wwPDB X-ray Structure Validation Summary Report (i)

Dec 10, 2023 – 04:57 pm GMT

PDB ID	:	1OB2
Title	:	E. coli elongation factor EF-Tu complexed with the antibiotic kirromycin, a GTP analog, and Phe-tRNA
Authors	:	Kristensen, O.; Nissen, P.; Nyborg, J.
Deposited on	:	2003-01-24
Resolution	:	3.35 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

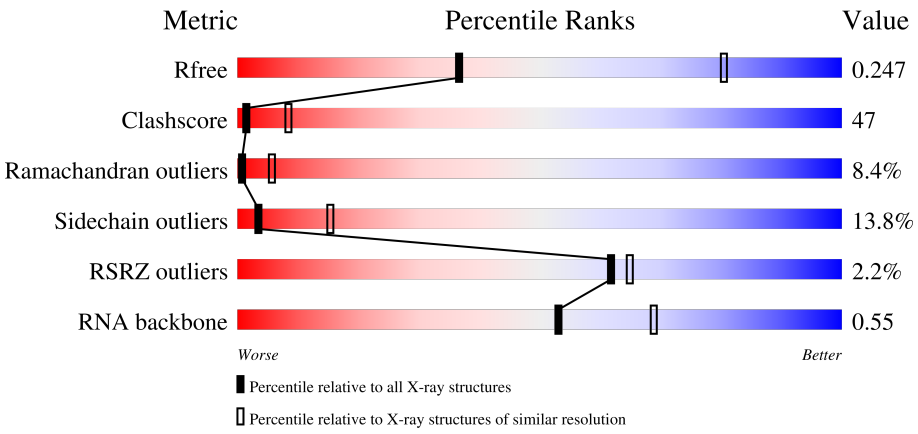
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.35 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	1558 (3.42-3.30)
Clashscore	141614	1627 (3.42-3.30)
Ramachandran outliers	138981	1599 (3.42-3.30)
Sidechain outliers	138945	1598 (3.42-3.30)
RSRZ outliers	127900	1507 (3.42-3.30)
RNA backbone	3102	1023 (3.80-2.92)

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 <=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	393	33% 52% 14% •
2	B	77	12% 26% 52% 21% •
3	C	2	50% 50%

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:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	OMC	B	32	-	-	-	X
2	OMG	B	34	-	-	-	X
2	YG	B	37	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 4810 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 ELONGATION FACTOR TU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	393	3035	1918	523	581	13	0	0	0

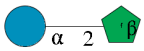
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	SER	conflict	UNP P0CE48

- Molecule 2 is a RNA chain called TRANSFER-RNA, PHE.

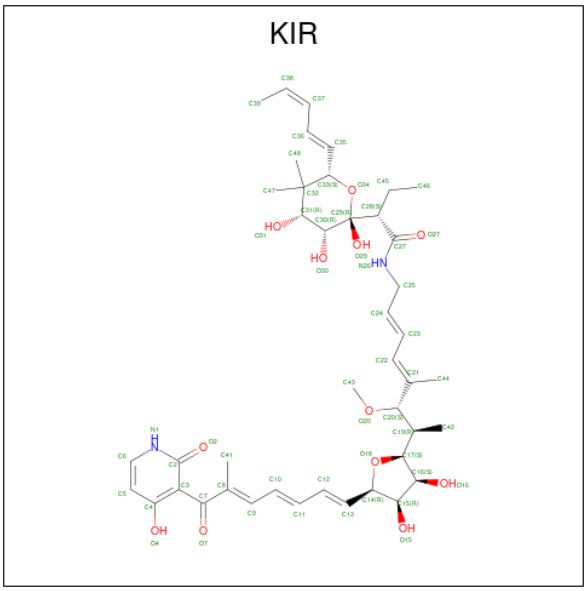
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	77	1662	754	295	537	76	0	0	0

- Molecule 3 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.



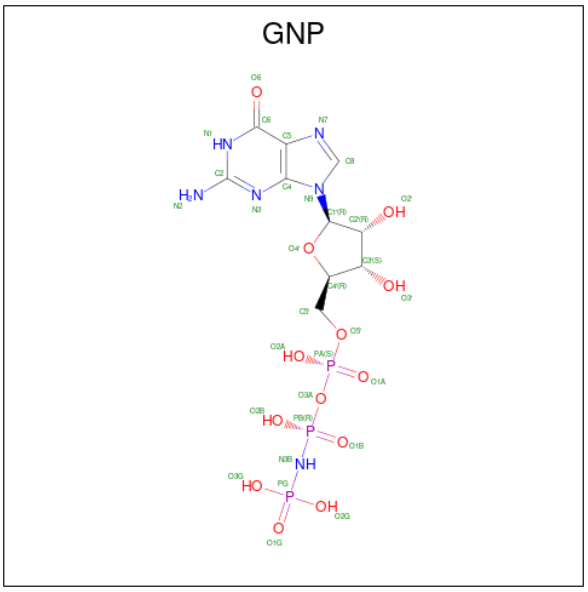
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
3	C	2	23	12	11	0	0	0

- Molecule 4 is KIRROMYCIN (three-letter code: KIR) (formula: $C_{43}H_{60}N_2O_{12}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	57	43	2	12	0	0

- Molecule 5 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	A	1	32	10	6	13	3	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

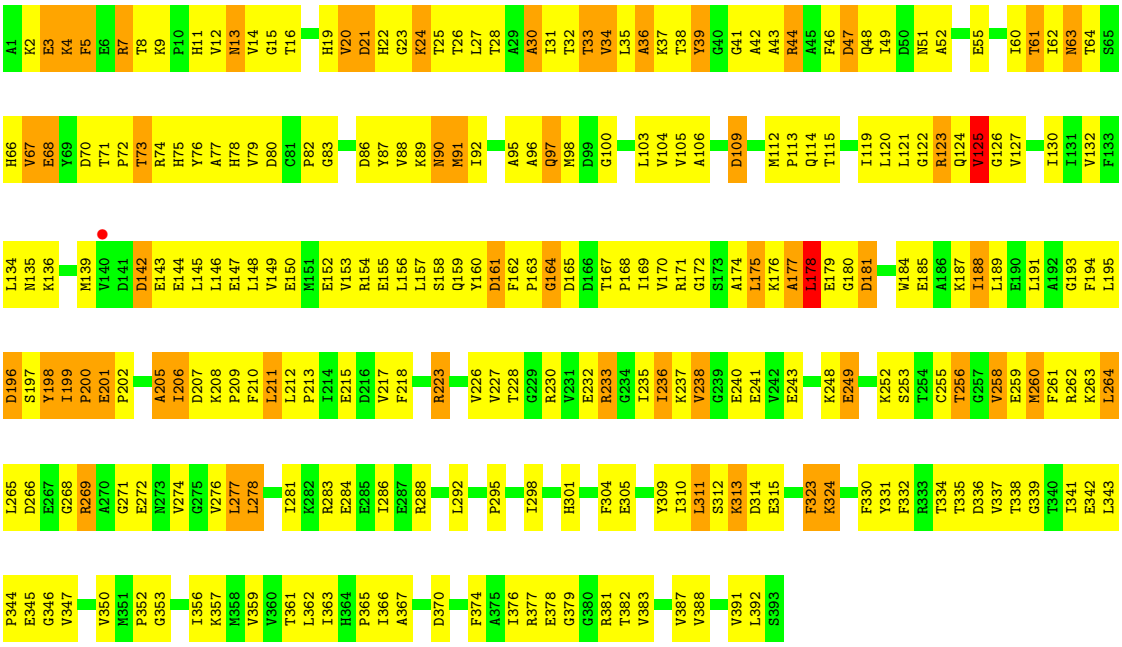
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
6	A	1	1	1	0	0

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.

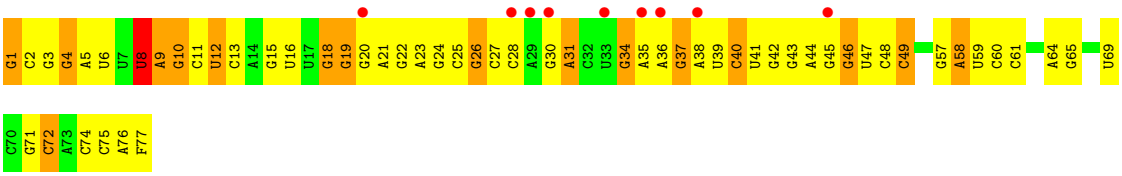
• Molecule 1: ELONGATION FACTOR TU

Chain A: 33% 52% 14%



• Molecule 2: TRANSFER-RNA, PHE

Chain B: 12% 26% 52% 21%



• Molecule 3: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain C: 50% 50%

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 3 2	Depositor
Cell constants a, b, c, α, β, γ	196.41Å 196.41Å 196.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.64 – 3.35 47.64 – 3.35	Depositor EDS
% Data completeness (in resolution range)	97.8 (47.64-3.35) 97.8 (47.64-3.35)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.01 (at 3.33Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.220 , 0.265 0.206 , 0.247	Depositor DCC
R_{free} test set	963 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å^2)	63.2	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 77.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	4810	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.93% 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: PSU, MG, 5MC, 2MG, YG, GNP, M2G, OMC, 7MG, PHA, FRU, KIR, GLC, OMG, 1MA, H2U

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	0.49	0/3091	0.81	0/4182
2	B	0.58	1/1509 (0.1%)	0.72	0/2349
All	All	0.52	1/4600 (0.0%)	0.78	0/6531

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
2	B	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	G	OP3-P	-7.00	1.52	1.61

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	22	G	Sidechain
2	B	8	U	Sidechain

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	3035	0	3051	354	0
2	B	1662	0	867	70	0
3	C	23	0	21	1	0
4	A	57	0	58	3	0
5	A	32	0	13	4	0
6	A	1	0	0	0	0
All	All	4810	0	4010	413	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 47.

The worst 5 of 413 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:199:ILE:HB	1:A:200:PRO:HA	1.18	1.12
1:A:74:ARG:HE	1:A:199:ILE:HD11	1.14	1.05
1:A:199:ILE:HB	1:A:200:PRO:CA	1.86	1.05
1:A:74:ARG:HE	1:A:199:ILE:CD1	1.74	1.00
1:A:123:ARG:HG2	1:A:162:PHE:HE2	1.28	0.98

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	391/393 (100%)	294 (75%)	64 (16%)	33 (8%)	1 6

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	GLU
1	A	21	ASP
1	A	24	LYS
1	A	127	VAL
1	A	143	GLU

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	325/325 (100%)	280 (86%)	45 (14%)	3 15

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	223	ARG
1	A	269	ARG
1	A	233	ARG
1	A	249	GLU
1	A	283	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	75	HIS
1	A	90	ASN
1	A	329	GLN
1	A	135	ASN
1	A	63	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	75/77 (97%)	15 (20%)	1 (1%)

5 of 15 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	4	G
2	B	8	U
2	B	9	A
2	B	12	U
2	B	18	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	18	G

5.4 Non-standard residues in protein, DNA, RNA chains (i)

14 non-standard protein/DNA/RNA residues 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	7MG	B	46	2	22,26,27	3.14	2 (9%)	29,39,42	1.45	2 (6%)
2	PHA	B	77	2	10,11,11	0.43	0	10,13,13	0.34	0
2	5MC	B	40	2	18,22,23	0.28	0	26,32,35	0.61	1 (3%)
2	H2U	B	17	2	18,21,22	0.54	0	21,30,33	0.67	0
2	YG	B	37	2	31,42,43	1.60	6 (19%)	33,62,65	2.35	12 (36%)
2	M2G	B	26	2	20,27,28	1.16	3 (15%)	22,40,43	0.78	1 (4%)
2	PSU	B	39	2	18,21,22	0.54	0	22,30,33	0.76	0
2	PSU	B	55	2	18,21,22	0.69	0	22,30,33	0.78	0
2	1MA	B	58	2	16,25,26	1.33	3 (18%)	18,37,40	1.04	2 (11%)
2	H2U	B	16	2	18,21,22	0.62	0	21,30,33	0.72	0
2	OMG	B	34	2	18,26,27	0.97	2 (11%)	19,38,41	0.84	1 (5%)
2	OMC	B	32	2	19,22,23	0.27	0	26,31,34	0.54	0
2	2MG	B	10	2	18,26,27	1.15	3 (16%)	16,38,41	0.90	1 (6%)
2	5MC	B	49	2	18,22,23	0.46	0	26,32,35	0.65	1 (3%)

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	7MG	B	46	2	-	0/7/37/38	0/3/3/3
2	PHA	B	77	2	-	0/5/6/6	0/1/1/1
2	5MC	B	40	2	-	0/7/25/26	0/2/2/2
2	H2U	B	17	2	-	2/7/38/39	0/2/2/2
2	YG	B	37	2	-	7/20/42/43	0/3/4/4
2	M2G	B	26	2	-	0/7/29/30	0/3/3/3
2	PSU	B	39	2	-	0/7/25/26	0/2/2/2
2	PSU	B	55	2	-	1/7/25/26	0/2/2/2
2	1MA	B	58	2	-	0/3/25/26	0/3/3/3
2	H2U	B	16	2	-	0/7/38/39	0/2/2/2
2	OMG	B	34	2	-	0/5/27/28	0/3/3/3
2	OMC	B	32	2	-	0/9/27/28	0/2/2/2
2	2MG	B	10	2	-	0/5/27/28	0/3/3/3
2	5MC	B	49	2	-	0/7/25/26	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	46	7MG	C8-N9	-14.40	1.37	1.46
2	B	37	YG	O23-C21	-5.01	1.25	1.34
2	B	58	1MA	C2-N3	3.37	1.33	1.29
2	B	37	YG	O18-C16	-3.15	1.25	1.33
2	B	10	2MG	C5-C6	-2.83	1.41	1.47

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	37	YG	C11-C12-N1	-6.33	102.96	106.53
2	B	46	7MG	N9-C8-N7	6.28	112.36	103.38
2	B	37	YG	C3-N3-C4	5.12	125.80	116.71
2	B	37	YG	O23-C21-N20	4.35	118.44	110.80
2	B	37	YG	O18-C16-C15	3.91	121.52	111.52

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	17	H2U	C2'-C1'-N1-C2

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Mol	Chain	Res	Type	Atoms
2	B	37	YG	C15-C16-O18-C19
2	B	37	YG	N20-C21-O23-C24
2	B	37	YG	O22-C21-O23-C24
2	B	37	YG	O17-C16-O18-C19

There are no ring outliers.

10 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	77	PHA	4	0
2	B	40	5MC	5	0
2	B	37	YG	5	0
2	B	26	M2G	1	0
2	B	39	PSU	4	0
2	B	58	1MA	2	0
2	B	16	H2U	1	0
2	B	34	OMG	1	0
2	B	10	2MG	1	0
2	B	49	5MC	1	0

5.5 Carbohydrates (i)

2 monosaccharides 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	$\#\|Z\| > 2$
3	GLC	C	1	3	11,11,12	1.44	2 (18%)	15,15,17	0.82	0
3	FRU	C	2	3	11,12,12	1.32	1 (9%)	10,18,18	0.80	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	GLC	C	1	3	-	2/2/19/22	0/1/1/1
3	FRU	C	2	3	-	5/5/24/24	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2	FRU	O2-C2	4.02	1.47	1.40
3	C	1	GLC	O5-C1	2.88	1.48	1.43
3	C	1	GLC	O5-C5	2.38	1.48	1.43

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	2	FRU	O1-C1-C2-O2
3	C	1	GLC	C4-C5-C6-O6
3	C	2	FRU	O1-C1-C2-O5
3	C	2	FRU	C4-C5-C6-O6
3	C	1	GLC	O5-C5-C6-O6

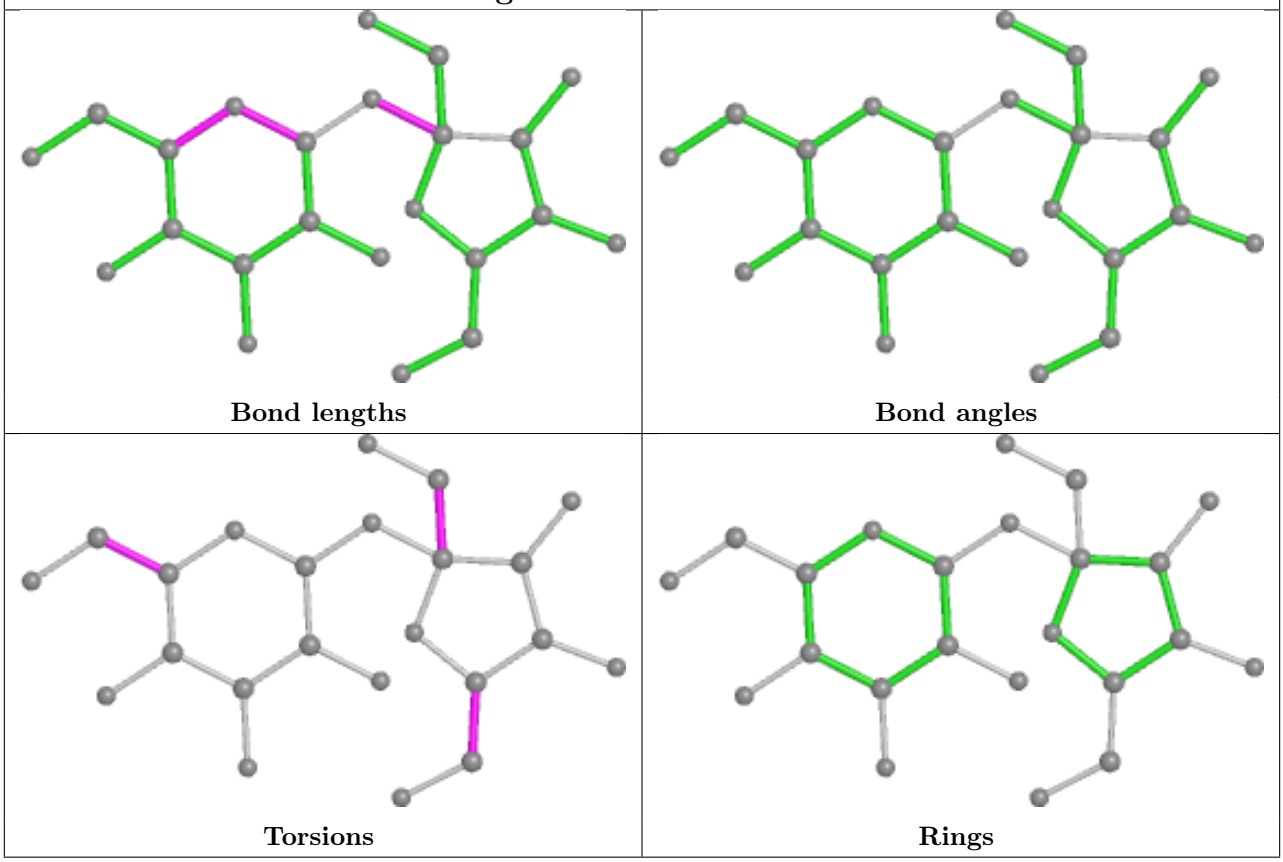
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2	FRU	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 oligosaccharide.

Oligosaccharide Chain C



5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	$\#\|Z\| > 2$
4	KIR	A	1394	-	56,59,59	3.15	14 (25%)	62,84,84	1.57	15 (24%)
5	GNP	A	1397	6	29,34,34	1.91	7 (24%)	33,54,54	2.36	8 (24%)

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
4	KIR	A	1394	-	-	2/54/98/98	0/3/3/3
5	GNP	A	1397	6	-	6/14/38/38	0/3/3/3

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1394	KIR	O18-C17	-15.55	1.21	1.44
4	A	1394	KIR	O30-C30	-12.96	1.16	1.42
5	A	1397	GNP	C6-N1	5.78	1.43	1.33
4	A	1394	KIR	C29-C28	4.10	1.62	1.54
4	A	1394	KIR	C27-N26	3.83	1.42	1.33

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	1397	GNP	C5-C6-N1	-7.65	112.97	123.43
5	A	1397	GNP	C2-N1-C6	5.29	124.33	115.93
5	A	1397	GNP	O1G-PG-N3B	-4.85	104.63	111.77
5	A	1397	GNP	O2G-PG-O3G	4.15	118.70	107.64
4	A	1394	KIR	O29-C29-O34	-3.92	103.63	110.21

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1397	GNP	PG-N3B-PB-O1B
5	A	1397	GNP	PA-O3A-PB-O1B
5	A	1397	GNP	PA-O3A-PB-O2B
5	A	1397	GNP	O4'-C4'-C5'-O5'
4	A	1394	KIR	C36-C37-C38-C39

There are no ring outliers.

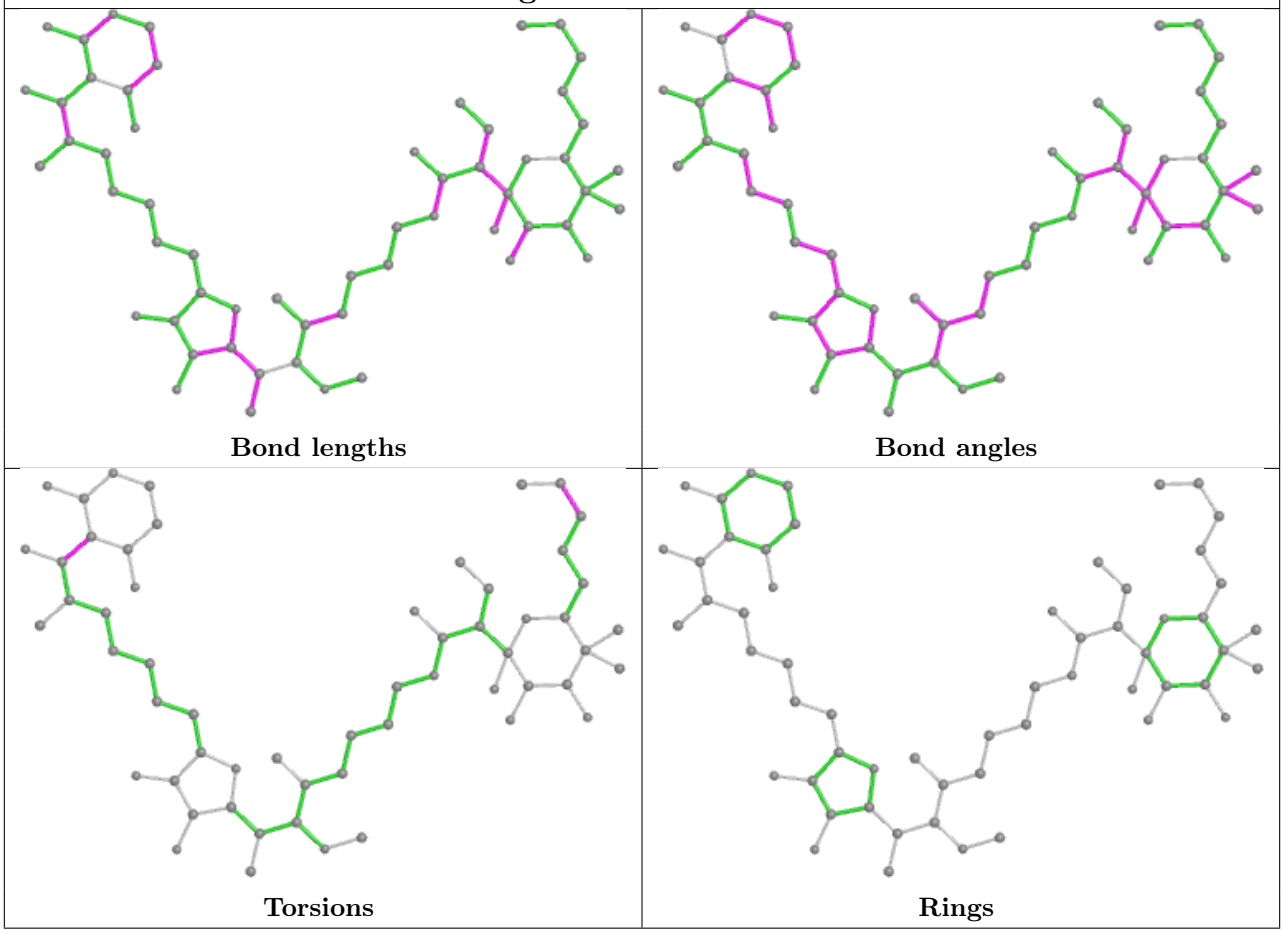
2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1394	KIR	3	0
5	A	1397	GNP	4	0

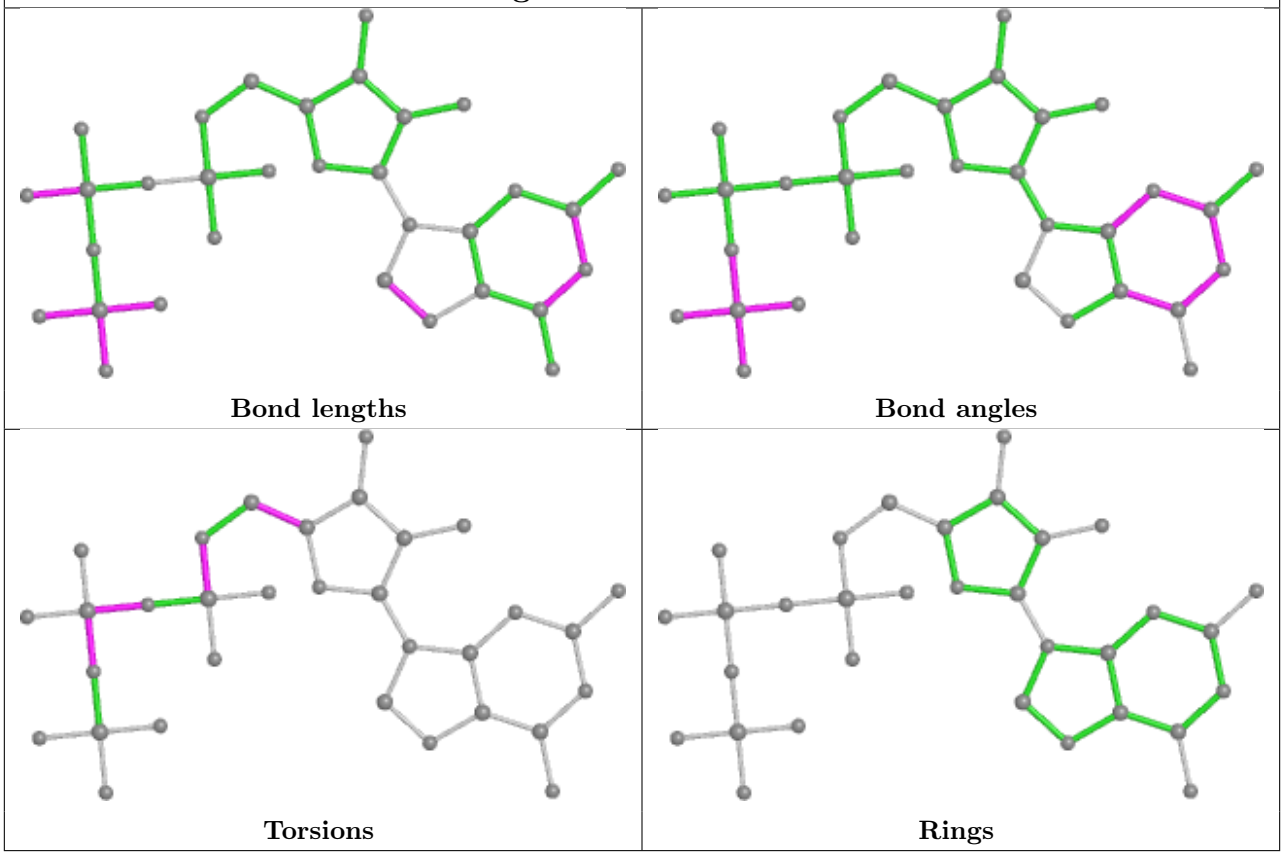
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 KIR A 1394



Ligand GNP A 1397



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	393/393 (100%)	-0.30	1 (0%) 94 95	2, 25, 64, 90	0
2	B	63/77 (81%)	0.66	9 (14%) 2 3	8, 36, 170, 199	0
All	All	456/470 (97%)	-0.16	10 (2%) 62 65	2, 26, 77, 199	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	33	U	5.7
2	B	36	A	4.1
2	B	35	A	3.7
2	B	38	A	3.3
2	B	20	G	3.3

6.2 Non-standard residues in protein, DNA, RNA chains (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
2	OMG	B	34	24/25	0.46	0.53	176,182,190,193	0
2	OMC	B	32	21/22	0.56	0.58	174,188,190,195	0
2	YG	B	37	39/40	0.58	0.74	194,198,199,199	0
2	PSU	B	39	20/21	0.71	0.30	142,149,168,170	0
2	5MC	B	40	21/22	0.82	0.20	140,149,159,159	0
2	M2G	B	26	25/26	0.94	0.32	55,68,72,81	0
2	H2U	B	17	20/21	0.94	0.23	57,69,86,87	0
2	H2U	B	16	20/21	0.95	0.21	52,59,63,67	0
2	2MG	B	10	24/25	0.95	0.26	20,40,49,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	7MG	B	46	24/25	0.95	0.30	41,51,60,68	0
2	PSU	B	55	20/21	0.97	0.21	17,35,43,49	0
2	1MA	B	58	23/24	0.97	0.24	13,22,33,41	0
2	PHA	B	77	11/11	0.97	0.19	1,14,23,23	0
2	5MC	B	49	21/22	0.98	0.19	0,16,22,34	0

6.3 Carbohydrates (i)

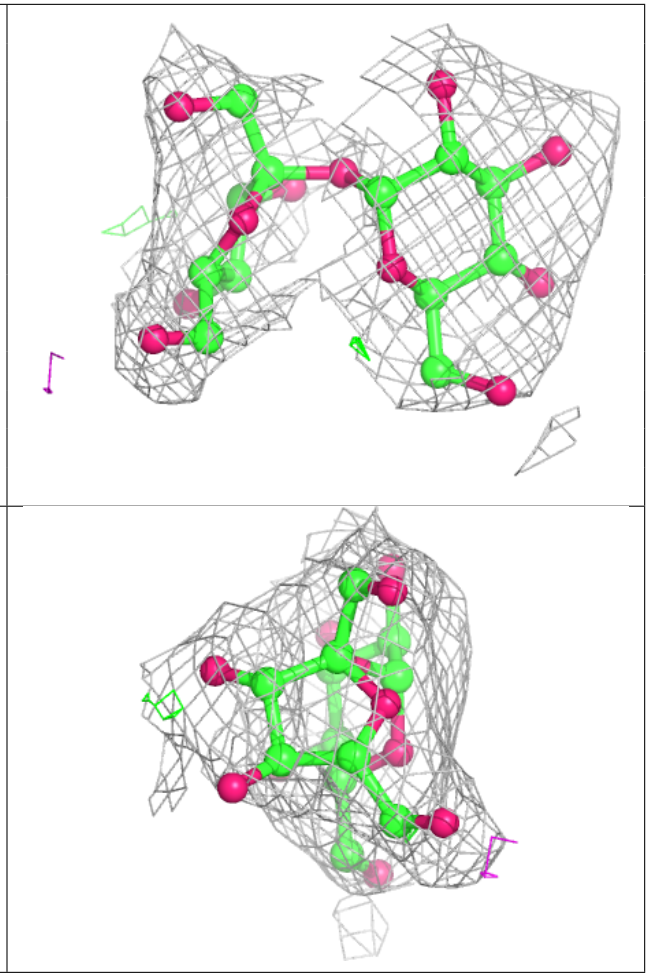
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	GLC	C	1	11/12	0.94	0.17	39,42,47,47	0
3	FRU	C	2	12/12	0.95	0.15	34,46,50,51	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

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



6.4 Ligands (i)

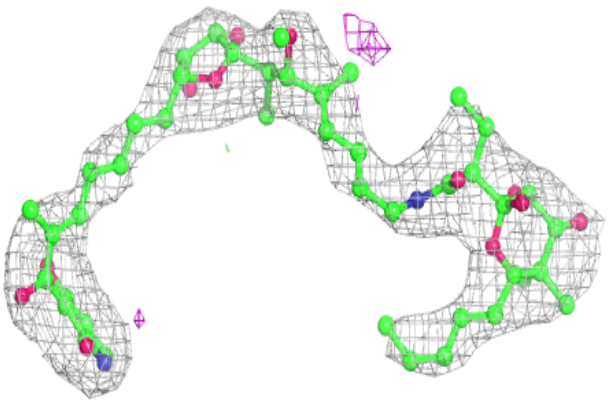
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

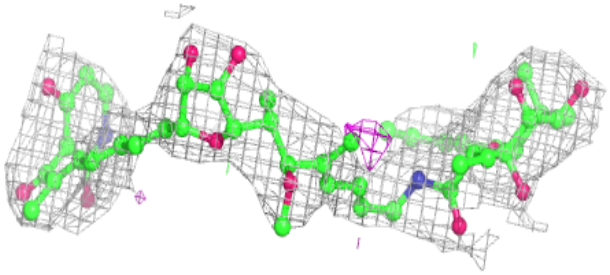
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	KIR	A	1394	57/57	0.93	0.29	7,21,40,48	0
5	GNP	A	1397	32/32	0.94	0.21	26,36,47,50	0
6	MG	A	1398	1/1	0.94	0.16	7,7,7,7	0

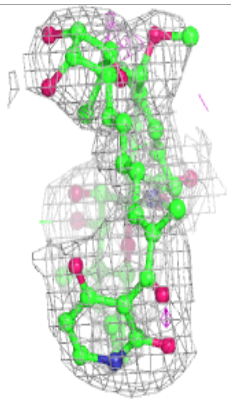
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around KIR A 1394:

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

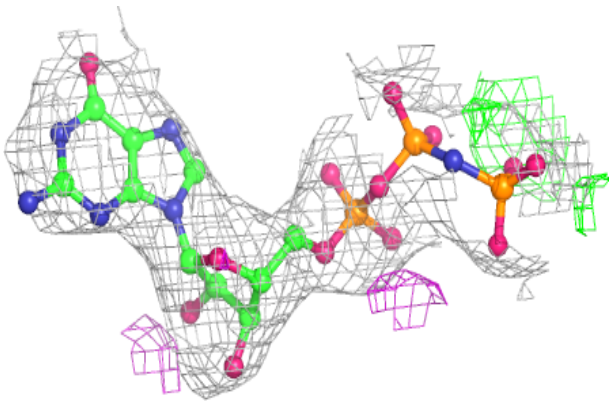


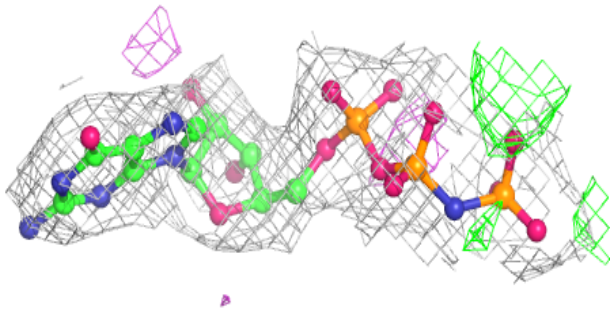


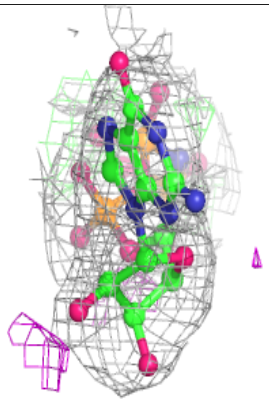


Electron density around GNP A 1397:

$2mF_o$-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.