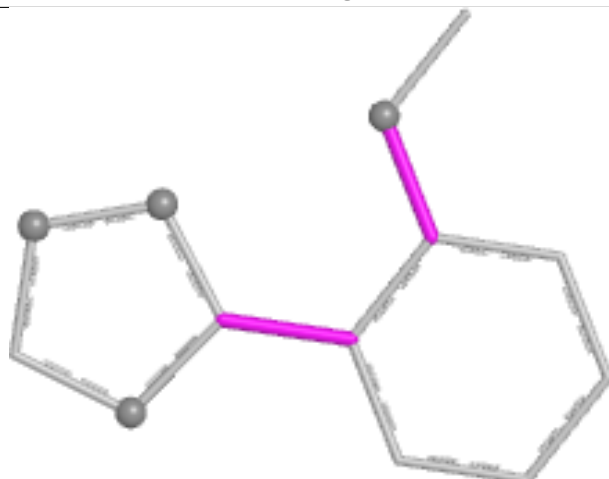
Ligand K6U A 1011



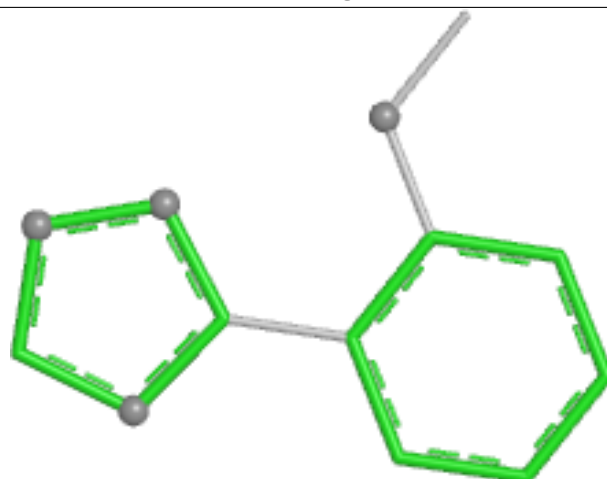
Bond lengths



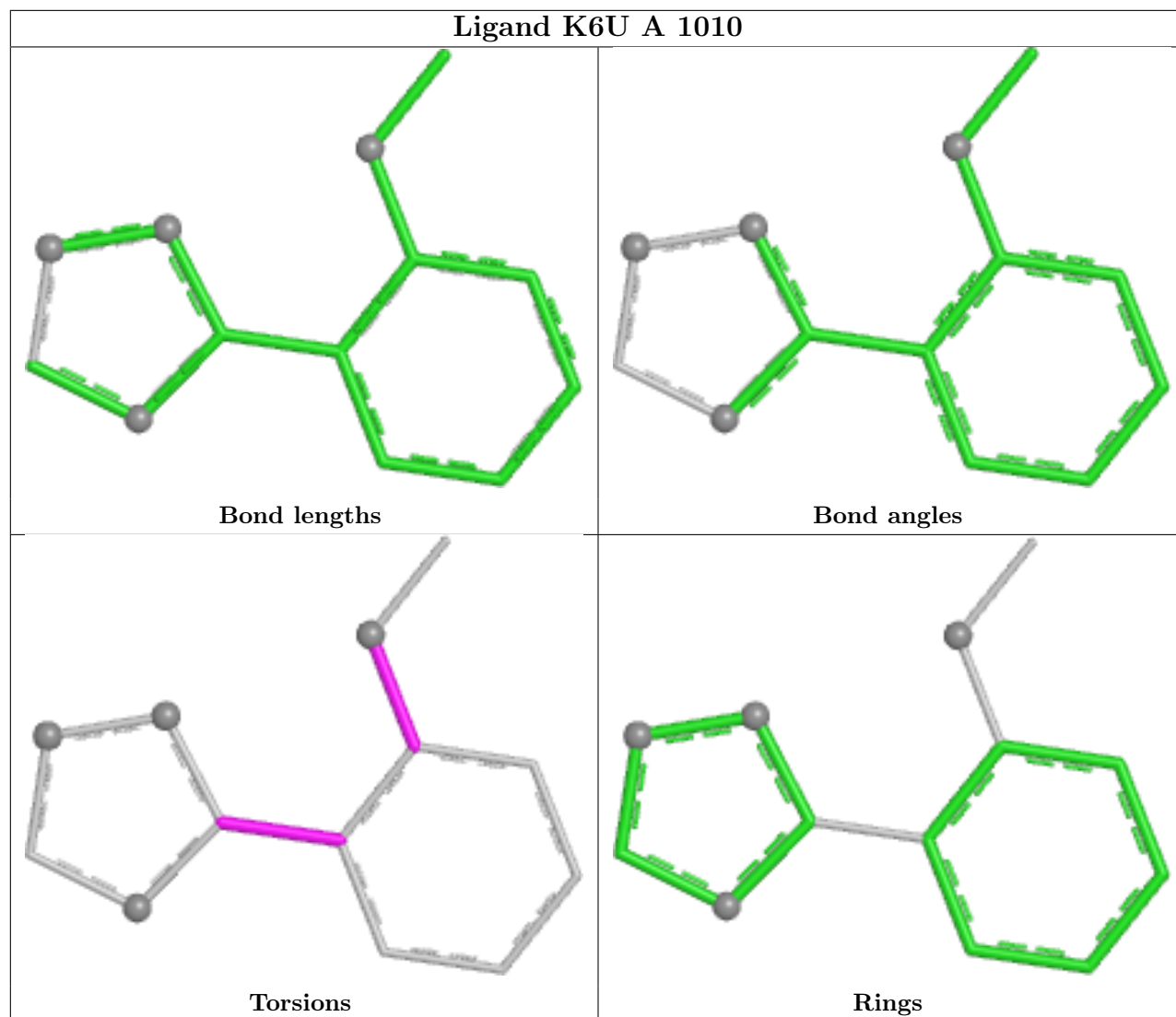
Bond angles



Torsions



Rings



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	567/637 (89%)	4.53	332 (58%) 0 0	8, 38, 93, 147	169 (29%)

All (332) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	505	SER	18.4
1	A	492	LEU	18.4
1	A	292	TRP	18.2
1	A	443	LEU	17.3
1	A	542	ILE	17.1
1	A	538	TRP	17.1
1	A	502	ASN	16.9
1	A	300	TYR	16.3
1	A	277	ILE	16.2
1	A	536	ALA	15.9
1	A	291	SER	15.6
1	A	535	THR	15.6
1	A	432	TRP	15.5
1	A	435	VAL	15.4
1	A	450	CYS	15.4
1	A	889	PHE	15.3
1	A	304	ALA	15.1
1	A	589	VAL	15.0
1	A	635	LEU	14.9
1	A	294	TYR	14.9
1	A	299	PRO	14.7
1	A	503	SER	14.7
1	A	495	ASP	14.6
1	A	801[A]	HIS	14.6
1	A	431	PHE	14.4
1	A	452	TYR	14.3
1	A	790	THR	14.3

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Mol	Chain	Res	Type	RSRZ
1	A	309	TYR	14.3
1	A	430	GLY	14.2
1	A	359	VAL	14.2
1	A	605	VAL	14.0
1	A	480	GLY	14.0
1	A	293	HIS	14.0
1	A	451	VAL	13.9
1	A	434	LEU	13.9
1	A	483	PHE	13.9
1	A	590	MET	13.7
1	A	445	GLY	13.7
1	A	594	SER	13.6
1	A	478	TRP	13.5
1	A	481	ALA	12.9
1	A	484	LEU	12.9
1	A	283	LYS	12.9
1	A	750	GLU	12.8
1	A	400	THR	12.6
1	A	584	THR	12.6
1	A	508	GLU	12.2
1	A	422	ALA	12.2
1	A	476	TYR	12.2
1	A	442	HIS	12.2
1	A	399	PHE	12.1
1	A	282	GLU	12.0
1	A	540	THR	12.0
1	A	595	ARG	11.9
1	A	298	HIS	11.9
1	A	537	GLY	11.8
1	A	541	ARG	11.8
1	A	426	VAL	11.7
1	A	449	THR	11.7
1	A	886	MET	11.6
1	A	405	SER	11.6
1	A	487	GLU	11.5
1	A	475	TRP	11.5
1	A	453	ASN	11.4
1	A	290	THR	11.4
1	A	830	VAL	11.3
1	A	425	ALA	11.3
1	A	493	ASN	11.3
1	A	774	LEU	11.2

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Mol	Chain	Res	Type	RSRZ
1	A	885	SER	11.2
1	A	479	LEU	11.2
1	A	637	VAL	11.1
1	A	398	GLU	11.1
1	A	295	ASP	11.0
1	A	650	VAL	11.0
1	A	544	LEU	10.8
1	A	428	ASP	10.8
1	A	636	THR	10.7
1	A	539	ASP	10.6
1	A	273	ASN	10.6
1	A	580	VAL	10.5
1	A	512[A]	LEU	10.3
1	A	716	LEU	10.2
1	A	401	ARG	9.8
1	A	888	ARG	9.6
1	A	311	THR	9.6
1	A	474	ILE	9.6
1	A	741[A]	SER	9.5
1	A	599	ARG	9.5
1	A	454	MET	9.5
1	A	485	GLU	9.5
1	A	360	ASP	9.4
1	A	604	VAL	9.4
1	A	598	GLN	9.4
1	A	380	TRP	9.4
1	A	791	SER	9.2
1	A	403	VAL	9.0
1	A	446	LYS	9.0
1	A	419	TRP	9.0
1	A	763[A]	SER	9.0
1	A	641	ILE	8.9
1	A	494	GLU	8.8
1	A	407	ALA	8.8
1	A	358	LYS	8.8
1	A	887	LYS	8.8
1	A	792	ARG	8.8
1	A	482	ARG	8.7
1	A	477	MET	8.7
1	A	448	GLU	8.7
1	A	429	SER	8.6
1	A	444	GLU	8.6

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Mol	Chain	Res	Type	RSRZ
1	A	433	GLU	8.5
1	A	638	THR	8.5
1	A	373	LEU	8.5
1	A	421	SER	8.4
1	A	278	GLY	8.4
1	A	836	ILE	8.3
1	A	287	GLU	8.3
1	A	719[A]	LYS	8.3
1	A	288	HIS	8.3
1	A	404	ARG	8.3
1	A	409	LEU	8.3
1	A	551	GLU	8.2
1	A	603	GLN	8.2
1	A	651	GLY	8.1
1	A	890	ARG	8.1
1	A	593	ILE	8.1
1	A	406	ASN	8.0
1	A	583	PRO	8.0
1	A	370	THR	8.0
1	A	860	ALA	8.0
1	A	402	LYS	7.8
1	A	717	ILE	7.6
1	A	634	HIS	7.6
1	A	296	GLN	7.6
1	A	455	MET	7.5
1	A	649	ARG	7.5
1	A	842	ARG	7.5
1	A	639	GLU	7.5
1	A	410	GLY	7.5
1	A	357	GLU	7.3
1	A	596	ARG	7.3
1	A	856	ARG	7.3
1	A	642	ALA	7.3
1	A	644	LYS	7.3
1	A	473	ALA	7.2
1	A	375	LYS	7.2
1	A	281	ILE	7.1
1	A	423	ARG	7.1
1	A	884	PRO	7.0
1	A	592	ILE	7.0
1	A	582	ARG	6.8
1	A	569	PHE	6.7

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Mol	Chain	Res	Type	RSRZ
1	A	633	GLN	6.7
1	A	441	LEU	6.7
1	A	297	ASP	6.6
1	A	408	ALA	6.6
1	A	411	ALA	6.6
1	A	891	ARG	6.6
1	A	729	ARG	6.5
1	A	640	GLU	6.5
1	A	745	GLY	6.5
1	A	344	THR	6.4
1	A	770	ARG	6.4
1	A	864[A]	GLN	6.4
1	A	843	GLU	6.3
1	A	374	MET	6.3
1	A	424	GLU	6.3
1	A	715	GLU	6.3
1	A	844	ASP	6.2
1	A	302	THR	6.2
1	A	882	TYR	6.2
1	A	648	VAL	6.1
1	A	600	GLY	6.0
1	A	286	GLN	5.9
1	A	785[A]	SER	5.9
1	A	420	LYS	5.8
1	A	597	ASP	5.8
1	A	883	MET	5.7
1	A	698	ARG	5.7
1	A	395	THR	5.6
1	A	562	LYS	5.6
1	A	364	GLN	5.6
1	A	371	LYS	5.5
1	A	303	TRP	5.4
1	A	743	GLY	5.4
1	A	647	LEU	5.4
1	A	832	SER	5.4
1	A	588	THR	5.3
1	A	834	GLU	5.3
1	A	799	ALA	5.2
1	A	835	GLU	5.2
1	A	564	LEU	5.1
1	A	744	ALA	4.9
1	A	670	LEU	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	652	ARG	4.9
1	A	308	SER	4.8
1	A	396	ARG	4.8
1	A	305	TYR	4.8
1	A	571	LEU	4.8
1	A	680	ALA	4.7
1	A	831	GLU	4.6
1	A	284	ILE	4.6
1	A	372	LYS	4.6
1	A	274	LEU	4.6
1	A	645	ASN	4.5
1	A	764	LEU	4.5
1	A	437	LYS	4.5
1	A	691	ILE	4.5
1	A	746	TRP	4.4
1	A	289	GLU	4.4
1	A	742	GLN	4.3
1	A	629	PHE	4.3
1	A	578	VAL	4.3
1	A	815	ARG	4.3
1	A	390	THR	4.2
1	A	800	THR	4.2
1	A	397	GLU	4.2
1	A	570	LYS	4.2
1	A	556	HIS	4.2
1	A	343	MET	4.1
1	A	552	MET	4.1
1	A	280	ARG	4.1
1	A	276	ILE	4.1
1	A	488	ALA	4.1
1	A	285	LYS	4.0
1	A	625	GLY	4.0
1	A	548	LYS	4.0
1	A	687	VAL	4.0
1	A	572	THR	3.9
1	A	379	GLU	3.9
1	A	558	GLU	3.9
1	A	566	GLU	3.9
1	A	427	GLU	3.9
1	A	880	THR	3.9
1	A	806	THR	3.8
1	A	306	HIS	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	581	GLN	3.7
1	A	279	LYS	3.7
1	A	319	SER	3.7
1	A	591	ASP	3.6
1	A	693	GLN	3.6
1	A	275	ASP	3.6
1	A	829	PRO	3.5
1	A	545	GLU	3.5
1	A	361	THR	3.4
1	A	447	CYS	3.4
1	A	820	GLU	3.4
1	A	575	ASN	3.4
1	A	363	THR	3.4
1	A	646	TRP	3.3
1	A	858	THR	3.3
1	A	307	GLY	3.3
1	A	827	LYS	3.3
1	A	740	ILE	3.2
1	A	365	GLU	3.2
1	A	576	LYS	3.1
1	A	613	THR	3.1
1	A	568	ILE	3.1
1	A	601	SER	3.1
1	A	855	SER	3.1
1	A	628	VAL	3.1
1	A	679	THR	3.0
1	A	627	GLY	3.0
1	A	393	MET	3.0
1	A	632	ILE	3.0
1	A	818	ILE	3.0
1	A	694	TRP	2.9
1	A	725	VAL	2.9
1	A	337	MET	2.9
1	A	555	ASN	2.9
1	A	524	LYS	2.9
1	A	808	ASP	2.9
1	A	301	LYS	2.9
1	A	579	ARG	2.8
1	A	664	ASP	2.8
1	A	825	GLU	2.8
1	A	848	GLY	2.8
1	A	383	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	643	VAL	2.8
1	A	439	ARG	2.8
1	A	553	VAL	2.8
1	A	630	LYS	2.7
1	A	854	THR	2.7
1	A	812	VAL	2.7
1	A	748	LEU	2.7
1	A	816	VAL	2.7
1	A	602	GLY	2.7
1	A	320	MET	2.7
1	A	366	PRO	2.7
1	A	436	ASP	2.6
1	A	321	VAL	2.6
1	A	683	ASP	2.6
1	A	868	ASN	2.6
1	A	486	PHE	2.6
1	A	684	MET	2.5
1	A	689	LYS	2.5
1	A	857	ALA	2.5
1	A	676	SER	2.5
1	A	381	LEU	2.5
1	A	878	GLU	2.5
1	A	828	THR	2.5
1	A	788	VAL	2.5
1	A	554	THR	2.4
1	A	862	ASN	2.4
1	A	718	MET	2.4
1	A	723	VAL	2.4
1	A	489	LEU	2.4
1	A	310	GLU	2.3
1	A	695	GLU	2.3
1	A	833	TRP	2.3
1	A	824	MET	2.3
1	A	369	GLY	2.3
1	A	720	ASP	2.3
1	A	807	GLU	2.3
1	A	677	ALA	2.2
1	A	624	GLU	2.2
1	A	521	ASP	2.2
1	A	368	GLU	2.2
1	A	504	LEU	2.2
1	A	804	MET	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	394	CYS	2.1
1	A	547	LEU	2.1
1	A	869	GLN	2.1
1	A	376	ILE	2.1
1	A	336	PRO	2.1
1	A	440	ASN	2.0
1	A	362	ARG	2.0
1	A	673	ARG	2.0
1	A	367	LYS	2.0
1	A	528	GLY	2.0
1	A	577	VAL	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	K6U	A	1010	13/13	0.55	0.57	52,54,57,58	13
7	K6U	A	1011	13/13	0.58	0.28	39,41,46,46	13
6	PEG	A	1009	7/7	0.73	0.20	70,77,86,87	0
5	PO4	A	1008	5/5	0.74	0.16	83,92,101,115	0
5	PO4	A	1007	5/5	0.80	0.13	42,46,55,81	0
4	DMS	A	1005	4/4	0.86	0.17	85,96,101,102	0
3	MES	A	1003[A]	12/12	0.93	0.25	767,781,797,797	12
3	MES	A	1003[B]	12/12	0.93	0.25	27,35,41,43	12
4	DMS	A	1004	4/4	0.94	0.14	49,57,58,64	0
4	DMS	A	1006	4/4	0.95	0.12	58,61,65,67	0
8	CL	A	1012	1/1	0.97	0.14	50,50,50,50	0
2	ZN	A	1002	1/1	0.98	0.04	60,60,60,60	0

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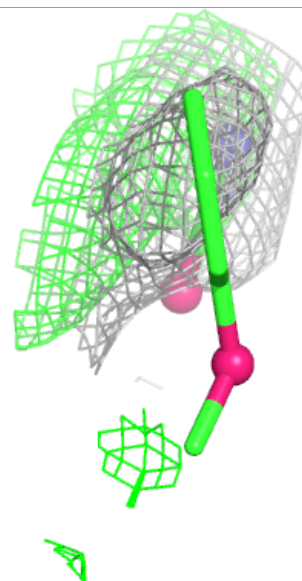
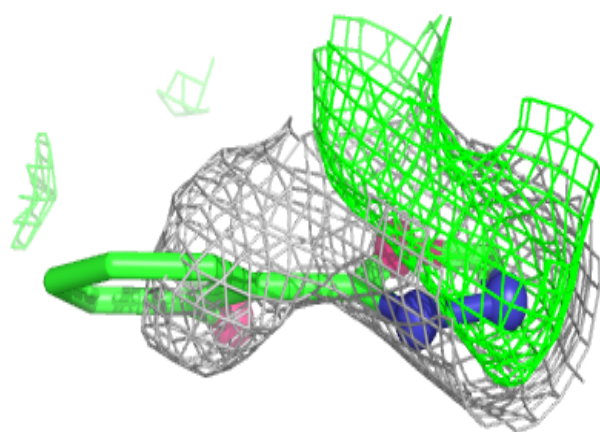
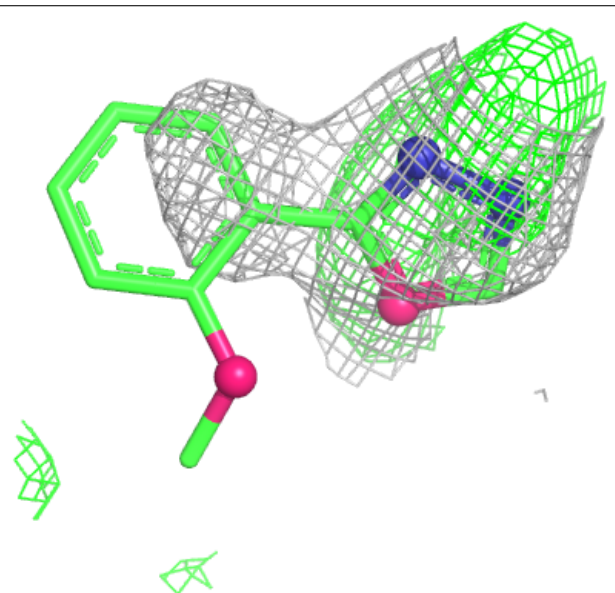
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	A	1001	1/1	1.00	0.01	30,30,30,30	0

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.

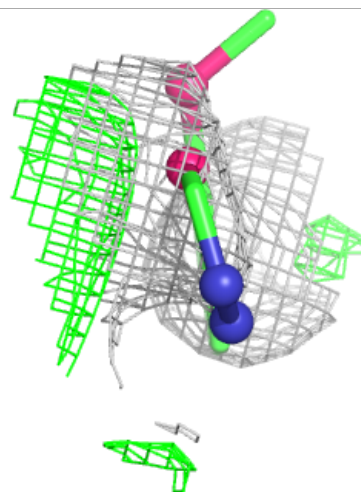
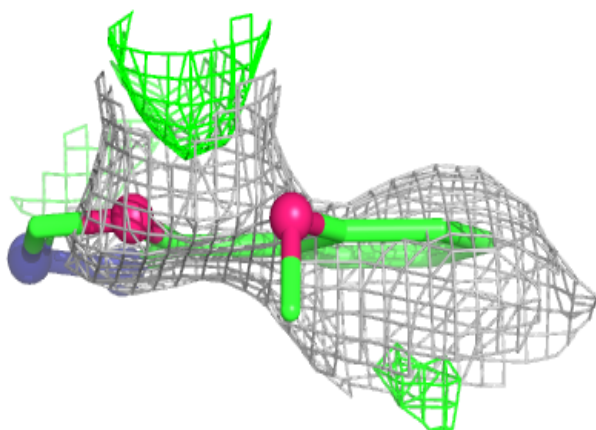
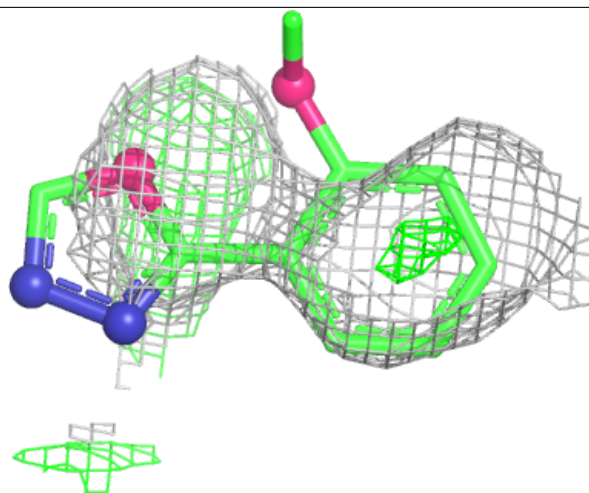
Electron density around K6U A 1010:

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 K6U A 1011:

$2mF_o-DF_c$ (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.