

Full wwPDB X-ray Structure Validation Report (i)

Nov 14, 2023 – 07:35 PM JST

:	6A38
:	MVM NS2 NES in complex with CRM1-Ran-RanBP1
:	Sun, Q.; Li, Y.
	2018-06-15
:	2.69 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 (1)) were used in the production of this report:

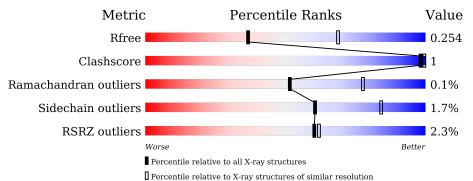
Xtriage (Phenix) EDS buster-report Percentile statistics	: : :	20191225.v01 (using entries in the PDB archive December 25th 2019)
-	:	
CCP4 Ideal geometry (proteins)		7.0.044 (Gargrove) Engh & Huber (2001)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.69 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	$\begin{array}{l} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	А	235	88%		• 11%
2	В	143	3%		• 10%
3	С	1003	2% 96%		•••
4	D	20	70%	15%	15%



2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 11075 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 GTP-binding nuclear protein Ran.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	А	210	Total 1677	C 1080	N 288	O 303	S 6	0	0	0

Chain	Residue	Modelled	Actual	Comment	Reference
А	-18	GLY	-	expression tag	UNP P62826
А	-17	SER	-	expression tag	UNP P62826
А	-16	SER	-	expression tag	UNP P62826
А	-15	HIS	-	expression tag	UNP P62826
А	-14	HIS	-	expression tag	UNP P62826
А	-13	HIS	-	expression tag	UNP P62826
А	-12	HIS	-	expression tag	UNP P62826
А	-11	HIS	-	expression tag	UNP P62826
А	-10	HIS	-	expression tag	UNP P62826
A	-9	SER	-	expression tag	UNP P62826
A	-8	SER	-	expression tag	UNP P62826
A	-7	GLY	-	expression tag	UNP P62826
А	-6	LEU	-	expression tag	UNP P62826
A	-5	VAL	-	expression tag	UNP P62826
A	-4	PRO	-	expression tag	UNP P62826
А	-3	ARG	-	expression tag	UNP P62826
А	-2	GLY	-	expression tag	UNP P62826
А	-1	SER	-	expression tag	UNP P62826
А	0	HIS	-	expression tag	UNP P62826
А	197	ALA	TYR	engineered mutation	UNP P62826

There are 20 discrepancies between the modelled and reference sequences:

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

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	В	129	Total 1058	C 672	N 184	0 197	${ m S}{ m 5}$	0	0	0



There are 3 discrepancies between the modelled and reference sequences:

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

• Molecule 3 is a protein called Exportin-1.

Mol	Chain	Residues		Α	toms		ZeroOcc	AltConf	Trace	
3	C	996	Total 8040	C 5169	N 1324	O 1506	S 41	0	1	0

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	-2	GLY	-	expression tag	UNP P30822
С	-1	GLY	-	expression tag	UNP P30822
С	0	SER	-	expression tag	UNP P30822
С	?	-	VAL	deletion	UNP P30822
С	?	-	GLN	deletion	UNP P30822
С	?	-	ARG	deletion	UNP P30822
С	?	-	LEU	deletion	UNP P30822
С	?	-	PRO	deletion	UNP P30822
С	?	-	ALA	deletion	UNP P30822
С	?	-	THR	deletion	UNP P30822
С	?	-	GLU	deletion	UNP P30822
С	?	-	MET	deletion	UNP P30822
С	?	-	SER	deletion	UNP P30822
С	?	-	PRO	deletion	UNP P30822
С	?	-	LEU	deletion	UNP P30822
С	?	-	ILE	deletion	UNP P30822
С	?	-	GLN	deletion	UNP P30822
С	?	-	LEU	deletion	UNP P30822
С	?	-	SER	deletion	UNP P30822
С	?	-	VAL	deletion	UNP P30822
С	?	-	GLY	deletion	UNP P30822
С	?	-	SER	deletion	UNP P30822
С	?	-	GLN	deletion	UNP P30822
С	?	-	ALA	deletion	UNP P30822
С	?	-	ILE	deletion	UNP P30822
С	?	-	SER	deletion	UNP P30822
С	?	-	THR	deletion	UNP P30822
С	?		GLY	deletion	UNP P30822



Chain	Residue	Modelled	Actual	Comment	Reference
С	?	-	SER	deletion	UNP P30822
С	?	_	GLY	deletion	UNP P30822
С	?	-	ALA	deletion	UNP P30822
C	?	_	LEU	deletion	UNP P30822
С	?	_	ASN	deletion	UNP P30822
С	?	_	PRO	deletion	UNP P30822
С	?	_	GLU	deletion	UNP P30822
С	?	-	TYR	deletion	UNP P30822
С	?	-	MET	deletion	UNP P30822
С	?	-	LYS	deletion	UNP P30822
С	?	-	ARG	deletion	UNP P30822
С	?	-	PHE	deletion	UNP P30822
С	?	-	VAL	deletion	UNP P30822
С	?	-	LEU	deletion	UNP P30822
С	?	_	VAL	deletion	UNP P30822
С	?	-	VAL	deletion	UNP P30822
С	?	_	GLU	deletion	UNP P30822
С	?	_	ASN	deletion	UNP P30822
С	?	_	ASP	deletion	UNP P30822
С	?	_	GLU	deletion	UNP P30822
С	?	_	GLY	deletion	UNP P30822
С	?	-	GLU	deletion	UNP P30822
С	?	-	ILE	deletion	UNP P30822
С	?	-	VAL	deletion	UNP P30822
С	?	-	ARG	deletion	UNP P30822
С	?	-	GLU	deletion	UNP P30822
С	?	-	PHE	deletion	UNP P30822
С	?	-	VAL	deletion	UNP P30822
С	?		LYS	deletion	UNP P30822
С	?	-	GLU	deletion	UNP P30822
С	?	-	SER	deletion	UNP P30822
С	?	-	ASP	deletion	UNP P30822
С	?	-	THR	deletion	UNP P30822
С	537	GLY	ASP	engineered mutation	UNP P30822
С	539	CYS	THR	engineered mutation	UNP P30822
С	540	GLU	VAL	engineered mutation	UNP P30822
С	541	GLN	LYS	engineered mutation	UNP P30822
С	1022	CYS	TYR	engineered mutation	UNP P30822

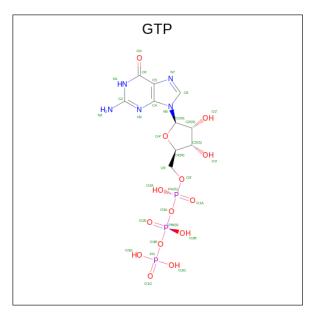
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• Molecule 4 is a protein called MVM NS2 NES.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	17	Total 133	C 83	N 21	O 28	S 1	0	0	0

• Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



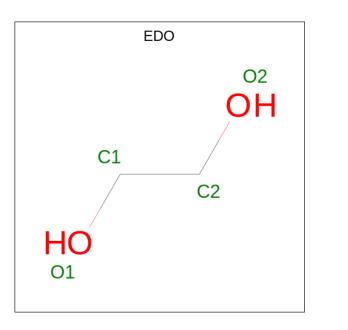
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
5	А	1	Total 32			0 14	Р 3	0	0

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

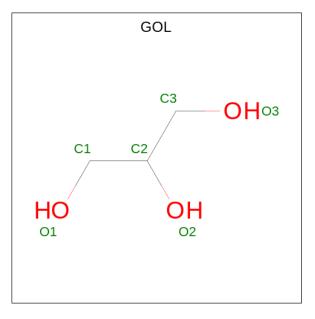
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	1	Total Mg 1 1	0	0

• Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
7	А	1	Total 4	С 2	O 2	0	0



[Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
	8	С	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
	8	С	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0

• Molecule 9 is SODIUM ION (three-letter code: NA) (formula: Na).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	С	1	Total Na 1 1	0	0

• Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	А	24	Total O 24 24	0	0
10	В	2	Total O 2 2	0	0
10	С	90	Total O 90 90	0	0
10	D	1	Total O 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.

- Chain A: 88% 11% • Molecule 2: Ran-specific GTPase-activating protein 1 Chain B: 86% 10% HIS LEU GLU CAL VAL VAL VAL VAL GLY SER ASF • Molecule 3: Exportin-1 Chain C: 96% • Molecule 4: MVM NS2 NES Chain D: 70% 15% 15%
- Molecule 1: GTP-binding nuclear protein Ran



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants	105.44Å 105.44Å 303.07Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.01 - 2.69	Depositor
Resolution (A)	46.59 - 2.69	EDS
% Data completeness	99.9 (50.01-2.69)	Depositor
(in resolution range)	99.9 (46.59 - 2.69)	EDS
R _{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.30 (at 2.69 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0131	Depositor
D D	0.218 , 0.256	Depositor
R, R_{free}	0.216 , 0.254	DCC
R_{free} test set	2369 reflections $(4.89%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	65.4	Xtriage
Anisotropy	0.094	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.28 , 34.4	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	0.94	EDS
Total number of atoms	11075	wwPDB-VP
Average B, all atoms $(Å^2)$	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.75% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: EDO, GOL, MG, GTP, NA

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		
	Unain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.38	0/1718	0.60	0/2329	
2	В	0.38	0/1077	0.60	0/1439	
3	С	0.39	0/8199	0.58	0/11110	
4	D	0.45	0/134	0.57	0/179	
All	All	0.39	0/11128	0.58	0/15057	

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 (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	А	1677	0	1681	1	0
2	В	1058	0	1054	2	0
3	С	8040	0	8132	11	0
4	D	133	0	131	3	0
5	А	32	0	12	0	0
6	А	1	0	0	0	0
7	А	4	0	6	0	0
8	С	12	0	16	0	0
9	С	1	0	0	0	0



	Ű	Non-H	1 0	H(added)	Clashes	Symm-Clashes
10	A	24	0	0	0	0
10	В	2	0	0	0	0
10	С	90	0	0	0	0
10	D	1	0	0	0	0
All	All	11075	0	11032	14	0

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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 (14) 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)
3:C:204:GLY:HA2	3:C:210:ILE:HD11	1.82	0.61
3:C:356:ARG:NH1	3:C:440:GLU:OE1	2.35	0.60
3:C:556:MET:HG3	3:C:598:THR:HG21	1.88	0.54
3:C:545:LYS:HB2	4:D:91:ILE:HG22	1.93	0.50
3:C:268:ASN:HD22	3:C:271:ILE:HD12	1.76	0.49
3:C:435:MET:HG3	3:C:511:ALA:HB2	1.98	0.46
4:D:91:ILE:N	4:D:91:ILE:HD12	2.32	0.45
2:B:103:TRP:CH2	2:B:175:ALA:HB2	2.52	0.44
3:C:699:ILE:HG21	3:C:731:LEU:HD21	2.00	0.44
3:C:894:LYS:NZ	3:C:938:GLU:OE1	2.51	0.43
3:C:469:ARG:HG3	3:C:514:SER:HB2	2.00	0.42
3:C:579:LYS:NZ	4:D:89:LEU:O	2.49	0.42
3:C:981:VAL:HG11	3:C:985:THR:HG21	2.01	0.41
1:A:216:LEU:HD11	2:B:90:ARG:HG2	2.04	0.40

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	Perce	entiles
1	А	208/235~(88%)	200~(96%)	8 (4%)	0	100	100
2	В	125/143~(87%)	117 (94%)	8 (6%)	0	100	100
3	С	995/1003~(99%)	974 (98%)	20~(2%)	1 (0%)	51	78
4	D	15/20~(75%)	15 (100%)	0	0	100	100
All	All	1343/1401~(96%)	1306~(97%)	36~(3%)	1 (0%)	51	78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	С	204	GLY

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	Perce	entiles
1	А	181/200~(90%)	178~(98%)	3~(2%)	60	84
2	В	111/122~(91%)	108~(97%)	3~(3%)	44	74
3	С	909/913~(100%)	895~(98%)	14~(2%)	65	86
4	D	16/17~(94%)	15~(94%)	1 (6%)	18	40
All	All	1217/1252~(97%)	1196 (98%)	21 (2%)	60	84

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	132	LYS
1	А	134	LYS
1	А	157	PHE
2	В	78	THR
2	В	157	VAL
2	В	186	LYS
3	С	35	GLN
3	С	136	GLU
3	С	291	MET
3	С	356	ARG



Contr	nueu jion	i previo	bus puge
Mol	Chain	\mathbf{Res}	Type
3	С	429	LEU
3	С	434	ASN
3	С	436	VAL
3	С	437	ARG
3	С	489	SER
3	С	594	MET
3	С	689	LEU
3	С	690	LEU
3	С	854	GLU
3	С	973	VAL
4	D	82	MET

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Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	196	GLN
3	С	30	GLN
3	С	268	ASN
3	С	345	GLN
3	С	426	GLN
3	С	730	GLN
3	С	896	ASN

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 6 ligands modelled in this entry, 2 are 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	Turne	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
	Type	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
8	GOL	С	1101	-	$5,\!5,\!5$	0.31	0	$5,\!5,\!5$	0.36	0
5	GTP	А	301	6	26,34,34	0.96	1 (3%)	$32,\!54,\!54$	1.46	<mark>5 (15%)</mark>
8	GOL	С	1102	-	$5,\!5,\!5$	0.28	0	$5,\!5,\!5$	0.32	0
7	EDO	А	303	-	3,3,3	0.54	0	2,2,2	0.18	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
8	GOL	С	1101	-	-	4/4/4/4	-
5	GTP	А	301	6	-	5/18/38/38	0/3/3/3
8	GOL	С	1102	-	-	0/4/4/4	-
7	EDO	A	303	-	_	0/1/1/1	_

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	А	301	GTP	C6-N1	-2.68	1.33	1.37

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
5	А	301	GTP	PB-O3B-PG	-3.49	120.86	132.83
5	А	301	GTP	PA-O3A-PB	-3.43	121.07	132.83
5	А	301	GTP	C3'-C2'-C1'	2.44	104.66	100.98
5	А	301	GTP	C8-N7-C5	2.42	107.59	102.99
5	А	301	GTP	C5-C6-N1	2.36	118.12	113.95

There are no chirality outliers.

All (9) torsion outliers are listed below:



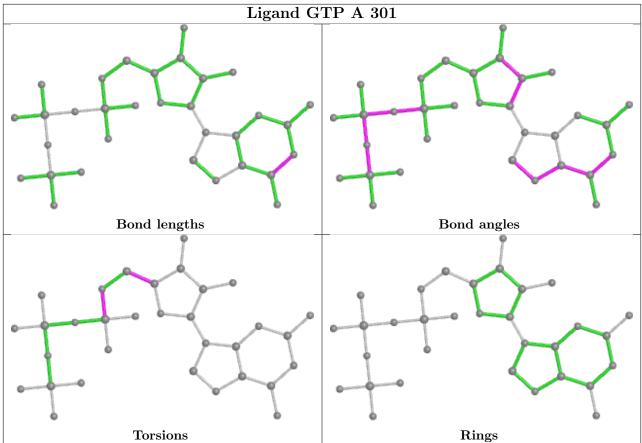
Mol	Chain	Res	Type	Atoms
5	А	301	GTP	C5'-O5'-PA-O1A
8	С	1101	GOL	O1-C1-C2-C3
5	А	301	GTP	O4'-C4'-C5'-O5'
5	А	301	GTP	C3'-C4'-C5'-O5'
8	С	1101	GOL	C1-C2-C3-O3
8	С	1101	GOL	O1-C1-C2-O2
8	С	1101	GOL	O2-C2-C3-O3
5	А	301	GTP	C5'-O5'-PA-O3A
5	А	301	GTP	C5'-O5'-PA-O2A

There are no ring outliers.

No monomer is involved in short contacts.

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.





Torsions

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, 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	$OWAB(Å^2)$	$\mathbf{Q}{<}0.9$
1	А	210/235~(89%)	-0.12	6 (2%) 51 52	54, 75, 131, 157	0
2	В	129/143~(90%)	-0.00	4 (3%) 49 49	71, 87, 125, 165	0
3	С	996/1003~(99%)	-0.10	21 (2%) 63 65	54, 78, 112, 144	0
4	D	17/20~(85%)	0.17	0 100 100	82, 95, 110, 121	0
All	All	1352/1401~(96%)	-0.09	31 (2%) 60 62	54, 79, 116, 165	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	101	LYS	4.2
3	С	-1	GLY	4.2
1	А	180	PRO	3.7
1	А	7	PRO	3.0
3	С	229	ILE	3.0
2	В	79	MET	2.9
2	В	65	PHE	2.8
3	С	978	GLU	2.7
3	С	0	SER	2.6
3	С	689	LEU	2.5
2	В	168	GLU	2.5
3	С	583	PHE	2.5
3	С	16	LEU	2.5
1	А	176	PHE	2.5
1	А	178	ALA	2.4
3	С	543	ARG	2.4
3	С	55	LEU	2.4
3	С	66	ILE	2.4
3	С	81	LEU	2.4
3	С	983	GLN	2.3
3	С	495	ILE	2.3



Mol	Chain	Res	Type	RSRZ	
3	С	572	PHE	2.2	
3	С	18	GLN	2.2	
1	А	187	VAL	2.1	
1	А	179	MET	2.1	
3	С	6	ASP	2.1	
3	С	1028	PHE	2.1	
3	С	690	LEU	2.0	
3	С	685	ALA	2.0	
3	С	7	PHE	2.0	
3	С	565	PHE	2.0	

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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.

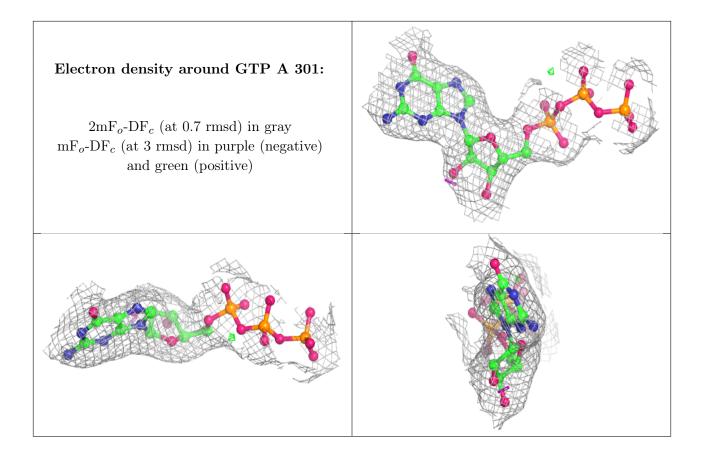
6.4 Ligands (i)

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
8	GOL	С	1102	6/6	0.74	0.33	108,109,109,110	0
8	GOL	С	1101	6/6	0.86	0.32	83,83,84,87	0
9	NA	С	1103	1/1	0.88	0.67	82,82,82,82	0
5	GTP	А	301	32/32	0.97	0.12	55,59,63,64	0
6	MG	А	302	1/1	0.97	0.14	75,75,75,75	0
7	EDO	A	303	4/4	0.97	0.23	77,77,80,80	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.

