



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 12:42 PM UTC

PDB ID : 2R7X / pdb_00002r7x
Title : Crystal Structure of Rotavirus SA11 VP1/RNA (UGUGACC)/GTP complex
Authors : Lu, X.; Harrison, S.C.; Tao, Y.J.; Patton, J.T.; Nibert, M.L.
Deposited on : 2007-09-10
Resolution : 2.80 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 ⓘ 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)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

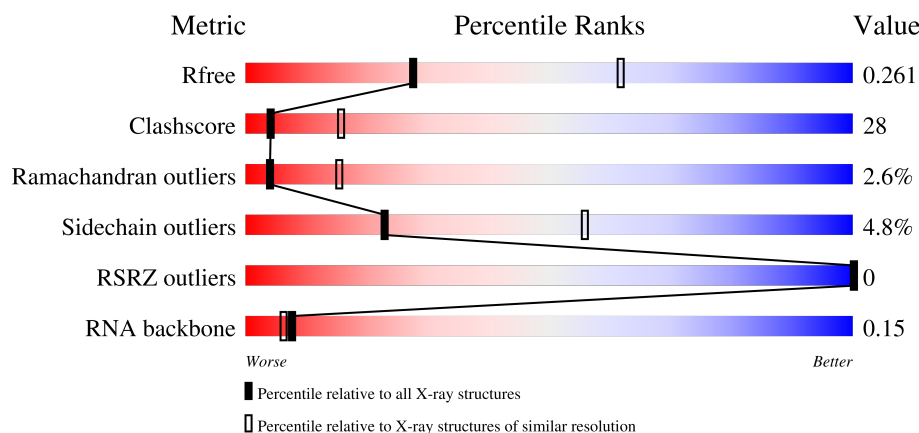
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)
RNA backbone	3983	1114 (3.00-2.60)

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	X	7	29% 29% 43%
1	Y	7	14% 43% 43%
2	A	1095	48% 43% 6% .
2	B	1095	49% 43% 6% ..

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 17744 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.

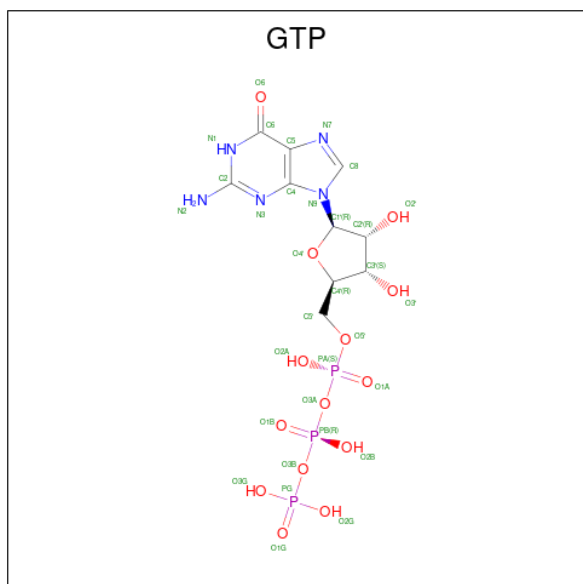
- Molecule 1 is a RNA chain called RNA (5'-R(*UP*GP*UP*GP*AP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	7	Total	C	N	O	P	0	0	0
			145	66	25	48	6			
1	Y	7	Total	C	N	O	P	0	0	0
			145	66	25	48	6			

- Molecule 2 is a protein called RNA-dependent RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	1073	Total	C	N	O	S	0	0	0
			8695	5576	1447	1634	38			
2	B	1073	Total	C	N	O	S	0	0	0
			8695	5576	1447	1634	38			

- Molecule 3 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
3	B	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

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: RNA (5'-R(*UP*GP*UP*GP*AP*CP*C)-3')

Chain X: 



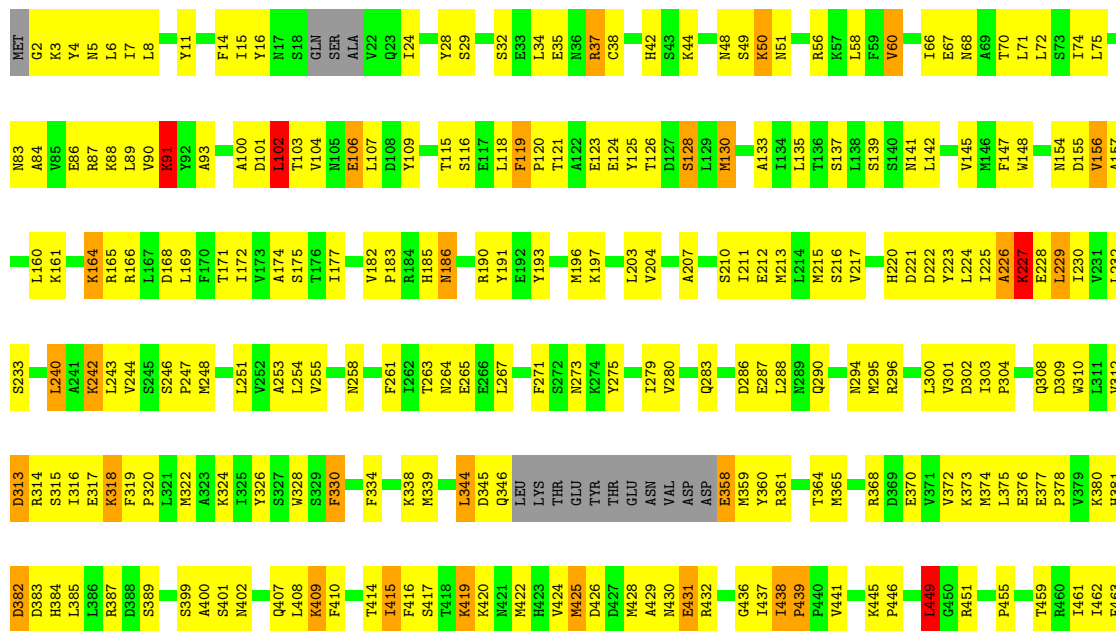
- Molecule 1: RNA (5'-R(*UP*GP*UP*GP*AP*CP*C)-3')

Chain Y: 



- Molecule 2: RNA-dependent RNA polymerase

Chain A: 





E376	W310	T230	A84	Met
E377	L311	V231	V85	G2
E378	V312	L232	E86	K3
V379	S233		R87	N4
	R314		K164	Y5
K380	S315	L240	R165	L6
H381	S316	A241	L166	I7
D382	L317	K242	L167	L8
D383	K318	L243	D168	
H384	K319	V244	L169	
L385	P320	S245	F170	Y11
L386	L321	S246	T171	
R387	M322	P247	I172	F14
D388	A323	M248	V173	I15
S389	K324		A174	Y16
	L325	L251	S175	M17
S399	K326	V252	T176	S18
A400	Y326	A253	I177	GLN
S401	S327	L254		SER
M402	K328	V255	V182	ALA
Q407	F330		P183	V22
L408		N258	R184	Q23
K409	F334		H185	I24
F410		F261	M186	
	K338	L262		Y28
L411	M339	T263	R190	S29
I415	L340	N264	L118	
F416		E265	V191	S32
S417	L344	F266	E192	E33
L418	Q345	L267	Y193	L34
K419	Q346			E35
K420	LEU	F271	M196	N36
M421	LVS	S272	K197	E124
M422	THR	N273	D198	R37
H423	GLU	K274	K199	C38
V424	TYR	Y275	L203	H42
	THR		V204	S43
M425	GLU	L279	L129	K44
D426	ASN	V280	M130	
D427	VAL		A207	N48
M428	ASP	Q283		S49
A429	ASP		S210	K50
M430			L135	N51
	E358	D286	T211	
R432	M359	E287	E212	R56
	V360	L288	M213	
G436	R361	N289	L214	K57
L437	F362	Q290	M215	L58
I438	V363		S216	F59
P439	L364	N294	V217	V60
V440	M365	P295	F218	
V441	L366	R296	S219	E67
	I367		H220	N68
K445	R368	L300	D221	A69
P446	D369	V301	D222	M146
	E370	S302	V223	T70
L449	V371	L303	L224	L71
G450	K372	P304	T225	
	F373		A226	S73
	M374	Q308	K227	I74
	L375	R309	E228	L75
			L156	
			A157	N52

S1061	L965	D880	T798	L722	D629	D551	T459
E1062	G966	I881	A799	R723	D632	A552	R460
M1063	I967	K882	D800	E726	E835	K553	I461
I1064	P968	E801	I802	T727	A835	V554	I462
K1065	K969	F884	E803	D728	F836	L555	P466
L1066	I970	F885	A803	R729	K637	Q556	Y467
W1067	A972	R887	A804	E730	Q638	T557	E468
K1068	D973	S888	K809	L733	F639	L558	E468
K1069	D974		N810	T734	F640	N559	E468
M1070	I975		Y811	T735	T641	L560	Y469
I1073	Y976	H891	L815	L736	E842	Y561	Q473
L1076	G977	L892	F874	Q737	V643	K562	H474
R1077	S978	I894	K823	M738	M647	Q563	A475
			N824	M739	I648	V573	V476
			F826	F739	Q649	Q574	V477
Y1080	K985	K896	I826	T744	D650	I575	K479
				T745			M480
A1083	T988	F899	R829	L748	D654	N579	K485
E1088	L989	P900	K901			I584	
PRO	Y992	T902	E835	F751	R661	Q585	A491
HIS	L996	L903	K836	F752	K665	Y586	
HIS	I997	P904	A837	S753	V666	S591	Y494
HIS	S998	Q908	K838	E754	K667	G592	S495
HIS	I999		Y842	R755		E508	R508
	N1000	Q912	A843	T758	S671	K594	F509
	Y1001		P844			Q595	
	L1002	R917	S846	T762	I675	T596	N512
	C1003	I918	C1003		E676	K597	N513
	Y1004	Y919	L847		I677	A598	T514
Q1005	Q1005	Q920	E248	F766	R680	A599	N515
L1006	L1006	I921	K849	D767		N600	V516
F1007	E922	R850	E248	S768		S601	L517
D1008	F008	D923	R851	E769	G684	I602	Y518
L1009	L1009	D924	A852	D770	I687	T519	D520
			Q853	F771		L605	V521
	K1016	S928	I954			A606	S522
L1017	L1017	R332	L857	T776	F689	L607	Q523
L1018	L1018		L858	T777	R690	I608	
R1019	L1020	S938	T859	T778	L695	K609	
I1020		V939	K860	V779	R696	T610	
			L861	D780	L696	V611	
I1026		I944	Q862	F782	R701	L612	
P1027		E945	K863	Y783	G702		
			P864	I784	Q703	I615	
L1035			R865	Q785			
Y1036		K949	T866	R786	Q706	K618	
A1037		V950	F867	A787	H619	F534	
		I951	F868	F788	D708	R535	
K1047		S952	S869	D789	Q709	F621	
		L953		M789		F621	
				S790		A822	
L1054			I872	L791		T623	
F1055		I958	T873	Q794		K624	
C1056		Q959	I874			I544	
N1057						I626	
Y1058		L962				R627	
P1059		I963	L878	S796		I626	
		S964	P870	T797		V629	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	76.00Å 143.77Å 112.83Å 90.00° 90.65° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80 30.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	83.1 (30.00-2.80) 80.8 (30.00-2.80)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.81Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.233 , 0.277 0.217 , 0.261	Depositor DCC
R_{free} test set	4650 reflections (8.06%)	wwPDB-VP
Wilson B-factor (Å ²)	55.4	Xtriage
Anisotropy	0.239	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 23.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.358 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	17744	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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: GTP

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	X	0.41	0/161	1.21	3/249 (1.2%)
1	Y	0.39	0/161	1.22	4/249 (1.6%)
2	A	0.49	0/8866	0.99	44/11985 (0.4%)
2	B	0.49	0/8866	0.99	45/11985 (0.4%)
All	All	0.49	0/18054	1.00	96/24468 (0.4%)

There are no bond length outliers.

The worst 5 of 96 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1026	ILE	CA-C-N	9.02	131.12	119.84
2	A	1026	ILE	C-N-CA	9.02	131.12	119.84
2	B	1026	ILE	CA-C-N	8.83	130.88	119.84
2	B	1026	ILE	C-N-CA	8.83	130.88	119.84
2	A	1020	ILE	N-CA-C	8.52	116.59	108.15

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	X	145	0	77	18	0
1	Y	145	0	77	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	8695	0	8782	481	0
2	B	8695	0	8782	479	0
3	A	32	0	12	2	0
3	B	32	0	12	2	0
All	All	17744	0	17742	977	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 28.

The worst 5 of 977 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)
2:A:865:VAL:HG13	2:A:866:THR:H	1.14	1.08
2:B:865:VAL:HG13	2:B:866:THR:H	1.14	1.08
2:B:734:THR:HA	2:B:737:MET:HE3	1.43	1.01
2:A:734:THR:HA	2:A:737:MET:HE3	1.44	1.00
2:B:520:ASP:HB3	2:B:667:LYS:HG2	1.45	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	
2	A	1067/1095 (97%)	915 (86%)	124 (12%)	28 (3%)	4	15
2	B	1067/1095 (97%)	919 (86%)	120 (11%)	28 (3%)	4	15
All	All	2134/2190 (97%)	1834 (86%)	244 (11%)	56 (3%)	4	15

5 of 56 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	866	THR
2	A	976	VAL
2	A	978	SER
2	B	866	THR
2	B	976	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	974/996 (98%)	928 (95%)	46 (5%)	23	57
2	B	974/996 (98%)	926 (95%)	48 (5%)	22	55
All	All	1948/1992 (98%)	1854 (95%)	94 (5%)	23	56

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	242	LYS
2	B	556	GLN
2	B	313	ASP
2	B	415	ILE
2	B	600	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	908	GLN
2	B	840	ASN
2	B	220	HIS
2	B	794	GLN
2	B	959	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	X	7/7 (100%)	4 (57%)	3 (42%)
1	Y	7/7 (100%)	4 (57%)	3 (42%)
All	All	14/14 (100%)	8 (57%)	6 (42%)

5 of 8 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	X	1102	G
1	X	1103	U
1	X	1104	G
1	X	1105	A
1	Y	1102	G

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	Y	1101	U
1	Y	1102	G
1	Y	1103	U
1	X	1102	G
1	X	1101	U

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](#)

2 ligands 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	GTP	B	1111	-	33,34,34	2.86	9 (27%)	50,54,54	3.28	18 (36%)
3	GTP	A	1111	-	33,34,34	2.67	8 (24%)	50,54,54	3.22	17 (34%)

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	GTP	B	1111	-	-	3/22/38/38	0/3/3/3
3	GTP	A	1111	-	-	2/22/38/38	0/3/3/3

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1111	GTP	PB-O3B	10.08	1.70	1.59
3	A	1111	GTP	PB-O3B	9.75	1.70	1.59
3	B	1111	GTP	PA-O3A	8.29	1.68	1.59
3	A	1111	GTP	PA-O3A	7.45	1.67	1.59
3	B	1111	GTP	PB-O3A	5.79	1.65	1.59

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1111	GTP	O3G-PG-O1G	-11.70	65.25	110.83
3	A	1111	GTP	O3G-PG-O1G	-11.67	65.36	110.83
3	A	1111	GTP	O2G-PG-O1G	-9.50	73.83	110.83
3	B	1111	GTP	O2G-PG-O1G	-9.14	75.20	110.83
3	B	1111	GTP	O4'-C4'-C5'	-9.11	80.14	109.33

There are no chirality outliers.

All (5) torsion outliers are listed below:

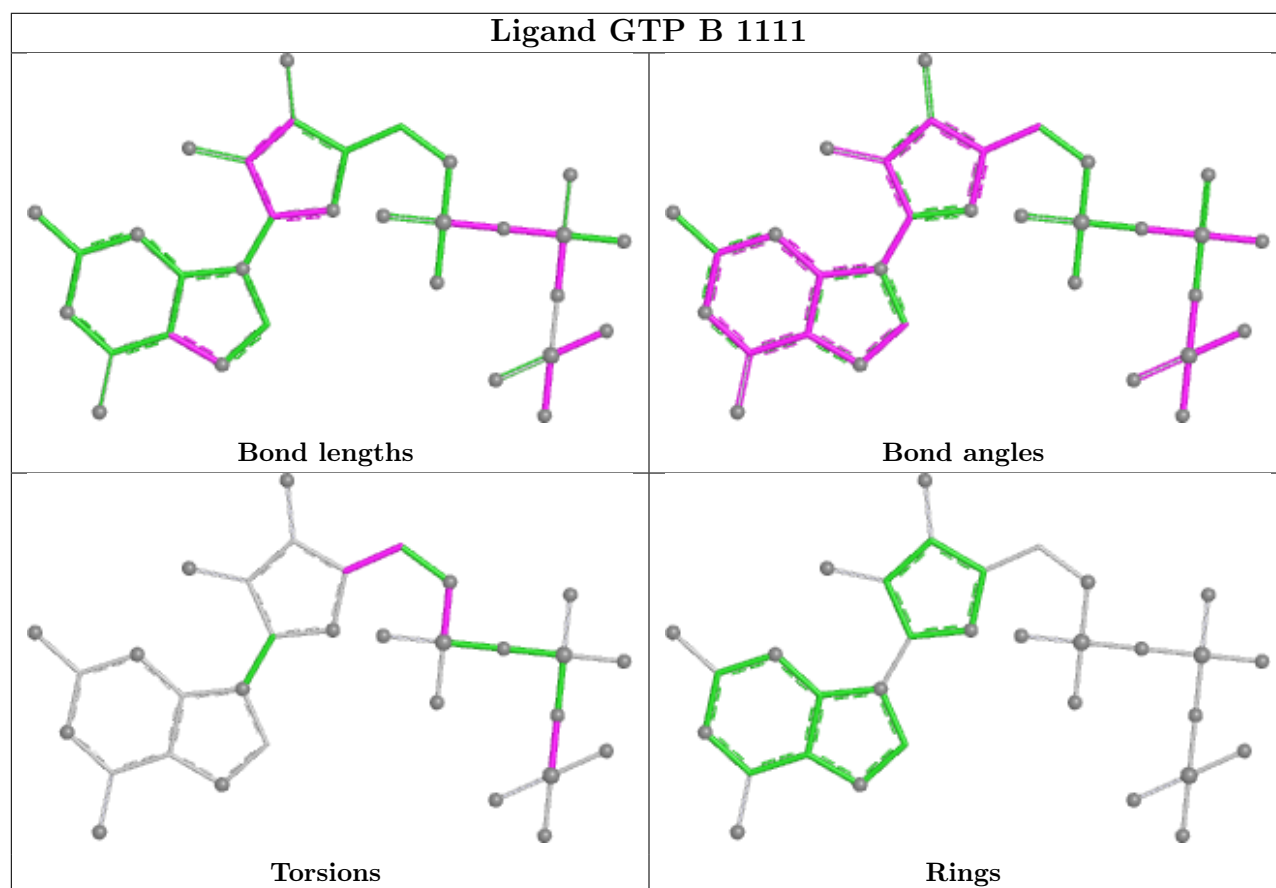
Mol	Chain	Res	Type	Atoms
3	B	1111	GTP	O4'-C4'-C5'-O5'
3	A	1111	GTP	O4'-C4'-C5'-O5'
3	B	1111	GTP	C5'-O5'-PA-O1A
3	A	1111	GTP	PB-O3B-PG-O1G
3	B	1111	GTP	PB-O3B-PG-O1G

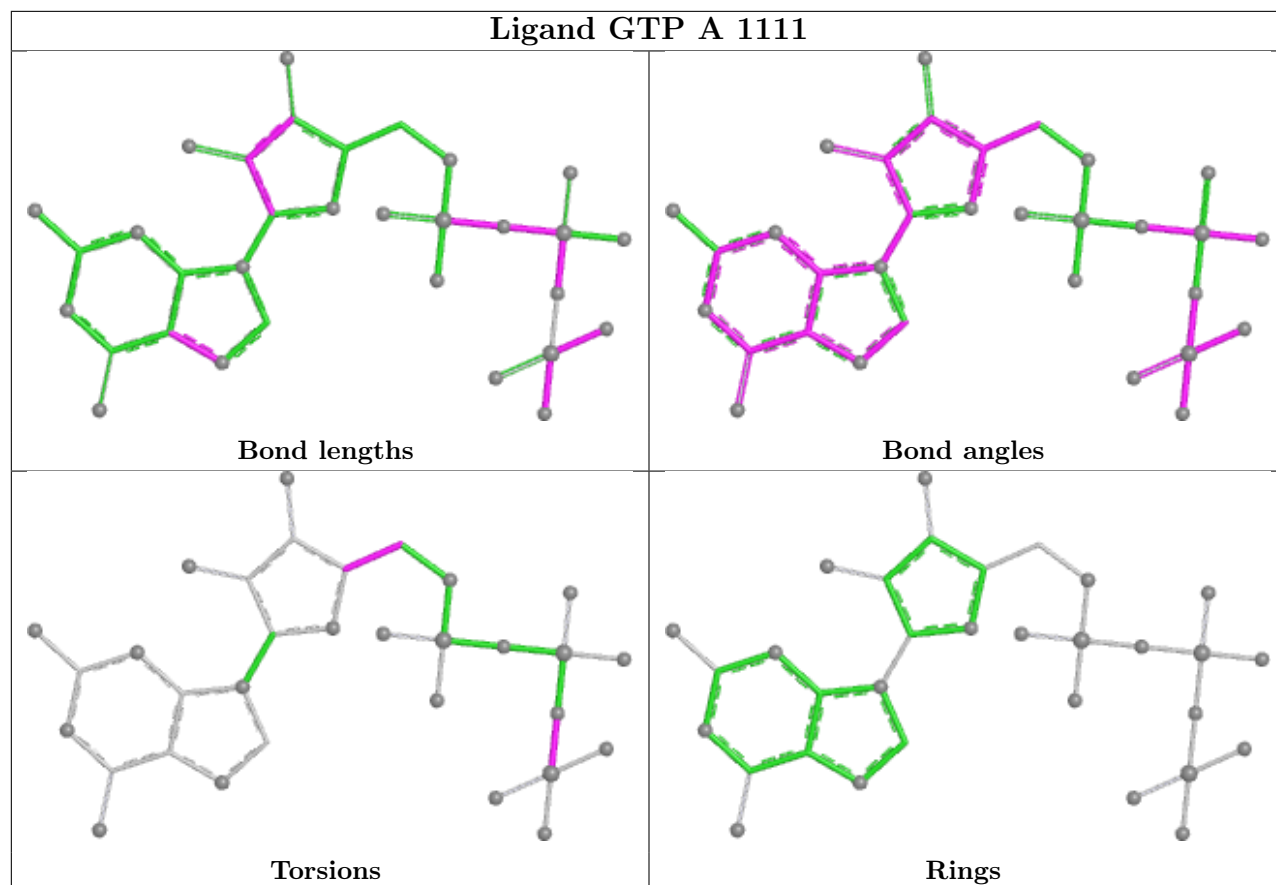
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1111	GTP	2	0
3	A	1111	GTP	2	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	X	7/7 (100%)	-1.77	0 100 100	47, 60, 73, 77	0
1	Y	7/7 (100%)	-1.69	0 100 100	47, 59, 72, 77	0
2	A	1073/1095 (97%)	-1.55	0 100 100	15, 49, 79, 120	0
2	B	1073/1095 (97%)	-1.54	0 100 100	17, 50, 80, 121	0
All	All	2160/2204 (98%)	-1.55	0 100 100	15, 50, 79, 121	0

There are no RSRZ outliers to report.

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.

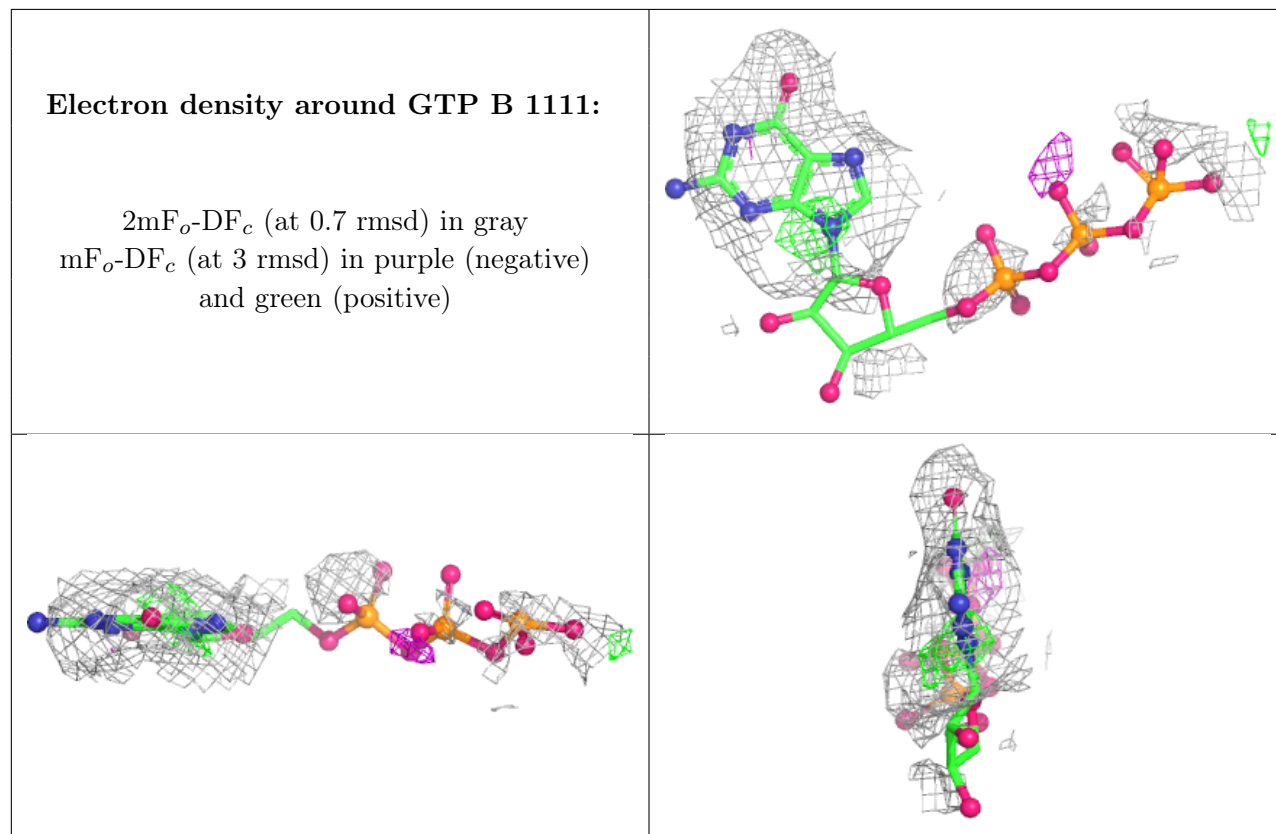
6.4 Ligands [i](#)

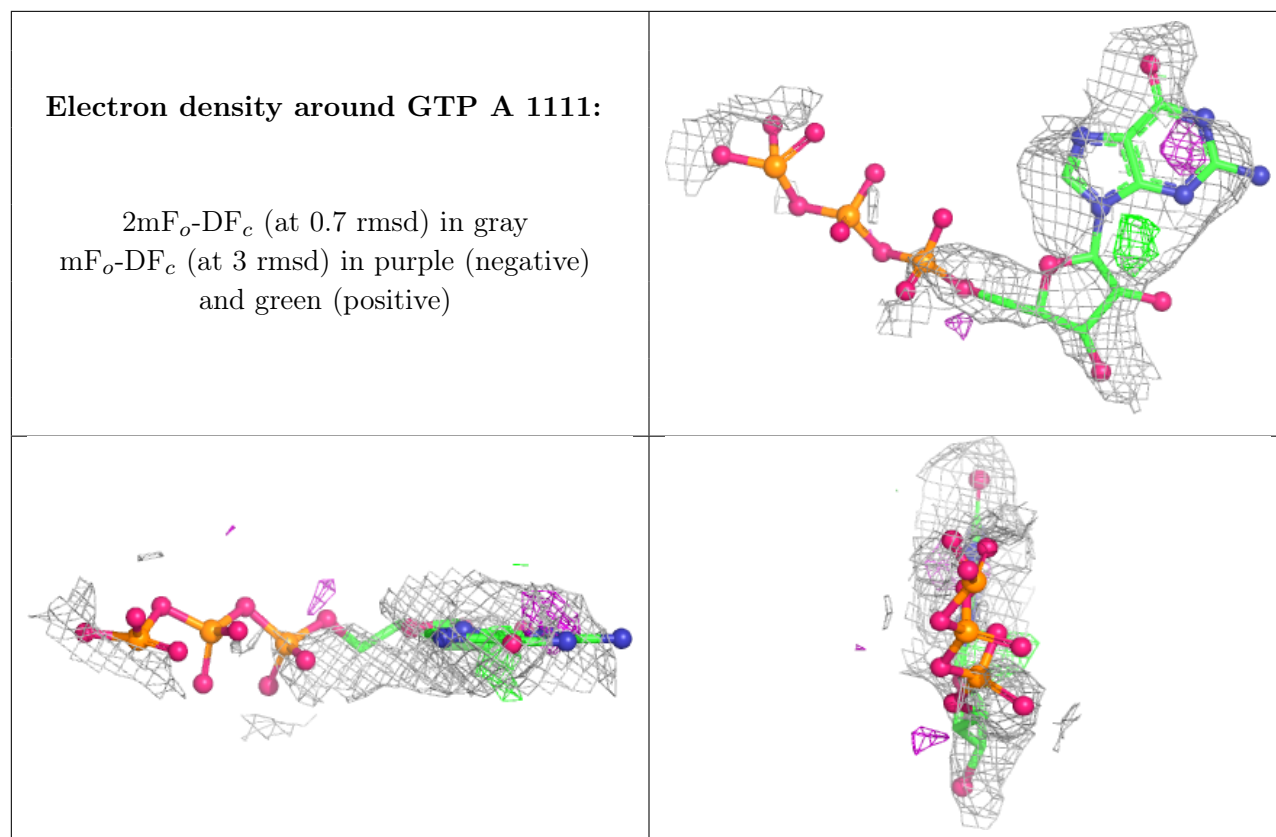
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GTP	B	1111	32/32	0.94	0.08	112,142,150,150	0
3	GTP	A	1111	32/32	0.95	0.09	107,137,145,145	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.