Full wwPDB X-ray Structure Validation Report (i)

Feb 29, 2024 – 09:34 AM EST

PDB ID	:	5UWS
Title	:	Crystal Structure of X11L2 NES Peptide in complex with CRM1-Ran-RanBP1
Authors	:	Fung, H.Y.J.; Chook, Y.M.
Deposited on	:	2017-02-21
Resolution	:	2.40 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 (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:

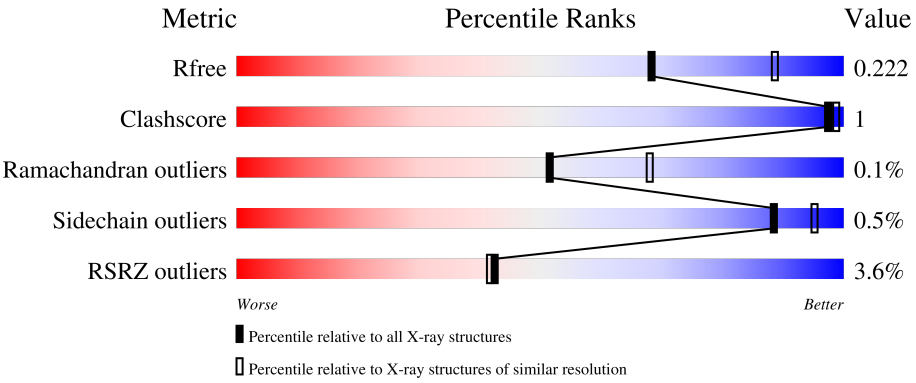
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	237	3% 86% · 13%
2	B	143	5% 89% · 9%
3	C	1024	3% 95% · ·
4	D	22	14% 68% 9% 23%

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
7	GOL	A	304	-	-	-	X

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 22517 atoms, of which 11142 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 GTP-binding nuclear protein Ran.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	206	3320	1071	1660	284	299	6	0	2	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP P62826
A	-19	GLU	-	expression tag	UNP P62826
A	-18	THR	-	expression tag	UNP P62826
A	-17	GLY	-	expression tag	UNP P62826
A	-16	SER	-	expression tag	UNP P62826
A	-15	SER	-	expression tag	UNP P62826
A	-14	HIS	-	expression tag	UNP P62826
A	-13	HIS	-	expression tag	UNP P62826
A	-12	HIS	-	expression tag	UNP P62826
A	-11	HIS	-	expression tag	UNP P62826
A	-10	HIS	-	expression tag	UNP P62826
A	-9	HIS	-	expression tag	UNP P62826
A	-8	SER	-	expression tag	UNP P62826
A	-7	SER	-	expression tag	UNP P62826
A	-6	GLY	-	expression tag	UNP P62826
A	-5	LEU	-	expression tag	UNP P62826
A	-4	PRO	-	expression tag	UNP P62826
A	-3	ARG	-	expression tag	UNP P62826
A	-2	GLY	-	expression tag	UNP P62826
A	-1	SER	-	expression tag	UNP P62826
A	0	HIS	-	expression tag	UNP P62826

- Molecule 2 is a protein called Ran-specific GTPase-activating protein 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	130	Total	C	H	N	O	S	0	2	0
			2151	682	1075	189	200	5			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	59	GLY	-	expression tag	UNP P41920
B	60	GLY	-	expression tag	UNP P41920
B	61	SER	-	expression tag	UNP P41920

- Molecule 3 is a protein called Exportin-1,Exportin-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	997	Total	C	H	N	O	S	0	23	0
			16384	5224	8250	1344	1521	45			

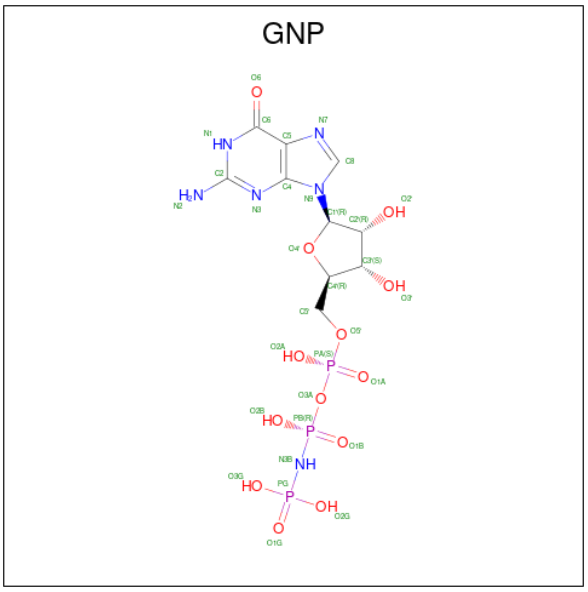
There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP P30822
C	-1	GLY	-	expression tag	UNP P30822
C	0	SER	-	expression tag	UNP P30822
C	441	ASP	VAL	conflict	UNP P30822
C	537	GLY	ASP	conflict	UNP P30822
C	539	CYS	THR	conflict	UNP P30822
C	540	GLU	VAL	conflict	UNP P30822
C	541	GLN	LYS	conflict	UNP P30822
C	1022	CYS	TYR	conflict	UNP P30822

- Molecule 4 is a protein called Amyloid beta A4 precursor protein-binding family A member 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	17	Total	C	H	N	O	0	0	0
			263	85	130	20	28			

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

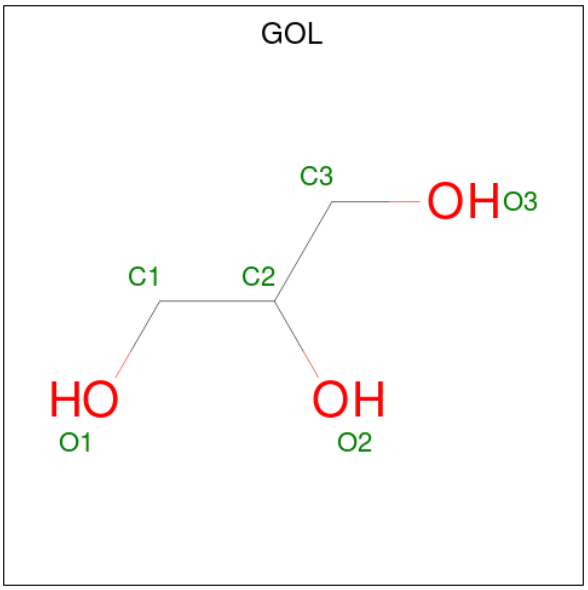


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	P	0	0
			44	10	12	6	13	3		

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

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

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	H	O	0	0
			11	3	5	3		
7	A	1	Total	C	H	O	0	0
			11	3	5	3		
7	C	1	Total	C	H	O	0	0
			11	3	5	3		

- Molecule 8 is water.

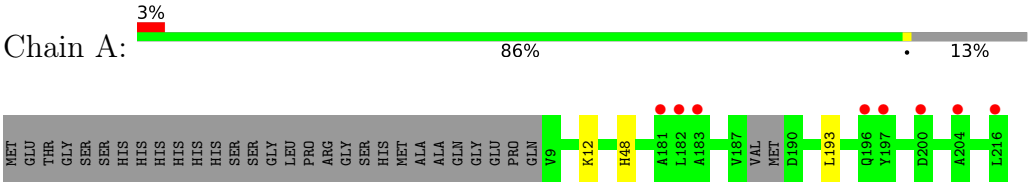
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	60	Total	O	0	0
			60	60		
8	B	12	Total	O	0	0
			12	12		
8	C	249	Total	O	0	0
			249	249		

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.

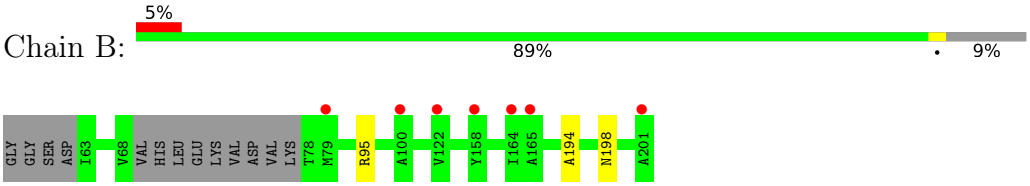
• Molecule 1: GTP-binding nuclear protein Ran

Chain A:



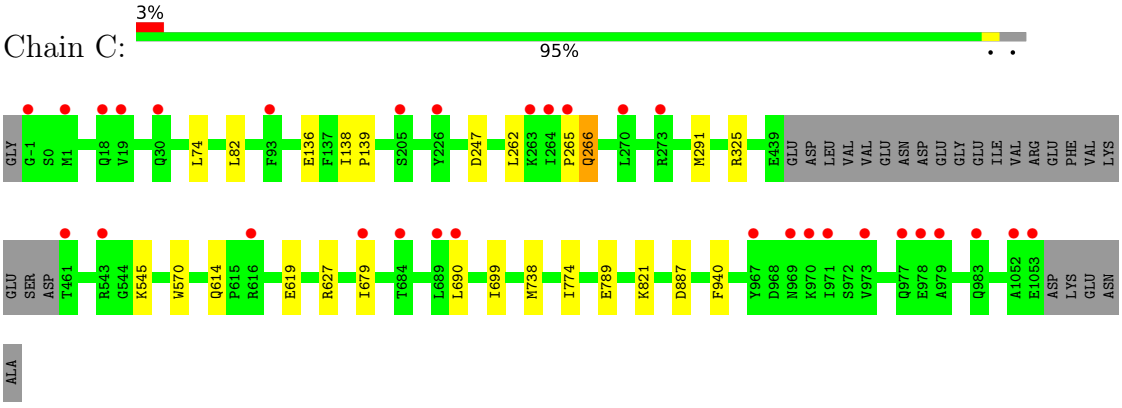
• Molecule 2: Ran-specific GTPase-activating protein 1

Chain B:



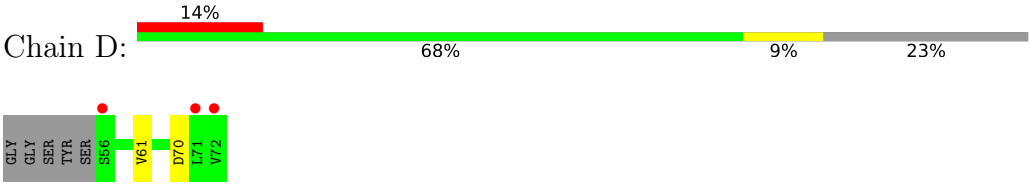
• Molecule 3: Exportin-1,Exportin-1

Chain C:



• Molecule 4: Amyloid beta A4 precursor protein-binding family A member 3

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	106.65Å 106.65Å 304.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.69 – 2.40 47.69 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.6 (47.69-2.40) 97.6 (47.69-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.34 (at 2.39Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.188 , 0.222 0.189 , 0.222	Depositor DCC
R_{free} test set	2003 reflections (2.95%)	wwPDB-VP
Wilson B-factor (Å^2)	36.1	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 39.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	22517	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, GNP, MG

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	0.25	0/1712	0.43	0/2320
2	B	0.24	0/1107	0.42	0/1477
3	C	0.24	0/8389	0.39	0/11362
4	D	0.24	0/134	0.34	0/180
All	All	0.24	0/11342	0.40	0/15339

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1660	1660	1650	2	0
2	B	1076	1075	1065	1	0
3	C	8134	8250	8168	15	0
4	D	133	130	130	1	0
5	A	32	12	12	0	0
6	A	1	0	0	0	0
7	A	12	10	16	1	0
7	C	6	5	8	1	0
8	A	60	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	B	12	0	0	0	0
8	C	249	0	0	2	0
All	All	11375	11142	11049	18	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 1.

All (18) 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:48:HIS:ND1	8:A:401:HOH:O	2.13	0.80
3:C:545:LYS:NZ	4:D:70:ASP:O	2.18	0.77
3:C:247:ASP:O	8:C:1201:HOH:O	2.13	0.67
2:B:194:ALA:O	2:B:198:ASN:ND2	2.40	0.55
3:C:265:PRO:O	3:C:266:GLN:HB2	2.09	0.53
3:C:619:GLU:OE2	3:C:627[A]:ARG:NH2	2.40	0.51
3:C:887:ASP:O	7:C:1101:GOL:H11	2.12	0.49
3:C:262:LEU:O	3:C:325:ARG:NH1	2.41	0.48
3:C:74:LEU:HD11	3:C:82:LEU:HD11	1.98	0.46
3:C:138:ILE:HB	3:C:139:PRO:HD3	1.98	0.44
3:C:265:PRO:O	3:C:266:GLN:CB	2.66	0.44
3:C:570:TRP:CG	3:C:614:GLN:HG2	2.53	0.44
3:C:690:LEU:HB2	3:C:738:MET:SD	2.59	0.43
1:A:12:LYS:HB2	7:A:304:GOL:H12	2.01	0.42
3:C:679:ILE:HD12	3:C:699:ILE:HG12	2.01	0.42
3:C:627[A]:ARG:NH1	8:C:1207:HOH:O	2.40	0.42
3:C:774:ILE:O	3:C:821:LYS:HD3	2.20	0.42
3:C:136:GLU:OE1	3:C:136:GLU:N	2.47	0.41

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	204/237 (86%)	197 (97%)	7 (3%)	0	100 100
2	B	128/143 (90%)	124 (97%)	4 (3%)	0	100 100
3	C	1016/1024 (99%)	996 (98%)	19 (2%)	1 (0%)	51 68
4	D	15/22 (68%)	15 (100%)	0	0	100 100
All	All	1363/1426 (96%)	1332 (98%)	30 (2%)	1 (0%)	51 68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	266	GLN

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	180/203 (89%)	179 (99%)	1 (1%)	86 94
2	B	113/122 (93%)	111 (98%)	2 (2%)	59 76
3	C	931/933 (100%)	928 (100%)	3 (0%)	92 97
4	D	15/18 (83%)	14 (93%)	1 (7%)	16 26
All	All	1239/1276 (97%)	1232 (99%)	7 (1%)	88 94

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	193	LEU
2	B	95[A]	ARG
2	B	95[B]	ARG
3	C	291	MET
3	C	789	GLU
3	C	940	PHE
4	D	61	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	$\#\|Z\| > 2$
5	GNP	A	301	6	29,34,34	4.44	9 (31%)	33,54,54	1.68	6 (18%)
7	GOL	C	1101	-	5,5,5	0.38	0	5,5,5	0.19	0
7	GOL	A	303	-	5,5,5	0.36	0	5,5,5	0.31	0
7	GOL	A	304	-	5,5,5	0.37	0	5,5,5	0.16	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
5	GNP	A	301	6	-	4/14/38/38	0/3/3/3
7	GOL	C	1101	-	-	2/4/4/4	-
7	GOL	A	303	-	-	2/4/4/4	-
7	GOL	A	304	-	-	4/4/4/4	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	301	GNP	C2'-C1'	-14.95	1.31	1.53
5	A	301	GNP	O4'-C1'	14.93	1.61	1.41
5	A	301	GNP	O4'-C4'	-6.31	1.30	1.45
5	A	301	GNP	C2-N2	4.23	1.42	1.33
5	A	301	GNP	PG-O1G	3.42	1.51	1.46
5	A	301	GNP	PB-O1B	3.40	1.51	1.46
5	A	301	GNP	O2'-C2'	2.89	1.49	1.43
5	A	301	GNP	O3'-C3'	-2.88	1.36	1.43
5	A	301	GNP	PG-O2G	-2.04	1.51	1.56

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	301	GNP	N3-C2-N1	-5.23	120.25	127.22
5	A	301	GNP	C2-N3-C4	4.05	119.98	115.36
5	A	301	GNP	C5-C6-N1	-2.56	119.93	123.43
5	A	301	GNP	C2-N1-C6	2.55	119.98	115.93
5	A	301	GNP	PB-O3A-PA	-2.25	124.71	132.62
5	A	301	GNP	O1G-PG-N3B	-2.18	108.55	111.77

There are no chirality outliers.

All (12) torsion outliers are listed below:

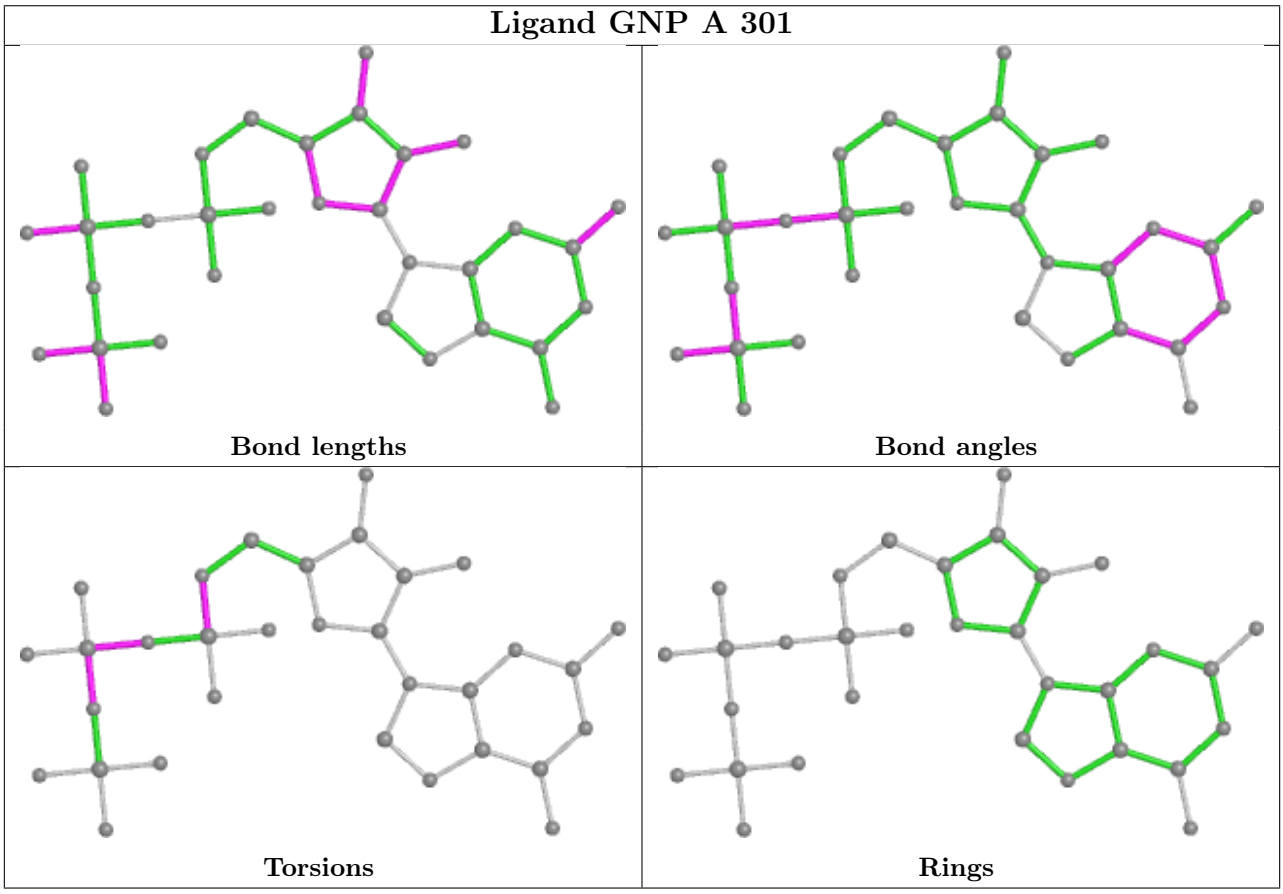
Mol	Chain	Res	Type	Atoms
5	A	301	GNP	PG-N3B-PB-O1B
5	A	301	GNP	PG-N3B-PB-O3A
5	A	301	GNP	C5'-O5'-PA-O1A
7	A	303	GOL	O1-C1-C2-C3
7	A	304	GOL	O1-C1-C2-C3
7	A	304	GOL	C1-C2-C3-O3
7	C	1101	GOL	O1-C1-C2-C3
7	A	303	GOL	O1-C1-C2-O2
7	C	1101	GOL	O1-C1-C2-O2
7	A	304	GOL	O1-C1-C2-O2
7	A	304	GOL	O2-C2-C3-O3
5	A	301	GNP	PA-O3A-PB-O2B

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	1101	GOL	1	0
7	A	304	GOL	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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, 95^{th} 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	206/237 (86%)	0.12	8 (3%) 39 38	22, 40, 96, 124	0
2	B	130/143 (90%)	0.40	7 (5%) 25 24	43, 62, 97, 113	0
3	C	997/1024 (97%)	0.08	31 (3%) 49 47	22, 42, 77, 117	0
4	D	17/22 (77%)	0.99	3 (17%) 1 1	52, 63, 77, 81	0
All	All	1350/1426 (94%)	0.13	49 (3%) 42 42	22, 44, 84, 124	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	182	LEU	5.8
3	C	-1	GLY	5.5
3	C	978	GLU	5.2
4	D	72	VAL	4.8
3	C	18	GLN	4.5
3	C	205	SER	4.3
3	C	979	ALA	4.1
3	C	30	GLN	4.0
2	B	79	MET	3.8
1	A	183	ALA	3.8
3	C	265	PRO	3.4
4	D	56	SER	3.4
1	A	197	TYR	3.4
3	C	226	TYR	3.3
3	C	1	MET	3.3
3	C	684	THR	3.2
3	C	1053	GLU	3.2
3	C	543	ARG	3.1
3	C	616	ARG	3.1
3	C	264	ILE	3.0
3	C	270	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
3	C	977	GLN	2.9
3	C	689	LEU	2.8
3	C	690	LEU	2.8
2	B	164	ILE	2.7
3	C	983	GLN	2.7
3	C	969	ASN	2.6
1	A	200	ASP	2.5
3	C	19	VAL	2.5
3	C	273	ARG	2.5
1	A	181	ALA	2.5
3	C	970	LYS	2.4
3	C	679	ILE	2.4
2	B	201	ALA	2.4
3	C	93	PHE	2.4
1	A	216	LEU	2.3
2	B	158	TYR	2.3
1	A	196	GLN	2.3
3	C	973	VAL	2.3
4	D	71	LEU	2.3
1	A	204	ALA	2.3
2	B	165	ALA	2.3
3	C	461	THR	2.3
2	B	122	VAL	2.1
3	C	967	TYR	2.1
3	C	1052	ALA	2.1
2	B	100	ALA	2.1
3	C	971	ILE	2.1
3	C	263	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 monosaccharides in this entry.

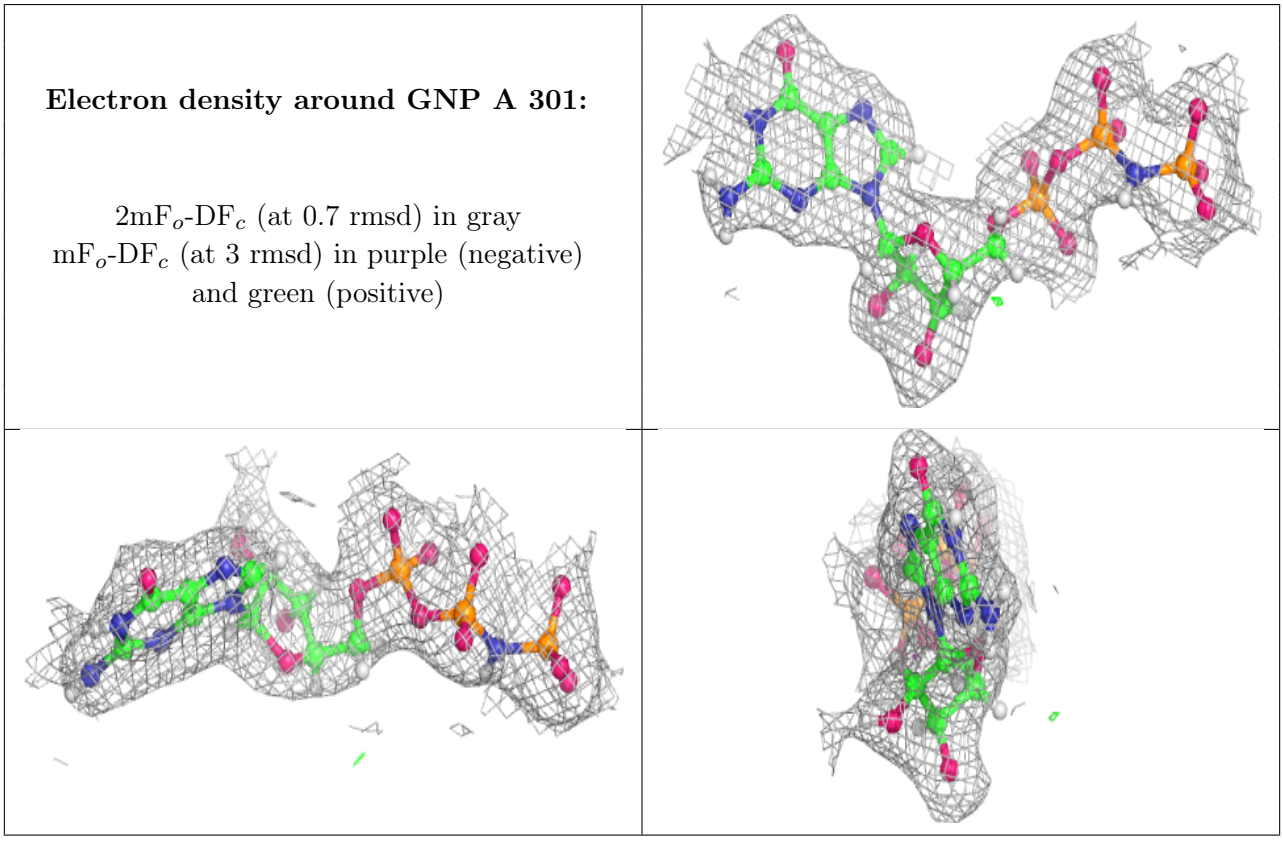
6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95^{th} 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	GOL	A	304	6/6	0.58	0.47	67,70,84,85	0
7	GOL	A	303	6/6	0.79	0.22	56,59,70,71	0
7	GOL	C	1101	6/6	0.84	0.26	63,66,78,80	0
6	MG	A	302	1/1	0.96	0.16	27,27,27,27	0
5	GNP	A	301	32/32	0.98	0.15	22,35,42,46	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.



6.5 Other polymers (i)

There are no such residues in this entry.